

# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 105281**

**TO: Vanessa L Ford**  
**Location: CM-1/8A16/8E12**  
**Art Unit: 1645**  
**Monday, October 06, 2003**

**Case Serial Number: 09/771382**

**From: David Schreiber**  
**Location: Biotech-Chem Library**  
**CM1-6A03**  
**Phone: 308-4292**

**david.schreiber@uspto.gov**

### **Search Notes**



## STIC-Biotech/ChemLib

105281

From: Pak, Michael  
Sent: Friday, October 03, 2003 10:39 AM  
T : STIC-Biotech/ChemLib  
Cc: Ford, Vanessa  
Subject: RE: IN Re: 09771382 Sequence search

Dear STIC,

Please search the multiple sequence search request set forth below. The search is necessary for the examination of the application.

thanks,

Mike Pak

-----Original Message-----

Fr m: Chan, Christina  
Sent: Friday, October 03, 2003 10:24 AM  
To: Ford, Vanessa; Pak, Michael; STIC-Biotech/ChemLib  
Subject: RE: IN Re: 09771382 Sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: Ford, Vanessa  
Sent: Thursday, October 02, 2003 6:46 PM  
To: Chan, Christina  
Subject: IN Re: 09771382 Sequence search

Please search SEQ ID NOs: 23-27 and 33-39. Please include interference searches. Please rush.

Vanessa L. Ford  
Biotechnology Patent Examiner  
Office: CM1 8A16  
Mailbox: CM1 8E12  
Phone: 703.308.4735  
Art Unit: 1645

Searcher: D. Schneider  
Phone: 308-427  
Location: CM1 6A03  
Date Picked Up: \_\_\_\_\_  
Date Completed: 10/6  
Searcher Prep/Review: 22  
Clerical: \_\_\_\_\_  
Online time: 8

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 12  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

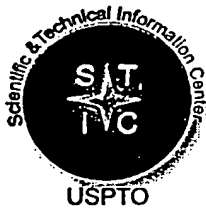
VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: Compugene  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

48 56

4 7

10 21





# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



091824206

09724512

09824588

10210296



PA (UYOU ) UNIV QUEENSLAND.  
XX  
XX PI Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
DR N-PSDB; AAS09172.  
XX  
XX New Nhba surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
XX  
PS Claim 12; Fig 5; 91pp: English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhba  
CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhba deletion mutant #1.  
XX  
SQ Sequence 512 AA:

Query Match

Best Local Similarity 100.0%; Score 2350; DB 22; Length 512;

Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNETDLTSVTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTL 60  
DB 52 NNETDLTSVTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTL 111  
QY 61 LMTGATTNTNDNVTDDEKKRAASVKDVNLNAGMNIKGVPPTTASDNDVFRTYDVEFL 120  
DB 112 LMTGATTNTNDNVTDDEKKRAASVKDVNLNAGMNIKGVPPTTASDNDVFRTYDVEFL 171  
QY 121 SADTKTTYNVESKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLVTA 180  
DB 172 SADTKTTYNVESKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLVTA 231  
QY 181 KEVIDAVNKGMRMKTITTTANGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTIV 240  
DB 232 KEVIDAVNKGMRMKTITTTANGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTIV 291  
QY 241 MTDVNVGDLNNOLONSGMNIDSKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 300  
DB 292 MTDVNVGDLNNOLONSGMNIDSKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 351  
QY 301 TTRNGKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVE 360  
DB 352 TTRNGKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVE 411  
QY 361 GDTVNVAOQLKGYAQNLLNNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG 420  
DB 412 GDTVNVAOQLKGYAQNLLNNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG 471  
QY 421 EAGYAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461  
DB 472 EAGYAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 512

RESULT 2

ID AAY27202 standard; Protein, 591 AA.

XX AAY27202;

XX 24-SEP-1999 (first entry)

XX

DE Amino acid sequence of N. meningitidis protein ORF40-1.

XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.

XX Neisseria meningitidis.

PN WO9336544-A2.

PD 22-JUL-1999.

PF 14-JAN-1999; 99WO-1B00103.

PR 09-OCT-1998; 98GB-0022143.

PR 14-JAN-1998; 98GB-0000760.

PR 01-SEP-1998; 98GB-0019015.

PA (CHTR-) CHIRON SPA.

PI Grandi G, Massignani V, Piazza M, Rappuoli R, Scarlato V;

DR WPI: 1999-444400/37.

XX N-PSDB; AAX99124.

PS Claim 1; Page 62; 123pp: English.

CC The invention provides proteins (AAY27201-245) from Neisseria

CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)

CC encoding the proteins. Compositions comprising the protein, nucleic acid

CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a

CC vaccine composition or a diagnostic composition. The composition is also

CC useful for treating or preventing an infection due to Neisseria

CC bacteria, especially Neisseria meningitidis.

SQ Sequence 591 AA:

Query Match

Best Local Similarity 100.0%; Score 2333; DB 20; Length 591;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTLMT 63  
DB 134 TDLTSVTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTLMT 193  
QY 64 GATTNVTNDNVTDDEKKRAASVKDVNLNAGMNIKGVPPTTASDNDVFRTYDVEFLSD 123  
DB 194 GATTNVTNDNVTDDEKKRAASVKDVNLNAGMNIKGVPPTTASDNDVFRTYDVEFLSD 253  
QY 124 TTTTYPNVVSKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLYAKEV 183  
DB 254 TTTTYPNVVSKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLYAKEV 313  
QY 184 IDAVNKGMRMKTITTTANGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTIVMD 243  
DB 314 IDAVNKGMRMKTITTTANGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTIVMD 373  
QY 244 VNVGDLNNOLONSGMNIDSKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEITRN 303  
DB 374 VNVGDLNNOLONSGMNIDSKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEITRN 433  
QY 304 GKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVEGDP 363  
DB 434 GKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVEGDP 493  
QY 364 TTVNVAQLKGYAQNLLNNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG 423  
DB 494 TTVNVAQLKGYAQNLLNNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG 553  
QY 424 VAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461

Db 554 YAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 591

## RESULT 3

AAV23741  
ID AAV23741 standard; Protein: 591 AA.

AC AAV23741;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KM Surface protein; surface glycoprotein; infection; vaccine;

KM Immunoreactive peptide.

OS Neisseria meningitidis.

PN WO931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU ) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI: 1999-418754/35.

DR N-PSDB; AAX85793.

PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 104-106; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 99.3%; Score 2333; DB 20; Length 591;

Best Local Similarity 100.0%; Pred. No. 1.1e-140;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISSTLTDTLLNT 63

Db 134 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISSTLTDTLLNT 193

QY 64 GATTNVNDVNTDDEKKRAASVVRKDVNLNAGNINIKGVKPGTTPASDNDVFRTYDVEFLSAD 123

Db 194 GATTNVNDVNTDDEKKRAASVVRKDVNLNAGNINIKGVKPGTTPASDNDVFRTYDVEFLSAD 253

QY 124 TKTTTVNVESEKDKGKTEVKIKGATSVIKERDKLVTGKDKGEGSSTDEGELVTAKEV 183

Db 254 TKTTTVNVESEKDKGKTEVKIKGATSVIKERDKLVTGKDKGEGSSTDEGELVTAKEV 313

QY 184 IDAVNRKGMKMTTANGOTGOADKPEVTSGTVFASGKGTATATSKDOGNTIYMD 243

Db 314 IDAVNRKGMKMTTANGOTGOADKPEVTSGTVFASGKGTATATSKDOGNTIYMD 373

QY 244 VNVGDALNVNQLNSGWNILDSKAVAGSSGKRVISGNSPSKGMDETIVNAGNNEITRN 303

Db 374 VNVGDALNVNQLNSGWNILDSKAVAGSSGKRVISGNSPSKGMDETIVNAGNNEITRN 433

QY 304 GKNDITATSMTPOFSSVSLGADAPTLISVDGALANGSKDKNPVITTVAPGVKGDV 363

Db 434 GKNDITATSMTPOFSSVSLGADAPTLISVDGALANGSKDKNPVITTVAPGVKGDV 493

QY 364 TNVAQLKGVANONLNRIIDVNDGNARAGIAQIATAGLVQAYLPKSSMAIIGCGTYRGEAG 423

Db 494 TNVAQLKGVANONLNRIIDVNDGNARAGIAQIATAGLVQAYLPKSSMAIIGCGTYRGEAG 553

QY 424 YAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 461

Db 554 YAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 591

## RESULT 4

AAV23746  
ID AAV23746 standard; Protein: 591 AA.

AC AAV23746;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KM Surface protein; surface glycoprotein; infection; vaccine;

KM Immunoreactive peptide.

OS Neisseria meningitidis.

PN WO931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU ) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI: 1999-418754/35.

DR N-PSDB; AAX85798.

PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 127-128; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 99.3%; Score 2333; DB 20; Length 591;

Best Local Similarity 100.0%; Pred. No. 1.1e-140;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISSTLTDTLLNT 63

Db 134 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISSTLTDTLLNT 193

QY 64 GATTNVNDVNTDDEKKRAASVVRKDVNLNAGNINIKGVKPGTTPASDNDVFRTYDVEFLSAD 123

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Db      194 GATTIVNTDNDVTDEKKRAASVKVDLNMGMNKGKPGTTASDNDVFRTYDTVEFLSAD 253
QY      124 TKTITVNVESKDNKGKTEYKIGAKTSVYKEKDGKLVYTGKDKGENSSSTDEGGLVYAKEV 183
Db      254 TKTITVNVESKDNKGKTEYKIGAKTSVYKEKDGKLVYTGKDKGENSSSTDEGGLVYAKEV 313
QY      184 IDAVNKAGWRMKTITTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVYMD 243
Db      314 IDAVNKAGWRMKTITTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVYMD 373
QY      244 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINMAGNNIEITRN 303
Db      374 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINMAGNNIEITRN 433
QY      304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVSGSKDNKPVRITTNVAPGVEGDV 363
Db      434 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVSGSKDNKPVRITTNVAPGVEGDV 493
QY      364 TNVAOLKGVAAQMLNRRIDNVDSGNARAGIAQAIAATAGLVQAVYLPKGSMAIIGGTYRGEG 423
Db      494 TNVAOLKGVAAQMLNRRIDNVDSGNARAGIAQAIAATAGLVQAVYLPKGSMAIIGGTYRGEG 553
QY      424 VAIGYSSISDGGNMIIKGTASGNSRGRHGSASVGYQW 461
Db      554 VAIGYSSISDGGNMIIKGTASGNSRGRHGSASVGYQW 591

RESULT 5
AAU06171
ID      AAU06171 standard. Protein: 591 AA.
XX      AAU06171;
XX      24-OCT-2001 (first entry)
DE      N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX      Surface antigen Nhha: meningococcal disease; meningitis vaccine.
XX      Neisseria meningitidis strain PMC21.
XX      Location/Qualifiers
FH      1..51
FT      Peptide
FT      /label= Signal_peptide
FT      1..50
FT      /label= C1
FT      /note= "Conserved region 1"
FT      51..108
FT      /label= V1
FT      /note= "Variable region 1"
FT      52..591
FT      /label= Mature_Nhha
FT      /note= "Predicted mature protein, specifically
FT      claimed in claim 12"
FT      109..120
FT      /label= C2
FT      /note= "Conserved region 2"
FT      121..124
FT      /label= V2
FT      /note= "Variable region 2"
FT      125..188
FT      /label= C3
FT      /note= "Conserved region 3"
FT      189..210
FT      /label= V3
FT      /note= "Variable region 3"
FT      211..229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
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FT      Region      237..591
FT      /label= C5
FT      /note= "Conserved region 5"
XX      WO20015182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX      (UYOU ) UNIV QUEENSLAND.
XX      Peak IRA, Jennings MP;
XX      WPI: 2001-488774/53.
XX      N-PSDB; AAS09161.
XX      New Nhha surface antigen polypeptides and polynucleotides from
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      preventing broad spectrum of Neisseria meningitidis -
XX      Claim 9; Fig 1; 91pp; English.
XX      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Nhha
XX      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX      characterised by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      CC medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC immunise against a broader spectrum of N. meningitidis strains than
XX      CC would be expected from a corresponding wild-type surface antigen.
XX      The present sequence representing the wild type surface antigen Nhha
XX      from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
SQ      Sequence      591 AA:
Query Match      99.3%; Score 2333; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.le-140;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 TDLTSVGTREKLSFSANGKVNITSDTKGINFKEKTAGNGDTVHLNGIGSTLPTLNT 63
Db      134 TDLTSVGTREKLSFSANGKVNITSDTKGINFKEKTAGNGDTVHLNGIGSTLPTLNT 193
QY      64 GATTIVNTDNDVTDEKKRAASVKVDLNMGMNKGKPGTTASDNDVFRTYDTVEFLSAD 123
Db      194 GATTIVNTDNDVTDEKKRAASVKVDLNMGMNKGKPGTTASDNDVFRTYDTVEFLSAD 253
QY      124 TKTITVNVESKDNKGKTEYKIGAKTSVYKEKDGKLVYTGKDKGENSSSTDEGGLVYAKEV 183
Db      254 TKTITVNVESKDNKGKTEYKIGAKTSVYKEKDGKLVYTGKDKGENSSSTDEGGLVYAKEV 313
QY      184 IDAVNKAGWRMKTITTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVYMD 243
Db      314 IDAVNKAGWRMKTITTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVYMD 373
QY      244 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINMAGNNIEITRN 303
Db      374 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINMAGNNIEITRN 433
QY      304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVSGSKDNKPVRITTNVAPGVEGDV 363
Db      434 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVSGSKDNKPVRITTNVAPGVEGDV 493
QY      364 TNVAOLKGVAAQMLNRRIDNVDSGNARAGIAQAIAATAGLVQAVYLPKGSMAIIGGTYRGEG 423
Db      494 TNVAOLKGVAAQMLNRRIDNVDSGNARAGIAQAIAATAGLVQAVYLPKGSMAIIGGTYRGEG 553
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QY 424 YAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 461  
|||||  
Db 554 YAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 591

RESULT 6  
AAU06175  
ID AAU06175 standard; Protein: 591 AA.  
XX  
AC AAU06175;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis EG329 surface antigen Noha polypeptide sequence.  
XX  
KW Surface antigen Noha; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain EG329.  
XX  
FH Key  
FT 1..50  
FT location/Qualifiers  
FT /label=C1  
FT /note="Conserved region 1"  
FT 51..108  
FT /label=V1  
FT /note="Variable region 1"  
FT 109..120  
FT /label=C2  
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FT 230..236  
FT /label=V4  
FT /note="Variable region 4"  
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FT /label=C5  
FT /note="Conserved region 5"  
XX  
PN W020015182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001MO-AU00069.  
XX  
PR 25-JAN-2000; 2000OUS-0177917.  
XX  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI: 2001-48874/53.  
XX  
DR N-PSDB: AAS09165.  
XX  
PT New Noha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 91pp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Noha  
CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Noha  
CC from N. meningitidis strain EG329 is 1 of 10 Noha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 591 AA;  
XX  
Query Match 99.3%; Score 2333; DB 22; Length 591;  
Best Local Similarity 100.0%; Pred. NO.1.1e-140;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TDLTSGTEKLSFSGANGKRVNITSDTKGLNFAKETAGTNGDPTVHLNGISGTLDTLNT 63  
Db 134 TDLTSGTEKLSFSGANGKRVNITSDTKGLNFAKETAGTNGDPTVHLNGISGTLDTLNT 193  
QY 64 GATTNVTNDVNTDDEKRAASVVDYLNAGWNKGVKPGTTASDNDVDFVRYDYVEFLSAD 123  
Db 194 GATTNVTNDVNTDDEKRAASVVDYLNAGWNKGVKPGTTASDNDVDFVRYDYVEFLSAD 253  
QY 124 TKTTTAVESKDNCKTEVKIGAKTSYKEKDGKLVYKXKMGESSTDEEGVLTAKEV 183  
Db 254 TKTTTAVESKDNCKTEVKIGAKTSYKEKDGKLVYKXKMGESSTDEEGVLTAKEV 313  
QY 184 IDAVNKAQWRKKTATTANGOTGOADKFEVTSCTVWFASGKGTATYSKDOGNITWYD 243  
Db 314 IDAVNKAQWRKKTATTANGOTGOADKFEVTSCTVWFASGKGTATYSKDOGNITWYD 373  
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGNSVPSKMDQETVNNAGNIEITRN 303  
Db 374 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGNSVPSKMDQETVNNAGNIEITRN 433  
QY 304 GKNIDIAQSMTPQSSVSLGAGADAPLTSVGDALNVGSKKDNKPVRTTNVAPGVKGDV 363  
Db 434 GKNIDIAQSMTPQSSVSLGAGADAPLTSVGDALNVGSKKDNKPVRTTNVAPGVKGDV 493  
QY 364 TTNVQLKGVAQNLNRRIDNDVGNARAGIAQIATAGLVAQAYLPKSMMAIGGTYRGEAG 423  
Db 494 TTNVQLKGVAQNLNRRIDNDVGNARAGIAQIATAGLVAQAYLPKSMMAIGGTYRGEAG 553  
QY 424 YAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 461  
Db 554 YAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 591

RESULT 7  
AA57045  
ID AA57045 standard; Protein: 591 AA.  
XX  
AC AA57045;  
XX  
DT 21-FEB-2000 (first entry)  
XX  
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
XX  
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
OS  
XX  
FH Key  
FT MISC-difference 90 location/Qualifiers  
FT MISC-difference 92 /note="Encoded by AAT"  
FT MISC-difference 92 /note="Encoded by GAT"  
FT MISC-difference 98 /note="Encoded by AAC"

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FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
FT /note= "Encoded by CGT"
XX WO9958683-A2.
XX 18-NOV-1999.
XX 07-MAY-1999; 99WO-EP03255.
XX 13-MAY-1998; 98GB-0010276.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA
XX PI Ruelle J;
XX WPI: 2000-053103/04.
XX DR N-PSDB; AAX39865.
XX PT New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal
XX PS Claim 4; Fig 2; 74pp; English.
XX
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fliDrl (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAX39864-239865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 591 AA:
Query Match 99.1%; Score 2330; DB 21; Length 591;
Best Local Similarity 99.8%; Pred. No. 1.7e-140;
Matches 457; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 63
DB 134 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 193
QY 64 GATTNVTNDNVTDDKKRAASVKDYLNAGWNKIKGVKPGTTASDNVDVFTYDTVEFLSAD 123
DB 194 GATTNVTNDNVTDDKKRAASVKDYLNAGWNKIKGVKPGTTASDNVDVFTYDTVEFLSAD 253
QY 124 TTTTNNVESKNGKRTVEKIGAKTSVIEKDKGLVTGDKGKNGSSSTEGEGLYTAKEV 183
DB 254 TTTTNNVESKNGKRTVEKIGAKTSVIEKDKGLVTGDKGKNGSSSTEGEGLYTAKEV 313
QY 184 IDAVNKAQKRMKTTTANGQTGADRFETVTSCTNVTFAAGKGTATVSKDDOGNTTVMYD 243
DB 314 IDAVNKAQKRMKTTTANGQTGADRFETVTSCTNVTFAAGKGTATVSKDDOGNTTVMYD 373
QY 244 VAVGALNNVOLONGSGWNLDSKAIVAGSSGKVIISGNVSPKGMDEFTVNIAGNNIEITRN 303
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DB 374 VAVGALNNVOLONGSGWNLDSKAIVAGSSGKVIISGNVSPKGMDEFTVNIAGNNIEITRN 433
QY 304 GKNIDIASTMTPOFSSVSLGAGADAPTLSDDDALNVGSKKNKPVRITNNVPGVKEGCV 363
DB 434 GKNIDIASTMTPOFSSVSLGAGADAPTLSDDDALNVGSKKNKPVRITNNVPGVKEGCV 493
QY 364 TNVAOLKGYAQNLLNNRIDNVGNARAGIAQAIAITAGLYOAYLPGKSMMAIGGTYRGAG 423
DB 494 TNVAOLKGYAQNLLNNRIDNVGNARAGIAQAIAITAGLYOAYLPGKSMMAIGGTYRGAG 553
QY 424 VAIGYSSTSDGGMWIKGTASGNSRGHRCASASVGTOW 461
DB 554 VAIGYSSTSDGGMWIKGTASGNSRGHRCASASVGTOW 591
RESULT 8
AAY23737
ID AAY23737 standard; Protein: 592 AA.
XX
AC AAY23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX (UYGU ) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI: 1999-418754/35.
XX DR N-PSDB; AAX85788.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 86-87; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA:
Query Match 99.1%; Score 2329; DB 20; Length 592;
Best Local Similarity 99.8%; Pred. No. 2e-140;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 63
DB 133 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 194
QY 64 GATTNVTNDNVTDDKKRAASVKDYLNAGWNKIKGVKPGTTASDNVDVFTYDTVEFLSAD 123
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|||||
Db 195 GATTNTNDVTDDEKRRASVYKDVYLNAGNNIKGVKPGTTASDNVDFVRTYDVEFLSAD 254
QY 124 TKTTTVEESKDKNGKTEVIGAKTSYIKERKDKLVYGRKNGEGSSTDGEGLYTAKEV 183
Db 255 TKTTTVEESKDKNGKTEVIGAKTSYIKERKDKLVYGRKNGEGSSTDGEGLYTAKEV 314
QY 184 IDAVNRKAGWRMKTTTANGOTGOADKFETVTSCTNVTVPASGKGTATVSKDOGNITVYMD 243
Db 315 IDAVNRKAGWRMKTTTANGOTGOADKFETVTSCTNVTVPASGKGTATVSKDOGNITVYMD 374
QY 244 VNVGDALNVNQLONGSNGLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIEITRN 303
Db 375 VNVGDALNVNQLONGSNGLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIEITRN 434
QY 304 GKNDIATSMTPQSSSVSLGAGADAPPLSYDGDALNVGSKDKNKPVRITNVAPGVKEGDV 363
Db 435 GKNDIATSMTPQSSSVSLGAGADAPPLSYDGDALNVGSKDKNKPVRITNVAPGVKEGDV 494
QY 364 TTNVAOLKGYAQNLNRRIDNVGNAIRAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAG 423
Db 495 TTNVAOLKGYAQNLNRRIDNVGNAIRAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAG 554
QY 424 YAIQYSSISDGGWMIITKGTASGNSRGHFGASASVGYQW 461
Db 555 YAIQYSSISDGGWMIITKGTASGNSRGHFGASASVGYQW 592

RESULT 9
AAI23740
ID AAI23740 standard; Protein: 594 AA.
XX
XX AAI23740;
AC
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
KM immunoreactive peptide.
XX
XX Neisseria meningitidis.
OS
XX
XX WO9931132-A1.
PN
XX
XX 24-JUN-1999.
PD
XX
XX 14-DEC-1998; 98WO-AU01031.
PF
XX
XX 12-DEC-1997; 97GB-0026398.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU ) UNIV QUEBENS LAND.
XX
XX
XX Jennings MP, Moxon ER, Peak IRA;
PI
XX
XX WPI; 1999-418754/35.
DR
XX
XX N-PSDB; AAX85792.
PT
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX
XX Claim 1; Page 100-101; 132pp; English.
XX
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
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XX
SQ Sequence 594 AA;
Query Match 96.28; Score 2260.5; DB 20; Length 594;
Best Local Similarity 97.48; Pred. No. 4.6e-136;
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSGANKNKNITSDPTGLNPAKFTAGTNDPTVHLNGISSTLDTLLNT 63
Db 136 TDLTSVTEKLSFSGANKNKNITSDPTGLNPAKFTAGTNDPTVHLNGISSTLDTLLNT 195
QY 64 GATTNTNDVTDDEKRRASVYKDVYLNAGNNIKGVKPGTTASDNVDFVRTYDVEFLSAD 123
Db 196 GATTNTNDVTDDEKRRASVYKDVYLNAGNNIKGVKPGTTASDNVDFVRTYDVEFLSAD 255
QY 124 TKTTTVEESKDKNGKTEVIGAKTSYIKERKDKLVYGRKNGEGSSTDGEGLYTAKEV 183
Db 256 TKTTTVEESKDKNGKTEVIGAKTSYIKERKDKLVYGRKNGEGSSTDGEGLYTAKEV 315
QY 184 IDAVNRKAGWRMKTTTANGOTGOADKFETVTSCTNVTVPASGKGTATVSKDOGNITVYMD 243
Db 316 IDAVNRKAGWRMKTTTANGOTGOADKFETVTSCTNVTVPASGKGTATVSKDOGNITVYMD 375
QY 364 TTNVAOLKGYAQNLNRRIDNVGNAIRAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAG 423
Db 496 TTNVAOLKGYAQNLNRRIDNVGNAIRAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAG 555
QY 423 GYAIGYSSISDGGWMIITKGTASGNSRGHFGASASVGYQW 461
Db 556 GYAIGYSSISDGGWMIITKGTASGNSRGHFGASASVGYQW 594

RESULT 10
AAI57044
ID AAI57044 standard; Protein: 594 AA.
XX
XX AAI57044;
AC
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
XX
XX BASB029; Neisseria meningitidis; surface fibrin protein; HSF; diagnosis;
KM infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
OS
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 104 /note="Encoded by AATC"
FT
XX
XX WO958683-A2.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-EP03255.
PF
XX
XX 13-MAY-1998; 98GB-0010276.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Ruelle J;
PI
XX
XX WPI; 2000-053103/04.
DR
XX
XX N-PSDB; AAZ39864.
```

XX New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal  
XX  
XX Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AA339864-239865) and  
CC polypeptide sequences (AA57044-57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with *Neisseria*  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
XX Sequence 594 AA;  
SQ

Query Match 96.2%; Score 2260.5; DB 21; Length 594;  
Best Local Similarity 97.4%; Pred. No. 4.6e-136;  
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSSANGKNGKNTSDTKGLNFAKETAGTGDITVHLNGISTLTDLTLMNT 63  
DB 136 TDLTSGTEKLSFSSANGKNGKNTSDTKGLNFAKETAGTGDITVHLNGISTLTDLTLMNT 195  
QY 64 GATTVNTDNTVTDDEKRRASVVDVNLNAGMNIKGVPPTTASDNDVETRYDTVEFLSAD 123  
DB 196 GATTVNTDNTVTDDEKRRASVVDVNLNAGMNIKGVPPTTASDNDVETRYDTVEFLSAD 255  
QY 124 TKTETVNVESKNGKRTVEKIGAKTSVYKEKDGKLVGTGDKENGSSDTBEGGLVYAKEV 183  
DB 256 TKTETVNVESKNGKRTVEKIGAKTSVYKEKDGKLVGTGDKENGSSDTBEGGLVYAKEV 315  
QY 184 IDAVKAGWRMKTITTAANGQTQADKFEYVTSCTNTVFASGKTATVSKDDGNTTAMD 243  
DB 316 IDAVKAGWRMKTITTAANGQTQADKFEYVTSCTNTVFASGKTATVSKDDGNTTAMD 375  
QY 244 VAVGDALNVNOLQNSGWNLDKRAVAGSSGKVIISGVNPSKGMDETVINAGNNIETRN 303  
DB 376 VAVGDALNVNOLQNSGWNLDKRAVAGSSGKVIISGVNPSKGMDETVINAGNNIETRN 435  
QY 304 GNIDILATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDKNRPVRTTNAAPGVKEGD 362  
DB 436 GNIDILATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDKNRPVRTTNAAPGVKEGD 495  
QY 363 VTNVAQLKGVNOLNLRIDNVGNARAGIATAGLQVAILPGKSMVIGGGYRGRA 422  
DB 496 VTNVAQLKGVNOLNLRIDNVGNARAGIATAGLQVAILPGKSMVIGGGYRGRA 555  
QY 423 GYAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461  
DB 556 GYAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594

XX N. meningitidis EG327 surface antigen Noha polypeptide sequence.  
DE Surface antigen Noha; meningococcal disease; meningitis vaccine.  
XX  
XX *Neisseria meningitidis* strain EG327.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1..50  
FT Region /label= C1  
FT /note= "Conserved region 1"  
FT 51..104  
FT Region /label= V1  
FT /note= "Variable region 1"  
FT 105..116  
FT Region /label= C2  
FT /note= "Conserved region 2"  
FT 117..126  
FT Region /label= V2  
FT /note= "Variable region 2"  
FT 127..190  
FT Region /label= C3  
FT /note= "Conserved region 3"  
FT 191..212  
FT Region /label= V3  
FT /note= "Variable region 3"  
FT 213..231  
FT Region /label= C4  
FT /note= "Conserved region 4"  
FT 232..238  
FT Region /label= V4  
FT /note= "Variable region 4"  
FT 239..594  
FT Region /label= C5  
FT /note= "Conserved region 5"  
XX  
XX WO20015182-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX  
XX (UYOU ) UNITV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
XX  
XX N-PSDB; AAS09164.  
XX  
XX New Noha surface antigen polypeptides and polynucleotides from  
PT *Neisseria meningitidis*, useful in producing vaccines for treating or  
PT preventing broad spectrum of *Neisseria meningitidis* -  
PS  
XX Claim 9; Fig 1; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel *Neisseria*  
XX meningitidis mutant polypeptides of the surface antigen Noha  
XX (AAU06182-AAU06186). The modified or mutant Noha polypeptides are  
XX characterised by deletions of non-conserved amino acids, particularly  
XX the deletion of variable regions. The deletion mutants are useful in  
XX diagnostics, therapeutic and prophylactic vaccines against a broader  
XX spectrum of *N. meningitidis*, and in designing and/or screening of  
XX medicaments. The mutant proteins when used as a vaccine can effectively  
XX immunise against a broader spectrum of *N. meningitidis* strains than  
XX would be expected from a corresponding wild-type surface antigen.  
XX The present sequence representing the wild type surface antigen Noha  
XX from *N. meningitidis* strain EG327 is 1 of 10 Noha polypeptide sequences  
XX (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
XX the present invention.  
XX  
XX Sequence 594 AA;  
SQ

Query Match 96.2%; Score 2260.5; DB 22; Length 594;  
Best Local Similarity 97.4%; Pred. No. 4.6e-136;  
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

```
QY 4 TDLTSTVTEKLSFGANGKRVNITSDFKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 63
DB 136 TDLTSTVTEKLSFGANGKRVNITSDFKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 135
QY 64 GATTNTVNDVNTDDEKRRASVYKDVNLNAGNINIGVYKPGTTASDNVDFVHTYDVEFLSAD 123
DB 196 GATTNTVNDVNTDDEKRRASVYKDVNLNAGNINIGVYKPGTTASDNVDFVHTYDVEFLSAD 255
QY 124 TKTITVNESKDKNGKTEVEIKGKTSYIKERDKLVYKDKGNGSSTDEGEGLVTAKEV 183
DB 256 TKTITVNESKDKNGKTEVEIKGKTSYIKERDKLVYKDKGNGSSTDEGEGLVTAKEV 315
QY 184 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMD 243
DB 316 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMD 375
QY 244 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303
DB 376 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 435
QY 304 GKNIDTATSMTPPFSSVSLGAGADAPTLISVDG-ALNVGSKDNKPVRITNVA PGYEGD 362
DB 436 GKNIDTATSMTPPFSSVSLGAGADAPTLISVDGALNVGSKDNKPVRITNVA PGYEGD 495
QY 363 VTNVAOLKGYAQNLLNRRIDNVGNARAGIAQAIAATAGLVQAYLPGKSMAIGGTYRGEA 422
DB 496 VTNVAOLKGYAQNLLNRRIDNVGNARAGIAQAIAATAGLVQAYLPGKSMAIGGTYRGEA 555
QY 423 GYAIIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
DB 556 GYAIIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594
```

RESULT 12  
ID AAY23743 standard; Protein; 599 AA.

XX AAY23743;  
XX 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

XX Surface protein; surface glycoprotein; infection; vaccine;  
KW Immunoreactive peptide.

XX Neisseria meningitidis.

OS WO931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98MO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

PA (UYOU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

DR WPI; 1999-418754/35.

XX N-PSDB; AAX85795.

PT Neisseria meningitidis surface proteins useful for treating N.

XX meningitidis infections  
PS Claim 1; Page 114-115; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 599 AA;

Query Match 96.1%; Score 2257.5; DB 20; Length 599;  
Best Local Similarity 97.4%; Pred. No. 7.2e-136;  
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

```
QY 4 TDLTSTVTEKLSFGANGKRVNITSDFKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 63
DB 141 TDLTSTVTEKLSFGANGKRVNITSDFKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 200
QY 64 GATTNTVNDVNTDDEKRRASVYKDVNLNAGNINIGVYKPGTTASDNVDFVHTYDVEFLSAD 123
DB 201 GATTNTVNDVNTDDEKRRASVYKDVNLNAGNINIGVYKPGTTASDNVDFVHTYDVEFLSAD 260
QY 124 TKTITVNESKDKNGKTEVEIKGKTSYIKERDKLVYKDKGNGSSTDEGEGLVTAKEV 183
DB 261 TKTITVNESKDKNGKTEVEIKGKTSYIKERDKLVYKDKGNGSSTDEGEGLVTAKEV 320
QY 184 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMD 243
DB 321 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMD 380
QY 321 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMD 380
DB 381 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 440
QY 244 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303
DB 381 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 440
QY 304 GKNIDTATSMTPPFSSVSLGAGADAPTLISVDG-DALNVGSKDNKPVRITNVA PGYEGD 362
DB 441 GKNIDTATSMTPPFSSVSLGAGADAPTLISVDGALNVGSKDNKPVRITNVA PGYEGD 500
QY 363 VTNVAOLKGYAQNLLNRRIDNVGNARAGIAQAIAATAGLVQAYLPGKSMAIGGTYRGEA 422
DB 501 VTNVAOLKGYAQNLLNRRIDNVGNARAGIAQAIAATAGLVQAYLPGKSMAIGGTYRGEA 560
QY 423 GYAIIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
DB 561 GYAIIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 599
```

RESULT 13  
ID AAU06176 standard; Protein; 599 AA.

XX AAU06176;

XX 24-OCT-2001 (first entry)

DE N. meningitidis H38 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain H38.

OS

XX Key Location/Qualifiers

XX 1..50 /label= C1

XX 51..105 /note= "Conserved region 1"

XX 106..117 /label= V1

XX 118..132 /note= "Variable region 1"

XX 133..147 /label= C2





QY 423 GYAIGYSSISDGGNWI IKGTASGNSRGHGASASVGYOW 461  
|||||  
DB 556 GYAIGYSSISDGGNWI IKGTASGNSRGHGASASVGYOW 594  
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Search completed: October 6, 2003, 09:22:41  
Job time : 41.5887 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 : Search time 12.3281 Seconds  
(without alignments)  
1582.188 Million cell updates/sec

Title: US-09-771-382-35  
Perfect score: 2330  
Sequence: 1 NNEIDLTSVGTETKLSFSAANG.....TASGNSRGHFGASASVGYOW 461

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2333	99.3	591	3	US-09-377-155-11 Sequence 11, Appl
2	2333	99.3	591	3	US-09-377-155-21 Sequence 21, Appl
3	2333	99.3	591	4	US-09-669-974-11 Sequence 11, Appl
4	2333	99.3	591	4	US-09-669-974-21 Sequence 21, Appl
5	2339	99.1	592	3	US-09-377-155-2 Sequence 2, Appl
6	2339	99.1	592	4	US-09-669-974-2 Sequence 2, Appl
7	2260.5	96.2	594	3	US-09-377-155-9 Sequence 9, Appl
8	2260.5	96.2	594	4	US-09-669-974-9 Sequence 9, Appl
9	2257.5	96.1	599	3	US-09-377-155-15 Sequence 15, Appl
10	2257.5	96.1	599	4	US-09-669-974-15 Sequence 15, Appl
11	2248.5	95.7	594	3	US-09-377-155-7 Sequence 7, Appl
12	2248.5	95.7	594	4	US-09-669-974-7 Sequence 7, Appl
13	2235.5	95.1	598	3	US-09-377-155-5 Sequence 5, Appl
14	2235.5	95.1	598	4	US-09-377-155-13 Sequence 13, Appl
15	2235.5	95.1	598	4	US-09-669-974-5 Sequence 5, Appl
16	2235.5	95.1	598	4	US-09-669-974-13 Sequence 13, Appl
17	2207.5	93.9	592	3	US-09-377-155-17 Sequence 17, Appl
18	2207.5	93.9	592	4	US-09-669-974-17 Sequence 17, Appl
19	2069.5	88.1	589	3	US-09-377-155-11 Sequence 11, Appl
20	2069.5	88.1	589	4	US-09-669-974-19 Sequence 19, Appl
21	901.5	38.4	2353	3	US-09-377-155-33 Sequence 33, Appl
22	901.5	38.4	2353	3	US-08-913-942-4 Sequence 4, Appl
23	901.5	38.4	2353	4	US-09-669-974-33 Sequence 33, Appl
24	901.5	38.4	2411	4	US-09-268-347-36 Sequence 36, Appl
25	895	38.1	2354	4	US-09-268-347-47 Sequence 47, Appl
26	889.5	37.9	1094	4	US-09-268-347-32 Sequence 32, Appl
27	875.5	37.3	1912	1	US-08-409-995-4 Sequence 4, Appl

28	875.5	37.3	1912	3	US-08-685-467-4 Sequence 4, Appl
29	874	37.2	1098	1	US-08-409-995-2 Sequence 2, Appl
30	874	37.2	1098	3	US-08-685-467-2 Sequence 2, Appl
31	874	37.2	1098	3	US-09-377-155-32 Sequence 32, Appl
32	874	37.2	1098	3	US-08-913-942-2 Sequence 2, Appl
33	874	37.2	1098	4	US-09-669-974-32 Sequence 32, Appl
34	874	37.2	1098	4	US-09-268-347-44 Sequence 44, Appl
35	856	36.4	658	1	US-08-409-995-5 Sequence 5, Appl
36	856	36.4	658	3	US-08-685-467-5 Sequence 5, Appl
37	856	36.4	658	3	US-08-913-942-5 Sequence 5, Appl
38	790.5	33.6	607	1	US-08-409-995-6 Sequence 6, Appl
39	790.5	33.6	607	3	US-08-685-467-6 Sequence 6, Appl
40	790.5	33.6	607	3	US-08-913-942-6 Sequence 6, Appl
41	652.5	27.8	679	3	US-08-913-942-15 Sequence 15, Appl
42	652.5	27.8	679	4	US-09-268-347-26 Sequence 26, Appl
43	564.5	24.0	1004	4	US-09-268-347-30 Sequence 30, Appl
44	560	23.8	1002	4	US-09-268-347-24 Sequence 24, Appl
45	525	22.3	1104	4	US-09-268-347-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
; US-09-377-155-11

Query Match 99.3%; Score 2333; DB 3; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-180;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	TDLTSGTETKLSFSAANGKVNITSDPKGLNFAKERTAGTGGDTVHLNGISTLTDTLLMT	63
DB	134	TDLTSGTETKLSFSAANGKVNITSDPKGLNFAKERTAGTGGDTVHLNGISTLTDTLLMT	193
QY	64	GATTNTNTNVNDDDEKRRASVYKVDVLAAGMNIKGVPCTTASNDVDFVTYDVEFLSAD	123
DB	194	GATTNTNTNVNDDDEKRRASVYKVDVLAAGMNIKGVPCTTASNDVDFVTYDVEFLSAD	253
QY	124	TTTTVNVESKDKGKTEVKIGAKTSVIEKEKDKLVTGDKENGSSDTDEGELVYAKEV	183
DB	254	TTTTVNVESKDKGKTEVKIGAKTSVIEKEKDKLVTGDKENGSSDTDEGELVYAKEV	313
QY	184	IDAVKAGRMRTTTTANGTGQADRFETYSCTNTYFASGKGTATVNSDDGNTVMD	243
DB	314	IDAVKAGRMRTTTTANGTGQADRFETYSCTNTYFASGKGTATVNSDDGNTVMD	373
QY	244	VWVGDLANNQOLNSGWNDSKAVAGSSGKTVISGNVSPKSKMDETVNINAGNIEITRN	303
DB	374	VWVGDLANNQOLNSGWNDSKAVAGSSGKTVISGNVSPKSKMDETVNINAGNIEITRN	433
QY	304	GNIDIAITSMTPQFSSSVISIGAGADAPTLISVDGDLNVGSKKDNKPVRITNVAAGYEGDV	363

Db 434 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVA PGVEGDV 493  
QY 364 TNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGVQAVLPGKSMMAIGGTYRGAG 423  
Db 494 TNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGVQAVLPGKSMMAIGGTYRGAG 553  
QY 424 YAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461  
Db 554 YAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

## RESULT 2

US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 99.3%; Score 2333; DB 3; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-180;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVGTETKLSFSANGKRVNITSPTKGLNFAKETAGTNGDTYVHLNGISGTLTDTLNT 63  
Db 134 TDLTSVGTETKLSFSANGKRVNITSPTKGLNFAKETAGTNGDTYVHLNGISGTLTDTLNT 193  
QY 64 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDVEEFLSAD 123  
Db 194 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDVEEFLSAD 253  
QY 124 TKTTTVNVESKDNKKTVEKIGAKTSVKEKDGKLVYTKDKGNGSSSTDEBEGVLTAKEV 183  
Db 254 TKTTTVNVESKDNKKTVEKIGAKTSVKEKDGKLVYTKDKGNGSSSTDEBEGVLTAKEV 313  
QY 184 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSNTVTFASGKGTATVASKDOGNITTYWD 243  
Db 314 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSNTVTFASGKGTATVASKDOGNITTYWD 373  
QY 244 VNVGDALNVNOLQNSGMNLDKKAAYAGSSGKVIISGNVSPSKGMDETVINAGNNIETRN 303  
Db 374 VNVGDALNVNOLQNSGMNLDKKAAYAGSSGKVIISGNVSPSKGMDETVINAGNNIETRN 433  
QY 304 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVA PGVEGDV 363  
Db 434 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVA PGVEGDV 493  
QY 364 TNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGVQAVLPGKSMMAIGGTYRGAG 423  
Db 494 TNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGVQAVLPGKSMMAIGGTYRGAG 553  
QY 424 YAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461  
Db 554 YAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

## RESULT 3

US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 99.3%; Score 2333; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-180;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVGTETKLSFSANGKRVNITSPTKGLNFAKETAGTNGDTYVHLNGISGTLTDTLNT 63  
Db 134 TDLTSVGTETKLSFSANGKRVNITSPTKGLNFAKETAGTNGDTYVHLNGISGTLTDTLNT 193  
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Db 194 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDVEEFLSAD 253  
QY 124 TKTTTVNVESKDNKKTVEKIGAKTSVKEKDGKLVYTKDKGNGSSSTDEBEGVLTAKEV 183  
Db 254 TKTTTVNVESKDNKKTVEKIGAKTSVKEKDGKLVYTKDKGNGSSSTDEBEGVLTAKEV 313  
QY 184 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSNTVTFASGKGTATVASKDOGNITTYWD 243  
Db 314 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSNTVTFASGKGTATVASKDOGNITTYWD 373  
QY 244 VNVGDALNVNOLQNSGMNLDKKAAYAGSSGKVIISGNVSPSKGMDETVINAGNNIETRN 303  
Db 374 VNVGDALNVNOLQNSGMNLDKKAAYAGSSGKVIISGNVSPSKGMDETVINAGNNIETRN 433  
QY 304 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVA PGVEGDV 363  
Db 434 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVA PGVEGDV 493  
QY 364 TNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGVQAVLPGKSMMAIGGTYRGAG 423  
Db 494 TNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGVQAVLPGKSMMAIGGTYRGAG 553  
QY 424 YAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461  
Db 554 YAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

## RESULT 4

US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974

Query Match 99.3%; Score 2333; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.5e-180;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21
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Query Match          99.3%; Score 2333; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,5e-180;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 134 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDTLLNT 193
QY 64 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKIKGKPGTTASDNVDFVRYDYVEFLSAD 123
DB 194 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKIKGKPGTTASDNVDFVRYDYVEFLSAD 253
QY 124 TKTTTAVESKDNCKKTEVKIGATSVYKEKDGKLVYKDKGNGSSSTDEBEGLVTAKEV 183
DB 254 TKTTTAVESKDNCKKTEVKIGATSVYKEKDGKLVYKDKGNGSSSTDEBEGLVTAKEV 313
QY 184 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDQGNITVYWD 243
DB 314 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDQGNITVYWD 373
QY 244 VNVGDALNVNOLQNSGMNLDKSKAVAGSSGKVISGNVSPSKGKMDETVINAGNNEIETRN 303
DB 374 VNVGDALNVNOLQNSGMNLDKSKAVAGSSGKVISGNVSPSKGKMDETVINAGNNEIETRN 433
QY 304 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNLSKDKNPVRTTNAAPGVKEDV 363
DB 434 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNLSKDKNPVRTTNAAPGVKEDV 493
QY 364 TNAQQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 423
DB 494 TNAQQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 553
QY 424 YAIYSSISDGNMIIRGTASGNSRGHFGASASVGYOW 461
DB 554 YAIYSSISDGNMIIRGTASGNSRGHFGASASVGYOW 591
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RESULT 5
US-09-377-155-2
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; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
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; ORGANISM: Neisseria meningitidis
US-09-377-155-2
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Query Match          99.1%; Score 2329; DB 3; Length 592;
Best Local Similarity 99.8%; Pred. No. 3,1e-180;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 135 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDTLLNT 194
QY 64 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKIKGKPGTTASDNVDFVRYDYVEFLSAD 123
DB 195 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKIKGKPGTTASDNVDFVRYDYVEFLSAD 254
QY 124 TKTTTAVESKDNCKKTEVKIGATSVYKEKDGKLVYKDKGNGSSSTDEBEGLVTAKEV 183
DB 255 TKTTTAVESKDNCKKTEVKIGATSVYKEKDGKLVYKDKGNGSSSTDEBEGLVTAKEV 314
QY 184 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDQGNITVYWD 243
DB 315 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDQGNITVYWD 374
QY 244 VNVGDALNVNOLQNSGMNLDKSKAVAGSSGKVISGNVSPSKGKMDETVINAGNNEIETRN 303
DB 375 VNVGDALNVNOLQNSGMNLDKSKAVAGSSGKVISGNVSPSKGKMDETVINAGNNEIETRN 434
QY 304 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNLSKDKNPVRTTNAAPGVKEDV 363
DB 435 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNLSKDKNPVRTTNAAPGVKEDV 494
QY 364 TNAQQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 423
DB 495 TNAQQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 554
QY 424 YAIYSSISDGNMIIRGTASGNSRGHFGASASVGYOW 461
DB 555 YAIYSSISDGNMIIRGTASGNSRGHFGASASVGYOW 592
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RESULT 6
US-09-669-974-2
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; Sequence 2, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2
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Query Match          99.1%; Score 2329; DB 4; Length 592;
Best Local Similarity 99.8%; Pred. No. 3,1e-180;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 4 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDTLLNT 63
DB 135 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDTLLNT 194
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QY	64	GATNTYNDNNTDDEKRRKRAASKYDVLNAGNNIKGKPGTTSQDNDVRYDYVEFLSAD	123
Db	195	GATNTYNDNNTDDEKRRKRAASKYDVLNAGNNIKGKPGTTSQDNDVRYDYVEFLSAD	254
QY	124	TKTTTVNESKNGKRRTEYKIGAKTSVIREKDGKLVYKDGKNGSGSTDEBEGLVTAKEY	183
Db	255	TKTTTVNESKNGKRRTEYKIGAKTSVIREKDGKLVYKDGKNGSGSTDEBEGLVTAKEY	314
QY	184	IDAIVKAGRRMKTITTAANGOTGQADKEFVYISGTVNTASAGKGTITAYSKDDGNTIYMD	243
Db	315	IDAIVKAGRRMKTITTAANGOTGQADKEFVYISGTVNTASAGKGTITAYSKDDGNTIYMD	374
QY	244	VNVGDALANTNOLNSGSMNLDSKAVNGSSGSKVYISGVNSPKKMDPYNINAGNNIETRN	303
Db	375	VNVGDALANTNOLNSGSMNLDSKAVNGSSGSKVYISGVNSPKKMDPYNINAGNNIETRN	434
QY	304	GKNIDTATSMTPOFSSVSLGAGADAPLTSVVDGDLANVSGSKDKNKPVRTVNAVPEKEDV	363
Db	435	GKNIDTATSMTPOFSSVSLGAGADAPLTSVVDGDLANVSGSKDKNKPVRTVNAVPEKEDV	494
QY	364	TNVAVLKGYAONLNNRIDNVDGNARAQIAQAIATPAGLVQAYLPKSKMMAIGGGTYRGEAG	423
Db	495	TNVAVLKGYAONLNNRIDNVDGNARAQIAQAIATPAGLVQAYLPKSKMMAIGGGTYRGEAG	554
QY	424	YATGYSSISDGGNWIITKGTAAGNSNGHGAASAVGYOW	461
Db	555	YATGYSSISDGGNWIITKGTAAGNSNGHGAASAVGYOW	592

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: RESULT 7
: US-09-377-155-9
: Sequence 9, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
:
: LENGTH: 594
:
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
: US-09-377-155-9

```

Query Match	96.2%;	Score 2260.5;	DB 3;	Length 594;
Best Local Similarity	97.4%;	Pred. No. 1.1e-174;		
Matches 447;	Conservative 4;	Mismatches 7;	Indels 1;	Gaps 1;

QY	4	TDLTISVGTGKLSFSSANGKNVNTISPTGKLNAPKAGNGBPTVHLNGISLTDLTPLNT	63
Db	136	TDLTISVGTGKLSFSSANGKNVNTISPTGKLNAPKAKTAETNGPTVHLNGISLTDLTPLNT	195
QY	64	GATTNTVNDNVTTDDEKKRAASVYKDLAANGWNIKGKPGTASDNDVDFRTDYVEEFLSAD	123
Db	196	GATTNTVNDNVTTDDEKKRAASVYKDLAANGWNIKGKPGTASDNDVDFRTDYVEEFLSAD	255
QY	124	TKTTTVNVESKDNGKKTVEYKIGAKTSVIERKDGKLVYTGKDGGENGSSTDEGEGLVYAAKEY	183
Db	256	TKTTTVNVESKDNGKKTVEYKIGAKTSVIERKDGKLVYTGKDGGENGSSTDEGEGLVYAAKEY	315
QY	184	DAVNAAGNRMTTANNGOTGADKDFEIVYISGTVNTPASGKGTATYATYAKDQNGIIVMYD	243
Db	316	DAVNAAGNRMTTANNGOTGADKDFEIVYISGTVNTPASGKGTATYATYAKDQNGIIVMYD	375

QY	244	VVVGDALNTNOLONGSMNLDSKAAVSSGSKYISGVPSKCKMDEYINAGNNIETRN	303
Db	376	VVVGDALNTNOLONGSMNLDSKAAVSSGSKYISGVPSKCKMDEYINAGNNIETRN	435
QY	304	GKNIDTATSMTPQFSSVSLGAGADAPTLTSLVGD -ALNNGSKKKDKPYRTITVAVPYVEGD	362
Db	436	GKNIDTATSMTPQFSSVSLGAGADAPTLTSLVDEGALNTGSKDANKPRTITVAVPYVEGD	495
QY	363	VTVNVAOLKVAONLNRRIDNDVGNARAGIAOAIATAGLVQAYLPFGKSMALGGCTYRGEA	422
Db	496	VTVNVAOLKVAONLNRRIDNDVGNARAGIAOAIATAGLVQAYLPFGKSMALGGCTYRGEA	555
QY	423	GYALIGYSSISDGGNNITIKGTASGNSRGHFGASASGYQW	461
Db	556	GYALIGYSSISDGGNNITIKGTASGNSRGHFGASASGYQW	594

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RESULT 8
US-09-669-974-9
: Sequence 9, Application US/09669974
: Patent No. 6331173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 594
: TYPE: PR1
: ORGANISM: Neisseria meningitidis
: US-09-669-974-9

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Query Match	96.28;	Score 2260.5;	DB 4;	Length 594;
Best Local Similarity	97.48;	Pred. No. 1.1e-174;		
Matches 447;	Conservative 4;	Mismatches 7;	Indels 1;	Gaps 1

QY	4	TDLTSTGTEKLSFESAGNKNVNTSPTKGINAKETAPAGNGBPTVHLNGISGTLDTLTLNT	63
Db	136	TDLTSTGTEKLSFESAGNKNVNTSPTKGINAKETAPAGNGBPTVHLNGISGTLDTLTLNT	195
QY	64	GATTNTVNTDNVTDDEKKRAASVKDYDLNAGWNIKGVPCGTTASDNVDVRYDYVEFLSAD	123
Db	196	GATTNTVNTDNVTDDEKKRAASVKDYDLNAGWNIKGVPCGTTASDNVDVRYDYVEFLSAD	255
QY	124	TKTTTVNVEBKONGKKEVEYKIGAKTSVIERKDGKLVYTKDKGENGSSSTDCEGLVTAKEY	183
Db	256	TKTTTVNVEBKONGKKEVEYKIGAKTSVIERKDGKLVYTKDKGENGSSSTDCEGLVTAKEY	315
QY	184	IDAVNKAAGRMTTTANGOTGADGKFEFVYTSNTNTPASGCGTTATVYSKDQGNITVYMD	243
Db	316	IDAVNKAAGRMTTTANGOTGADGKFEFVYTSNTNTPASGCGTTATVYSKDQGNITVYMD	375
QY	244	VNVGDALNNTOLONGSMNLDSKAIVAGSSGSKVISCNVSPSKCKMDEYNINAGNIETLRN	303
Db	376	VNVGDALNNTOLONGSMNLDSKAIVAGSSGSKVISCNVSPSKCKMDEYNINAGNIETLRN	435
QY	304	GKNIDATSMTPQOFSSVSLGAGADAPLTSLVYGD - ALANGSKDKMKPRITVNAVAGVEGD	362
Db	436	GKNIDATSMTPQOFSSVSLGAGADAPLTSLVYGD - ALANGSKDKMKPRITVNAVAGVEGD	495
QY	363	VTVNVADLKVCAONLNRRIDNVGNNRAGIAQAIATAGLVQAVYLPFGKSMIAIGGGTVRGEA	422

Db 496 VTNVADLKGVAQNLNNHIDNVGSMARAGTAQAIAFAGLYQAYLFGKSMMAIGGTTYGEA 555  
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 Qy 423 GYAIGYSSISDGGNMWIKKTASGNSRGHFGASASVGYOM 461  
 |||||  
 Db 556 GYAIGYSSISDGGNMWIKKTASGNSRGHFGASASVGYOM 594  
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1 RESULT 9
2 US-09-377-155-15
3 : Sequence 15, Application US/09377155
4 : Patent No. 6197312
5 : GENERAL INFORMATION:
6 : APPLICANT: PEAK, Ian Richard Anselm
7 : APPLICANT: JENNINGS, Michael Paul
8 : APPLICANT: MOXON, E. Richard
9 : TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
10 : FILE REFERENCE: 065064/0128
11 : CURRENT APPLICATION NUMBER: US/09/377,155
12 : CURRENT FILING DATE: 1999-08-19
13 : PRIOR APPLICATION NUMBER: PCT/AU98/01031
14 : PRIOR FILING DATE: 1998-12-14
15 : PRIOR APPLICATION NUMBER: GB 9726398.2
16 : PRIOR FILING DATE: 1997-12-12
17 : NUMBER OF SEQ ID NOS: 33
18 : SOFTWARE: PatentIn Ver. 2.0
19 : SEQ ID NO 15
20 : LENGTH: 599
21 : TYPE: PRT
22 : ORGANISM: Neisseria meningitidis
23 : US-09-377-155-15

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Query Match	96.1%;	Score 2257.5;	DB 3;	Length 599;
Best Local Similarity	97.4%;	Pred. No. 1.9e-174;		
Matches 447;	Conservative 2;	Mismatches 9;	Indels 1;	Gaps 1.
QY	4	TDLTSVGT EKLSF SANGKNVYITSDYFKGLNFAKETAGTNGDTYVHLNIGSTLDDTLTNT	63	
Db	141	TDLTSVETEKLSF SANGKNVYITSDYFKGLNFAKETAGTNGDTYVHLNIGSTLDDTLTNT	200	
QY	64	GATTNVINDNTYDDEKKRAASVKQVYLANGMNIIKGKPGCTPSDNDVFRYTDYVEFLSAD	123	
Db	201	GATTNVINDNTYDDEKKRAASVKQVYLANGMNIIKGKPGCTPSDNDVFRYTDYVEFLSAD	260	
QY	124	TKTTTVNVESKDNDCKTEVKGIGAKTSVYKEKDKGLVTKEDKDGENGSTYDEEGCLYTAKEV	183	
Db	261	TKTTTVNVESKDNDCKTEVKGIGAKTSVYKEKDKGLVTKEDKDGENGSTYDEEGCLYTAKEV	320	
QY	184	IDAVNRKAGRRKKT TTANGQTQADKFEVYVTSCTNVTFAFSGKGTATVSKDDOGNTTMYD	243	
Db	321	IDAVNRKAGRRKKT TTANGQTQADKFEVYVTSCTNVTFAFSGKGTATVSKDDOGNTTMYD	380	
QY	244	VNVGDALNVNDLQNSGWNIDSKAAVAGSSGKVIYSGNVSPSKGMDETVINMGNNIETIRN	303	
Db	381	VNVGDALNVNDLQNSGWNIDSKAAVAGSSGKVIYSGNVSPSKGMDETVINMGNNIETIRN	440	
QY	304	GKNIDITATSMTPQFSSVSLGAGADPTLSVDC-DALNIGSKDKDKPVRIITVAPGVKCGD	362	
Db	441	GKNIDITATSMTPQFSSVSLGAGADPTLSVDCGALNIGSKDKDKPVRIITVAPGVKCGD	500	
QY	363	VTNTAOLKGVANQNLNNRINDVNDGNARAGIAQAIATAGLVQVYALPCKSMIAIGCGTYREBA	422	
Db	501	VTNTAOLKGVANQNLNNRINDVNDGNARAGIAQAIATAGLVQVYALPCKSMIAIGCGTYREBA	560	
QY	423	GYAIGYSSISDGGWIIKGTASGNSRGHFAGSASVGYOW	461	
Db	561	GYAIGYSSISDGGWIIKGTASGNSRGHFAGSASVGYOW	599	

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1  GENERAL INFORMATION:
2  APPLICANT:  peak, jan Richard Anselm
3  APPLICANT:  JENNINGS, Michael Paul
4  APPLICANT:  MOXON, E. Richard
5  TITLE OF INVENTION:  NOVEL SURFACE ANTIGEN
6  FILE REFERENCE:  065064/0128
7  CURRENT APPLICATION NUMBER:  US/09/669,974
8  CURRENT FILING DATE:  2000-09-26
9  PRIOR APPLICATION NUMBER:  US 09/377,155
10 PRIOR FILING DATE:  1998-08-19
11 PRIOR APPLICATION NUMBER:  PCT/AU98/01031
12 PRIOR FILING DATE:  1998-12-14
13 PRIOR APPLICATION NUMBER:  GB 9726398.2
14 PRIOR FILING DATE:  1997-12-12
15 NUMBER OF SEQ ID NOS:  33
16 SOFTWARE:  PatentIn Ver. 2.0
17 SEQ ID NO 15
18 LENGTH:  599
19 TYPE:  PRT
20 ORGANISM:  Neisseria meningitidis
21 US-09-669-974-15

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Query Match	Similarity	96.1%;	Score 2257.5;	DB 4;	Length 599;
Best Local	Similarity	97.4%;	Pred. No. 1.9e-174;		
Matches	447;	Conservative	2;	Mismatches	9;
				Indels	1;
				Gaps	1
QY	4	TDLTSVGTETKLSFSANGKNKVNITSDPTKGLNFAKETAGTNGDITVHLNIGISTLTDTLLNT	63		
DB	141	TDLTSVETEKLSFGANGKNVNITSDPTKGLNFAKETAGTNGDITVHLNIGISTLTDTLLNT	200		
QY	64	GATNNTVTDNDYTDDEKKRRAASVKVDLNGMNLKGVKPGCTASDNDVFWYTYTVEFLSD	123		
DB	201	GATNNTVTDNDYTDDEKKRRAASVKVDLNGMNLKGVKPGCTASDNDVFWHTYTFVEFLSD	260		
QY	124	TKTTTVNVESKDNCKRTEVKGAKTVSIREKDKLVYTGKDKGENSSDTEGBGLYTAKEV	183		
DB	261	TKTTTVNVESKDNCKRTEVKGAKTVSIREKDKLVYTGKDKGENSSDTEGBGLYTAKEV	320		
QY	184	IDAVNKKAGRRKKTITTANGOTGOADKFEFVYTSSTNTFASGKGTATVSKDDOGNTTVMYD	243		
DB	321	IDAVNKKAGRRKKTITTANGOTGOADKFEFVYTSSTNTFASGKGTATVSKDDOGNTTVMYD	380		
QY	244	VNVGDALVNDLONSGMNLDSKAAVAGSSGKVTSGNVSPSKGKMDFTVINAAGNIETFTN	303		
DB	381	VNVGDALVNDLONSGMNLDSKAAVAGSSGKVTSGNVSPSKGKMDFTVINAAGNIETFTN	440		
QY	304	GKNIDIASMTPPQFSVSVLGAGADAPTLISVDC-DALNVGSKKDKNPVRTTNNAPGVKEED	362		
DB	441	GKNIDIASMTPPQFSVSVLGAGADAPTLISVDDKGLANVGSKANKPVRTTNNAPGVKEED	500		
QY	363	VTVNAQLKGVANQNLNLRIDNDVGNARACIAQAIATAGLVAQVLPKSMMAIGCTYRGEA	422		
DB	501	VTVNAQLKGVANQNLNLRIDNDVGNARACIAQAIATAGLVAQVLPKSMMAIGCTYRGEA	560		
QY	423	GYAIGYSSISDGGNNITKGTASGNSRGHFGASASGYQW 461			
DB	561	GYAIGYSSISDGGNNITKGTASGNSRGHFGASASGYQW 599			

OY	363	VTNVAOLKGVAAQNNNNRINDVNGNARAGIAOAIITAGIYVOAYLPGRKSMMAIGGTYRGEA	422
.			
.			
Db	501	VTNVAOLKGVAAQNNNNRINDVNGNARAGIAOAIITAGIYVOAYLPGRKSMMAIGGTYRGEA	560
OY	423	GVAIGYSSISDGCNMIIKGTASGNSRGHFGASASVGYOW	461
.			
.			
Db	561	GVAIGYSSISDGCNMIIKGTASGNSRGHFGASASVGYOW	599
RESULT 10			
US-09-669-974-15			
: Sequence 15, Application US/09669974			
: Patent No. 6333173			

;; PRIOR APPLICATION NUMBER: GB 9726398.2  
;; PRIOR FILING DATE: 1997-12-12  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: Patentl Ver. 2.0  
;; SEQ ID NO 7  
;; LENGTH: 594  
;; TYPE: PR1  
;; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 95.7%; Score 2248.5; DB 3; Length 594;  
Best Local Similarity 97.2%; Pred. No. 1e-173;  
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 4 TDLTSTGTEKLSFSANGNKVNITSDPKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLMT 63  
DB 136 TDLTSTGTEKLSFGANGNKVNITSDPKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLMT 195  
QY 64 GATTNTNDNVTDDEKKRAASYKDVNLNAGMNKGVKPGTTASDNVDFVRTYDVEFLSAD 123  
DB 196 GATTNTNDNVTDDEKKRAASYKDVNLNAGMNKGVKPGTTASDNVDFVRTYDVEFLSAD 255  
QY 124 TTTTYYNVESKDNKGKTEVKIGAKTSVIEKDGKLVTKGDKGNGSSTDEGBGLYAKEV 183  
DB 256 TTTTYYNVESKDNKGKTEVKIGAKTSVIEKDGKLVTKGDKGNGSSTDEGBGLYAKEV 315  
QY 184 IDAVNKGWRMKTNTTANGOTGADKRETVTSGTNVTFASGKGTATVSRDDGNTVMD 243  
DB 316 IDAVNKGWRMKTNTTANGOTGADKRETVTSGTNVTFASGKGTATVSRDDGNTVMD 375  
QY 244 VNVGDLANVNOJLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVNNAGNIEITRN 303  
DB 376 VNVGDLANVNOJLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVNNAGNIEITRN 435  
QY 304 GNKIDTATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVSKDNKPVRTTNVAPGVKEGD 362  
DB 436 GNKIDTATSMTPQFSSVSLGAGADAPTLVSVDGALNVSKDNKPVRTTNVAPGVKEGD 495  
QY 363 VTINVAOLKVAOVLNRRIDNVGNARAGIAQATATAGLVQAVLPKGSMAIGGDTYRGEA 422  
DB 496 VTINVAOLKVAOVLNRRIDNVGNARAGIAQATATAGLVQAVLPKGSMAIGGDTYRGEA 555  
QY 423 GYALIGYSSISDGGNMIKGTASGNSRHHGASASVGYOW 461  
DB 556 GYALIGYSSISDGGNMIKGTASGNSRHHGASASVGYOW 594

## RESULT 12

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentl Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PR1  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 95.7%; Score 2248.5; DB 4; Length 594;  
Best Local Similarity 97.2%; Pred. No. 1e-173;  
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 4 TDLTSTGTEKLSFSANGNKVNITSDPKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLMT 63  
DB 136 TDLTSTGTEKLSFGANGNKVNITSDPKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLMT 195  
QY 64 GATTNTNDNVTDDEKKRAASYKDVNLNAGMNKGVKPGTTASDNVDFVRTYDVEFLSAD 123  
DB 196 GATTNTNDNVTDDEKKRAASYKDVNLNAGMNKGVKPGTTASDNVDFVRTYDVEFLSAD 255  
QY 124 TTTTYYNVESKDNKGKTEVKIGAKTSVIEKDGKLVTKGDKGNGSSTDEGBGLYAKEV 183  
DB 256 TTTTYYNVESKDNKGKTEVKIGAKTSVIEKDGKLVTKGDKGNGSSTDEGBGLYAKEV 315  
QY 184 IDAVNKGWRMKTNTTANGOTGADKRETVTSGTNVTFASGKGTATVSRDDGNTVMD 243  
DB 316 IDAVNKGWRMKTNTTANGOTGADKRETVTSGTNVTFASGKGTATVSRDDGNTVMD 375  
QY 244 VNVGDLANVNOJLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVNNAGNIEITRN 303  
DB 376 VNVGDLANVNOJLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVNNAGNIEITRN 435  
QY 304 GNKIDTATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVSKDNKPVRTTNVAPGVKEGD 362  
DB 436 GNKIDTATSMTPQFSSVSLGAGADAPTLVSVDGALNVSKDNKPVRTTNVAPGVKEGD 495  
QY 363 VTINVAOLKVAOVLNRRIDNVGNARAGIAQATATAGLVQAVLPKGSMAIGGDTYRGEA 422  
DB 496 VTINVAOLKVAOVLNRRIDNVGNARAGIAQATATAGLVQAVLPKGSMAIGGDTYRGEA 555  
QY 423 GYALIGYSSISDGGNMIKGTASGNSRHHGASASVGYOW 461  
DB 556 GYALIGYSSISDGGNMIKGTASGNSRHHGASASVGYOW 594

## RESULT 13

US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentl Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PR1  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 95.1%; Score 2235.5; DB 3; Length 598;  
Best Local Similarity 96.3%; Pred. No. 1.2e-172;  
Matches 442; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

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DB 140 TDLTSTGTEKLSFGANGNKVNITSDPKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLMT 199  
QY 64 GATTNTNDNVTDDEKKRAASYKDVNLNAGMNKGVKPGTTASDNVDFVRTYDVEFLSAD 123  
DB 200 GATTNTNDNVTDDEKKRAASYKDVNLNAGMNKGVKPGTTASDNVDFVRTYDVEFLSAD 259



Mon Oct 6 12:38:47 2003

us-09-771-382-35.ra1

Page 8

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Job time : 13.3281 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:31:05 ; Search time 23.0934 Seconds  
(Without alignments)  
3158.312 Million cell updates/sec

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Perfect score: 2350  
Sequence: 1 NNETDLTVGTEKLSFSGANG.....TASGNRHHGASASVGYOW 461

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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2: /cgn2\_6/ptodata/2/pubppa/PCF\_NEW\_PUB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
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16: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2350	100.0	461	US-09-771-382-35	Sequence 35, App1
2	2350	100.0	512	US-09-771-382-23	Sequence 23, App1
3	2333	99.3	591	US-09-797-862-11	Sequence 11, App1
4	2333	99.3	591	US-09-797-862-21	Sequence 21, App1
5	2333	99.3	591	US-09-771-382-1	Sequence 1, App1
6	2333	99.3	591	US-09-771-382-5	Sequence 5, App1
7	2329	99.1	592	US-09-797-862-2	Sequence 2, App1
8	2328	99.1	540	US-09-771-382-33	Sequence 33, App1
9	2260.5	96.2	594	US-09-797-862-9	Sequence 9, App1
10	2260.5	96.2	594	US-09-771-382-4	Sequence 4, App1
11	2257.5	96.1	599	US-09-797-862-15	Sequence 15, App1
12	2257.5	96.1	599	US-09-771-382-6	Sequence 6, App1
13	2248.5	95.7	594	US-09-797-862-7	Sequence 7, App1
14	2248.5	95.7	594	US-09-771-382-9	Sequence 9, App1
15	2235.5	95.1	598	US-09-797-862-5	Sequence 5, App1

16	2235.5	95.1	598	10	US-09-797-862-13	Sequence 13, App1
17	2235.5	95.1	598	10	US-09-771-382-7	Sequence 7, App1
18	2235.5	95.1	598	10	US-09-771-382-8	Sequence 8, App1
19	2213.5	94.2	462	10	US-09-771-382-36	Sequence 36, App1
20	2213.5	94.2	513	10	US-09-771-382-24	Sequence 24, App1
21	2207.5	93.9	541	10	US-09-771-382-34	Sequence 34, App1
22	2207.5	93.9	592	10	US-09-797-862-17	Sequence 17, App1
23	2207.5	93.9	592	10	US-09-771-382-2	Sequence 2, App1
24	2148.5	91.4	502	10	US-09-771-382-27	Sequence 27, App1
25	2089.5	88.9	592	10	US-09-771-382-10	Sequence 10, App1
26	2069.5	88.1	589	10	US-09-797-862-19	Sequence 19, App1
27	2069.5	88.1	589	10	US-09-771-382-3	Sequence 3, App1
28	1946.5	82.8	604	10	US-09-771-382-11	Sequence 11, App1
29	1941	82.6	433	10	US-09-771-382-26	Sequence 26, App1
30	1941	82.6	433	10	US-09-771-382-35	Sequence 35, App1
31	1822	77.5	407	10	US-09-771-382-25	Sequence 25, App1
32	1808	76.9	356	10	US-09-771-382-37	Sequence 37, App1
33	901.5	38.4	2353	10	US-09-797-862-33	Sequence 33, App1
34	874	37.2	1098	10	US-09-797-862-32	Sequence 32, App1
35	864.5	36.8	201	10	US-09-771-382-39	Sequence 39, App1
36	358	15.2	2122	10	US-09-813-214A-9	Sequence 9, App1
37	356	15.1	1833	12	US-10-175-275-4	Sequence 4, App1
38	356	15.1	1833	12	US-10-175-282-4	Sequence 4, App1
39	356	15.1	1992	12	US-10-175-275-3	Sequence 3, App1
40	356	15.1	1992	12	US-10-175-282-3	Sequence 3, App1
41	350.5	14.9	1778	12	US-10-238-075-749	Sequence 749, App
42	298	12.7	2039	15	US-10-192-584-7	Sequence 7, App1
43	262.5	11.2	2042	15	US-10-192-584-6	Sequence 6, App1
44	217.5	9.3	1180	12	US-10-193-764-61	Sequence 61, App1
45	217.5	9.3	1188	12	US-10-193-764-59	Sequence 59, App1

ALIGNMENTS

RESULT 1  
US-09-771-382-35  
: Sequence 35, Application US/09771382  
: Patent No. US20020160016A1  
: GENERAL INFORMATION:  
: APPLICANT: Peak, Ian  
: TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN  
: FILE REFERENCE: 8795-2401  
: CURRENT APPLICATION NUMBER: US/09/771,382  
: CURRENT FILING DATE: 2001-01-25  
: PRIOR APPLICATION NUMBER: US 60/177,917  
: PRIOR FILING DATE: 2000-01-25  
: NUMBER OF SEQ ID NOS: 52  
: SOFTWARE: PatentIn version 3.0  
: SEQ ID NO 35  
: LENGTH: 461  
: TYPE: PRT  
: ORGANISM: Neisseria meningitidis  
US-09-771-382-35

Query Match	100.0%	Score 2350:	DB 10:	Length 461:
Best Local Similarity	100.0%	Pred. No. 3.7e-175:		
Matches 461:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Qy	1	NNETDLTVGTEKLSFSGANGKNVITSDTKGLNFAKKTAGTNGDTVHLNIGSTLNDTL	60	
Db	1	NNETDLTVGTEKLSFSGANGKNVITSDTKGLNFAKKTAGTNGDTVHLNIGSTLNDTL	60	
Qy	61	LNTGATNTVNDNTDDEKRRASVKOVNLNAGNKKVKGPTTASDVNDVRYTYVEFL	120	
Db	61	LNTGATNTVNDNTDDEKRRASVKOVNLNAGNKKVKGPTTASDVNDVRYTYVEFL	120	
Qy	121	SADKTTTVNVESSDKNKKTEVKTGATSVYKKEGDLVNGKDGSSGSSDBEGGLVTA	180	
Db	121	SADKTTTVNVESSDKNKKTEVKTGATSVYKKEGDLVNGKDGSSGSSDBEGGLVTA	180	
Qy	181	KEVIDAVNKGWRKKTTTANGOTGOADKFTVTSGTNVTASGKGTATVSKDQGNITV	240	

Db 181 KEVIDAVNKAGRMKTTTANGOTGADKREYVTSCTNVTFSAGSKGTTATVSKDDGNTIV 240  
OY 241 MYDVNVGDLANVNOLONSGWNLSKRAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 300  
Db 241 MYDVNVGDLANVNOLONSGWNLSKRAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 300  
OY 301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNPVRITNVAPGVE 360  
Db 301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNPVRITNVAPGVE 360  
OY 361 GGVTVNAOLKGYAONLNRRIDNVGDNARAGIAOAIATAGLVQAYILPGKSMMAIGGTYRG 420  
Db 361 GGVTVNAOLKGYAONLNRRIDNVGDNARAGIAOAIATAGLVQAYILPGKSMMAIGGTYRG 420  
OY 421 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461  
Db 421 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461

RESULT 2  
US-09-771-382-23  
; Sequence 23, Application US/09771382  
; Patent No. US20020160016A1  
; GENERAL INFORMATION:  
; APPLICANT: Peak, Ian  
; APPLICANT: Jennings, Michael  
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN  
; FILE REFERENCE: 8795-24U1  
; CURRENT APPLICATION NUMBER: US/09/771,382  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/177,917  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 512  
; TYPE: PRF  
; ORGANISM: Neisseria meningitidis  
US-09-771-382-23

Query Match 100.0%; Score 2350; DB 10; Length 512;  
Best Local Similarity 100.0%; Pred. No. 4.2e-175;  
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNETDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISLTDTL 60  
Db 52 NNETDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISLTDTL 111  
OY 61 LNTGATTNVTNDVTDDEKRAASVYKVDVLAAGMNIKGVKPGTTASDNVDFVRTYDVEFL 120  
Db 112 LNTGATTNVTNDVTDDEKRAASVYKVDVLAAGMNIKGVKPGTTASDNVDFVRTYDVEFL 171  
OY 121 SADRTTYYNVSKDNGKTEYKIGAKTSVIEKDGKLVYTKDGKNGSSTDEGELVYA 180  
Db 172 SADRTTYYNVSKDNGKTEYKIGAKTSVIEKDGKLVYTKDGKNGSSTDEGELVYA 231  
OY 181 KEVIDAVNKAGRMKTTTANGOTGADKREYVTSCTNVTFSAGSKGTTATVSKDDGNTIV 240  
Db 232 KEVIDAVNKAGRMKTTTANGOTGADKREYVTSCTNVTFSAGSKGTTATVSKDDGNTIV 291  
OY 241 MYDVNVGDLANVNOLONSGWNLSKRAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 300  
Db 292 MYDVNVGDLANVNOLONSGWNLSKRAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 351  
OY 301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNPVRITNVAPGVE 360  
Db 352 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNPVRITNVAPGVE 411  
OY 361 GGVTVNAOLKGYAONLNRRIDNVGDNARAGIAOAIATAGLVQAYILPGKSMMAIGGTYRG 420  
Db 412 GGVTVNAOLKGYAONLNRRIDNVGDNARAGIAOAIATAGLVQAYILPGKSMMAIGGTYRG 471

OY 421 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461  
Db 472 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 512

RESULT 3  
US-09-797-862-11  
; Sequence 11, Application US/09797862  
; Patent No. US20020102276A1  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, IAN RICHARD ANSELM  
; APPLICANT: MOXON, E. RICHARD  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0134  
; CURRENT APPLICATION NUMBER: US/09/797,862  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRF  
; ORGANISM: Neisseria meningitidis  
US-09-797-862-11

Query Match 99.3%; Score 2333; DB 10; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.1e-173;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TDLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISLTDTL 63  
Db 134 TDLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISLTDTL 193  
OY 64 GATTNVTNDVTDDEKRAASVYKVDVLAAGMNIKGVKPGTTASDNVDFVRTYDVEFLSAD 123  
Db 194 GATTNVTNDVTDDEKRAASVYKVDVLAAGMNIKGVKPGTTASDNVDFVRTYDVEFLSAD 253  
OY 124 TKTTTYYNVSKDNGKTEYKIGAKTSVIEKDGKLVYTKDGKNGSSTDEGELVYAKEV 183  
Db 254 TKTTTYYNVSKDNGKTEYKIGAKTSVIEKDGKLVYTKDGKNGSSTDEGELVYAKEV 313  
OY 184 IDAVNKAGRMKTTTANGOTGADKREYVTSCTNVTFSAGSKGTTATVSKDDGNTIVMD 243  
Db 314 IDAVNKAGRMKTTTANGOTGADKREYVTSCTNVTFSAGSKGTTATVSKDDGNTIVMD 373  
OY 244 VNVGDLANVNOLONSGWNLSKRAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEITRN 303  
Db 374 VNVGDLANVNOLONSGWNLSKRAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEITRN 433  
OY 304 GNKIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNPVRITNVAPGVEGV 363  
Db 434 GNKIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNPVRITNVAPGVEGV 493  
OY 364 TNAVOLKGYAONLNRRIDNVGDNARAGIAOAIATAGLVQAYILPGKSMMAIGGTYRGEAG 423  
Db 494 TNAVOLKGYAONLNRRIDNVGDNARAGIAOAIATAGLVQAYILPGKSMMAIGGTYRGEAG 553  
OY 424 VAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461  
Db 554 VAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 4  
US-09-797-862-21  
; Sequence 21, Application US/09797862  
; Patent No. US20020102276A1  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, IAN RICHARD ANSELM  
; APPLICANT: JENNINGS, MICHAEL PAUL



APPLICANT: MOXON, E. RICHARD  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0134  
CURRENT APPLICATION NUMBER: US/09/797,862  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: PCT/A098/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 591  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-797-862-21

Query Match 99.3%; Score 2333; DB 10; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1,1e-173;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKETAAGTNGDTYVHLNGISGLTDLTLNT 63  
DB 134 TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKETAAGTNGDTYVHLNGISGLTDLTLNT 193  
QY 64 GATTNVNDVNTDEDEKRAASVYKDYLNAGNNIKVKGKGTASDVDFVRYTDVEFLSAD 123  
DB 194 GATTNVNDVNTDEDEKRAASVYKDYLNAGNNIKVKGKGTASDVDFVRYTDVEFLSAD 253  
QY 124 TKTTTVNESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENSGSTDEGEGLVTAKEV 183  
DB 254 TKTTTVNESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENSGSTDEGEGLVTAKEV 313  
QY 184 IDAVNKGWRKKTITANGOTQADKFEFVTSCTVWTFASGKTATVSKDDOGNITWYD 243  
DB 314 IDAVNKGWRKKTITANGOTQADKFEFVTSCTVWTFASGKTATVSKDDOGNITWYD 373  
QY 244 VNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 303  
DB 374 VNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 433  
QY 304 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGALNVGSKDKNPVRTNVAPEGVKGEDV 363  
DB 434 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGALNVGSKDKNPVRTNVAPEGVKGEDV 493  
QY 364 TNAQLKGVAQNLRNDNDGNARAGIAQAIAATAGLVQAVLPKSMMAIGGCTYRGEAG 423  
DB 494 TNAQLKGVAQNLRNDNDGNARAGIAQAIAATAGLVQAVLPKSMMAIGGCTYRGEAG 553  
QY 424 YALGYSSISDGGNMIIGKTASGNSRGHFGASASVGYOM 461  
DB 554 YALGYSSISDGGNMIIGKTASGNSRGHFGASASVGYOM 591

RESULT 5  
US-09-771-382-1

Sequence 1, Application US/09771382  
Patent No. US20020160016A1

GENERAL INFORMATION:

APPLICANT: Peak, Ian  
APPLICANT: Jennings, Michael  
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN  
FILE REFERENCE: 8795-2401

CURRENT APPLICATION NUMBER: US/09/771,382  
CURRENT FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: US 60/177,917  
PRIOR FILING DATE: 2000-01-25

NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1  
LENGTH: 591

TYPE: PRT  
ORGANISM: Neisseria meningitidis

US-09-771-382-1

Query Match 99.3%; Score 2333; DB 10; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1,1e-173;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKETAAGTNGDTYVHLNGISGLTDLTLNT 63  
DB 134 TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKETAAGTNGDTYVHLNGISGLTDLTLNT 193  
QY 64 GATTNVNDVNTDEDEKRAASVYKDYLNAGNNIKVKGKGTASDVDFVRYTDVEFLSAD 123  
DB 194 GATTNVNDVNTDEDEKRAASVYKDYLNAGNNIKVKGKGTASDVDFVRYTDVEFLSAD 253  
QY 124 TKTTTVNESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENSGSTDEGEGLVTAKEV 183  
DB 254 TKTTTVNESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENSGSTDEGEGLVTAKEV 313  
QY 184 IDAVNKGWRKKTITANGOTQADKFEFVTSCTVWTFASGKTATVSKDDOGNITWYD 243  
DB 314 IDAVNKGWRKKTITANGOTQADKFEFVTSCTVWTFASGKTATVSKDDOGNITWYD 373  
QY 244 VNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 303  
DB 374 VNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 433  
QY 304 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGALNVGSKDKNPVRTNVAPEGVKGEDV 363  
DB 434 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGALNVGSKDKNPVRTNVAPEGVKGEDV 493  
QY 364 TNAQLKGVAQNLRNDNDGNARAGIAQAIAATAGLVQAVLPKSMMAIGGCTYRGEAG 423  
DB 494 TNAQLKGVAQNLRNDNDGNARAGIAQAIAATAGLVQAVLPKSMMAIGGCTYRGEAG 553  
QY 424 YALGYSSISDGGNMIIGKTASGNSRGHFGASASVGYOM 461  
DB 554 YALGYSSISDGGNMIIGKTASGNSRGHFGASASVGYOM 591

RESULT 6

US-09-771-382-5  
Sequence 5, Application US/09771382  
Patent No. US20020160016A1

GENERAL INFORMATION:

APPLICANT: Peak, Ian  
APPLICANT: Jennings, Michael  
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN  
FILE REFERENCE: 8795-2401

CURRENT APPLICATION NUMBER: US/09/771,382  
CURRENT FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: US 60/177,917  
PRIOR FILING DATE: 2000-01-25

NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 5  
LENGTH: 591

TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-771-382-5

Query Match 99.3%; Score 2333; DB 10; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1,1e-173;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKETAAGTNGDTYVHLNGISGLTDLTLNT 63  
DB 134 TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKETAAGTNGDTYVHLNGISGLTDLTLNT 193  
QY 64 GATTNVNDVNTDEDEKRAASVYKDYLNAGNNIKVKGKGTASDVDFVRYTDVEFLSAD 123  
DB 194 GATTNVNDVNTDEDEKRAASVYKDYLNAGNNIKVKGKGTASDVDFVRYTDVEFLSAD 253  
QY 124 TKTTTVNESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENSGSTDEGEGLVTAKEV 183

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Db 254 TKTTVNVESKDNKGKTEYKIGAKTSVLIKEDGKLVTKDCKENGSSSTDEGGLVTAKEY 313
OY 184 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVFASGKGTATTATVSKDDGNTTVMYD 243
Db 314 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVFASGKGTATTATVSKDDGNTTVMYD 373
OY 244 VNVGDALVNNQLONSGWNLDKSAVAGSSGKVTISGNVSPSKGMDETNTNINAGNNIEITRN 303
Db 374 VNVGDALVNNQLONSGWNLDKSAVAGSSGKVTISGNVSPSKGMDETNTNINAGNNIEITRN 433
OY 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPVRITNVAPEGYEGDV 363
Db 434 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPVRITNVAPEGYEGDV 493
OY 364 TNVAOLKGYAQNLRNLRIDVNDGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYRGEAG 423
Db 494 TNVAOLKGYAQNLRNLRIDVNDGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYRGEAG 553
OY 424 VAIGYSSISDGGNMWIKGTASGNSRGHFGASASVGYOW 461
Db 554 VAIGYSSISDGGNMWIKGTASGNSRGHFGASASVGYOW 591
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RESULT 7
US-09-797-862-2
; Sequence 2, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797, 862
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-2
```

```
Query Match 99.1%; Score 2329; DB 10; Length 592;
Best Local Similarity 99.8%; Pred. No. 2.2e-173;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 4 TDLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT 63
Db 135 TDLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT 194
OY 64 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGYKPGTTASDNVDFVATYPTVEFLSD 123
Db 195 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGYKPGTTASDNVDFVATYPTVEFLSD 254
OY 124 TKTTVNVESKDNKGKTEYKIGAKTSVLIKEDGKLVTKDCKENGSSSTDEGGLVTAKEY 183
Db 255 TKTTVNVESKDNKGKTEYKIGAKTSVLIKEDGKLVTKDCKENGSSSTDEGGLVTAKEY 314
OY 184 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVFASGKGTATTATVSKDDGNTTVMYD 243
Db 315 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVFASGKGTATTATVSKDDGNTTVMYD 374
OY 244 VNVGDALVNNQLONSGWNLDKSAVAGSSGKVTISGNVSPSKGMDETNTNINAGNNIEITRN 303
Db 375 VNVGDALVNNQLONSGWNLDKSAVAGSSGKVTISGNVSPSKGMDETNTNINAGNNIEITRN 434
OY 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPVRITNVAPEGYEGDV 363
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Db 435 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPVRITNVAPEGYEGDV 494
OY 364 TNVAOLKGYAQNLRNLRIDVNDGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYRGEAG 423
Db 495 TNVAOLKGYAQNLRNLRIDVNDGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYRGEAG 554
OY 424 VAIGYSSISDGGNMWIKGTASGNSRGHFGASASVGYOW 461
Db 555 VAIGYSSISDGGNMWIKGTASGNSRGHFGASASVGYOW 592
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RESULT 8
US-09-771-382-33
; Sequence 33, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-24U1
; CURRENT APPLICATION NUMBER: US/09/771, 382
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177, 917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 33
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-771-382-33
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Query Match 99.1%; Score 2328; DB 10; Length 540;
Best Local Similarity 99.8%; Pred. No. 2.4e-173;
Matches 457; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 4 TDLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT 63
Db 83 TDLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT 142
OY 64 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGYKPGTTASDNVDFVATYPTVEFLSD 123
Db 143 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGYKPGTTASDNVDFVATYPTVEFLSD 202
OY 124 TKTTVNVESKDNKGKTEYKIGAKTSVLIKEDGKLVTKDCKENGSSSTDEGGLVTAKEY 183
Db 203 TKTTVNVESKDNKGKTEYKIGAKTSVLIKEDGKLVTKDCKENGSSSTDEGGLVTAKEY 262
OY 184 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVFASGKGTATTATVSKDDGNTTVMYD 243
Db 263 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVFASGKGTATTATVSKDDGNTTVMYD 322
OY 244 VNVGDALVNNQLONSGWNLDKSAVAGSSGKVTISGNVSPSKGMDETNTNINAGNNIEITRN 303
Db 323 VNVGDALVNNQLONSGWNLDKSAVAGSSGKVTISGNVSPSKGMDETNTNINAGNNIEITRN 382
OY 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPVRITNVAPEGYEGDV 363
Db 383 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPVRITNVAPEGYEGDV 442
OY 364 TNVAOLKGYAQNLRNLRIDVNDGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYRGEAG 423
Db 443 TNVAOLKGYAQNLRNLRIDVNDGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYRGEAG 502
OY 424 VAIGYSSISDGGNMWIKGTASGNSRGHFGASASVGYOW 461
Db 503 VAIGYSSISDGGNMWIKGTASGNSRGHFGASASVGYOW 540
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RESULT 9
US-09-797-862-9
; Sequence 9, Application US/09797862
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; Patent No. US20020102276A1  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, IAN RICHARD ANSELM  
; APPLICANT: JENNINGS, MICHAEL PAUL  
; APPLICANT: MOXON, E. RICHARD  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0134  
; CURRENT APPLICATION NUMBER: US/09/797,862  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-797-862-9

Query Match 96.2%; Score 2260.5; DB 10; Length 594;  
Best Local Similarity 97.4%; Pred. No. 5e-168;  
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVHLNGISGTLTDLTLNT 63  
DB 136 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVHLNGISGTLTDLTLNT 195  
QY 64 GATTNVTNDVNTDDEKRRASVSKVDVLNAGNNIKGVKPGTTASDNDVDFRYDVEFLSAD 123  
DB 196 GATTNVTNDVNTDDEKRRASVSKVDVLNAGNNIKGVKPGTTASDNDVDFRYDVEFLSAD 255  
QY 124 TKTTTVAVESKDNCKRTEVKIGAKTSYIKEDGKLVTKDKGENGSTDEEGELVTAKEV 183  
DB 256 TKTTTVAVESKDNCKRTEVKIGAKTSYIKEDGKLVTKDKGENGSTDEEGELVTAKEV 315  
QY 184 IDAVNKAQWRRKTTTANGOTGOADKFETVTSCTNVTFAASGKTATVSKDDOGNITYWYD 243  
DB 316 IDAVNKAQWRRKTTTANGOTGOADKFETVTSCTNVTFAASGKTATVSKDDOGNITYWYD 375  
QY 244 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVNINAGNIEITRN 303  
DB 376 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVNINAGNIEITRN 435  
QY 304 GKNIDITSMTPQSSSVSLGADAPFLSYDGD-ALNVGSKDNKPVRITNVAVGVEGD 362  
DB 436 GKNIDITSMTPQSSSVSLGADAPFLSYDDEGALNVGSKDNKPVRITNVAVGVEGD 495  
QY 363 VTNYAOLKGYAQNINNHIDNVGNARAGIAQAIATAGIYQAYLPKGSMAIIGGCTYRGEA 422  
DB 496 VTNYAOLKGYAQNINNHIDNVGNARAGIAQAIATAGIYQAYLPKGSMAIIGGCTYRGEA 555  
QY 423 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 461  
DB 556 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 10  
US-09-771-382-4  
; Sequence 4, Application US/09771382  
; Patent No. US2002010016A1  
; GENERAL INFORMATION:  
; APPLICANT: Peak, Ian  
; APPLICANT: Jennings, Michael  
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN  
; FILE REFERENCE: 8795-2401  
; CURRENT APPLICATION NUMBER: US/09/771,382  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/177,917  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patentln version 3.0

; SEQ ID NO 4  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-771-382-4

Query Match 96.2%; Score 2260.5; DB 10; Length 594;  
Best Local Similarity 97.4%; Pred. No. 5e-168;  
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVHLNGISGTLTDLTLNT 63  
DB 136 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVHLNGISGTLTDLTLNT 195  
QY 64 GATTNVTNDVNTDDEKRRASVSKVDVLNAGNNIKGVKPGTTASDNDVDFRYDVEFLSAD 123  
DB 196 GATTNVTNDVNTDDEKRRASVSKVDVLNAGNNIKGVKPGTTASDNDVDFRYDVEFLSAD 255  
QY 124 TKTTTVAVESKDNCKRTEVKIGAKTSYIKEDGKLVTKDKGENGSTDEEGELVTAKEV 183  
DB 256 TKTTTVAVESKDNCKRTEVKIGAKTSYIKEDGKLVTKDKGENGSTDEEGELVTAKEV 315  
QY 184 IDAVNKAQWRRKTTTANGOTGOADKFETVTSCTNVTFAASGKTATVSKDDOGNITYWYD 243  
DB 316 IDAVNKAQWRRKTTTANGOTGOADKFETVTSCTNVTFAASGKTATVSKDDOGNITYWYD 375  
QY 244 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVNINAGNIEITRN 303  
DB 376 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVNINAGNIEITRN 435  
QY 304 GKNIDITSMTPQSSSVSLGADAPFLSYDGD-ALNVGSKDNKPVRITNVAVGVEGD 362  
DB 436 GKNIDITSMTPQSSSVSLGADAPFLSYDDEGALNVGSKDNKPVRITNVAVGVEGD 495  
QY 363 VTNYAOLKGYAQNINNHIDNVGNARAGIAQAIATAGIYQAYLPKGSMAIIGGCTYRGEA 422  
DB 496 VTNYAOLKGYAQNINNHIDNVGNARAGIAQAIATAGIYQAYLPKGSMAIIGGCTYRGEA 555  
QY 423 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 461  
DB 556 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 11  
US-09-797-862-15  
; Sequence 15, Application US/09797862  
; Patent No. US20020102276A1  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, IAN RICHARD ANSELM  
; APPLICANT: JENNINGS, MICHAEL PAUL  
; APPLICANT: MOXON, E. RICHARD  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0134  
; CURRENT APPLICATION NUMBER: US/09/797,862  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-797-862-15

Query Match 96.1%; Score 2257.5; DB 10; Length 599;  
Best Local Similarity 97.4%; Pred. No. 8.6e-168;  
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;  
QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVHLNGISGTLTDLTLNT 63  
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Db 141 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLLNT 200
Qy 64 GATTNVTNDNTDDEKKRAASVKDYVLNAGMNKGVKPGTTASDNVDFVTTYDVEFLSAD 123
Db 201 GATTNVTNDNTDDEKKRAASVKDYVLNAGMNKGVKPGTTASDNVDFVTTYDVEFLSAD 260
Qy 124 TTTTIVNESKNGKRTVEKIGAKTSVLEKEDKLVTKGDKENSSSTDEGGLVYAKEV 183
Db 261 TTTTIVNESKNGKRTVEKIGAKTSVLEKEDKLVTKGDKENSSSTDEGGLVYAKEV 320
Qy 184 IDAVKAGRMKMTTANAGOTGOADKFEVYTSCTNTVTFASGKGTATVSKDDGNTIVMD 243
Db 321 IDAVKAGRMKMTTANAGOTGOADKFEVYTSCTNTVTFASGKGTATVSKDDGNTIVMD 380
Qy 244 VNVGALNVNOLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 303
Db 381 VNVGALNVNOLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 440
Qy 304 GKNIDIASMTPOFSSVSLGAGADAPTLSDG-DALNVSKKDNKPVRTTNPAPGVKEGD 362
Db 441 GKNIDIASMTPOFSSVSLGAGADAPTLSDGKALNVSCKDNKPVRTTNPAPGVKEGD 500
Qy 363 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVQAVLPGKSMAIGGTYRGEA 422
Db 501 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVQAVLPGKSMAIGGTYRGEA 560
Qy 423 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 461
Db 561 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 599
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## RESULT 12

```
US-09-771-382-6
; Sequence 6, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; TITLE OF INVENTION: Jemmings, Michael
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-771-382-6
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Query Match 96.1%; Score 2257.5; DB 10; Length 599;
Best Local Similarity 97.4%; Pred. No. 8.6e-168;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
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Qy 4 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLLNT 63
Db 141 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLLNT 200
Qy 64 GATTNVTNDNTDDEKKRAASVKDYVLNAGMNKGVKPGTTASDNVDFVTTYDVEFLSAD 123
Db 201 GATTNVTNDNTDDEKKRAASVKDYVLNAGMNKGVKPGTTASDNVDFVTTYDVEFLSAD 260
Qy 124 TTTTIVNESKNGKRTVEKIGAKTSVLEKEDKLVTKGDKENSSSTDEGGLVYAKEV 183
Db 261 TTTTIVNESKNGKRTVEKIGAKTSVLEKEDKLVTKGDKENSSSTDEGGLVYAKEV 320
Qy 184 IDAVKAGRMKMTTANAGOTGOADKFEVYTSCTNTVTFASGKGTATVSKDDGNTIVMD 243
Db 321 IDAVKAGRMKMTTANAGOTGOADKFEVYTSCTNTVTFASGKGTATVSKDDGNTIVMD 380
Qy 244 VNVGALNVNOLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 303
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Db 381 VNVGALNVNOLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 440
Qy 304 GKNIDIASMTPOFSSVSLGAGADAPTLSDG-DALNVSCKDNKPVRTTNPAPGVKEGD 362
Db 441 GKNIDIASMTPOFSSVSLGAGADAPTLSDGKALNVSCKDNKPVRTTNPAPGVKEGD 500
Qy 363 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVQAVLPGKSMAIGGTYRGEA 422
Db 501 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVQAVLPGKSMAIGGTYRGEA 560
Qy 423 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 461
Db 561 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 599
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## RESULT 13

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US-09-797-862-7
; Sequence 7, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-7
```

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Query Match 95.7%; Score 2248.5; DB 10; Length 594;
Best Local Similarity 97.2%; Pred. No. 4.3e-167;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;
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Qy 4 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLLNT 63
Db 136 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLLNT 195
Qy 64 GATTNVTNDNTDDEKKRAASVKDYVLNAGMNKGVKPGTTASDNVDFVTTYDVEFLSAD 123
Db 196 GATTNVTNDNTDDEKKRAASVKDYVLNAGMNKGVKPGTTASDNVDFVTTYDVEFLSAD 255
Qy 124 TTTTIVNESKNGKRTVEKIGAKTSVLEKEDKLVTKGDKENSSSTDEGGLVYAKEV 183
Db 256 TTTTIVNESKNGKRTVEKIGAKTSVLEKEDKLVTKGDKENSSSTDEGGLVYAKEV 315
Qy 184 IDAVKAGRMKMTTANAGOTGOADKFEVYTSCTNTVTFASGKGTATVSKDDGNTIVMD 243
Db 316 IDAVKAGRMKMTTANAGOTGOADKFEVYTSCTNTVTFASGKGTATVSKDDGNTIVMD 375
Qy 244 VNVGALNVNOLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 303
Db 376 VNVGALNVNOLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 435
Qy 304 GKNIDIASMTPOFSSVSLGAGADAPTLSDG-DALNVSCKDNKPVRTTNPAPGVKEGD 362
Db 436 GKNIDIASMTPOFSSVSLGAGADAPTLSDGKALNVSCKDNKPVRTTNPAPGVKEGD 495
Qy 363 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVQAVLPGKSMAIGGTYRGEA 422
Db 496 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVQAVLPGKSMAIGGTYRGEA 555
Qy 423 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 461
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Db 556 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

# RESULT 14

US-09-771-382-9  
 ; Sequence 9, Application US/09771382  
 ; Patent No. US20020160016A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Peak, Ian  
 ; APPLICANT: Jennings, Michael  
 ; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN  
 ; FILE REFERENCE: 8795-2401  
 ; CURRENT APPLICATION NUMBER: US/09/771,382  
 ; CURRENT FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: US 60/177,917  
 ; PRIOR FILING DATE: 2000-01-25  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 594  
 ; TYPE: PRP  
 ; ORGANISM: Neisseria meningitidis  
 US-09-771-382-9

Query Match 95.7%; Score 2248.5; DB 10; Length 594;

Best Local Similarity 97.2%; Pred. No. 4.3e-167;  
 Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 63  
 DB 136 TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 195  
 QY 64 GATTNTNDNVTDDEKRRASVADVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 123  
 DB 196 GATTNTNDNVTDDEKRRASVADVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 255  
 QY 124 TTTTNNVSKDNGKRTVEKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 183  
 DB 256 TTTTNNVSKDNGKRTVEKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 315  
 QY 184 IDAVNAGWRMKTTTANGOTGQADKFEVTSCTNVTFAFGKGTATVSKDDGNTVMYD 243  
 DB 316 IDAVNAGWRMKTTTANGOTGQADKFEVTSCTNVTFAFGKGTATVSKDDGNTVMYD 375  
 QY 244 VNVGDLNNOLONSGMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303  
 DB 376 VNVGDLNNOLONSGMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 435  
 QY 304 GKNIDATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVGSKDNKPVRTITNAPGYKEG 362  
 DB 436 GKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDNKPVRTITNAPGYKEG 495  
 QY 363 VTNVAQLKGVQNLNRRIDNVGNARAGIAQALATAGLVQAYLPGKSMAIGGTYRGEA 422  
 DB 496 VTNVAQLKGVQNLNRRIDNVGNARAGIAQALATAGLVQAYLPGKSMAIGGTYRGEA 555  
 QY 423 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461  
 DB 556 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

# RESULT 15

US-09-797-862-5  
 ; Sequence 5, Application US/09797862  
 ; Patent No. US20020102276A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, IAN RICHARD ANSELM  
 ; APPLICANT: JENNINGS, MICHAEL PAUL  
 ; APPLICANT: MOXON, E. RICHARD  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0134  
 ; CURRENT APPLICATION NUMBER: US/09/797,862

; CURRENT FILING DATE: 2001-05-03  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 598  
 ; TYPE: PRP  
 ; ORGANISM: Neisseria meningitidis  
 US-09-797-862-5

Query Match 95.1%; Score 2235.5; DB 10; Length 598;

Best Local Similarity 96.3%; Pred. No. 4.5e-166;  
 Matches 442; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 63  
 DB 140 TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 199  
 QY 64 GATTNTNDNVTDDEKRRASVADVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 123  
 DB 200 GATTNTNDNVTDDEKRRASVADVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 259  
 QY 124 TTTTNNVSKDNGKRTVEKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 183  
 DB 260 TTTTNNVSKDNGKRTVEKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 319  
 QY 184 IDAVNAGWRMKTTTANGOTGQADKFEVTSCTNVTFAFGKGTATVSKDDGNTVMYD 243  
 DB 320 IDAVNAGWRMKTTTANGOTGQADKFEVTSCTNVTFAFGKGTATVSKDDGNTVMYD 379  
 QY 244 VNVGDLNNOLONSGMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303  
 DB 380 VNVGDLNNOLONSGMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 439  
 QY 304 GKNIDATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVGSKDNKPVRTITNAPGYKEG 362  
 DB 440 GKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDNKPVRTITNAPGYKEG 499  
 QY 363 VTNVAQLKGVQNLNRRIDNVGNARAGIAQALATAGLVQAYLPGKSMAIGGTYRGEA 422  
 DB 500 VTNVAQLKGVQNLNRRIDNVGNARAGIAQALATAGLVQAYLPGKSMAIGGTYRGEA 559  
 QY 423 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461  
 DB 560 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 33.8588 Seconds  
(without alignments)  
3513.485 Million cell updates/sec

Title: US-09-771-382-35  
Perfect score: 2350  
Sequence: 1 NNETDLTSGTEKLSFSANG.....TASGNSRGHFGASASVGYQW 461

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
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2	2333	99.3	591	09JPS7	09jps7 neisseria m
3	2333	99.3	591	09JRI8	09jri8 neisseria m
4	2329	99.1	592	09AOF0	09afo0 neisseria m
5	2296	97.7	526	09JPS4	09jps4 neisseria m
6	2296	97.7	530	09JPS1	09jps1 neisseria m
7	2291	97.5	600	09JPS6	09jps6 neisseria m
8	2281.5	97.1	590	09JPS3	09jps3 neisseria m
9	2260.5	96.2	594	0930Y4	093qy4 neisseria m
10	2257.5	96.1	594	09JPI3	09jpi3 neisseria m
11	2257.5	96.1	594	09JPS2	09jps2 neisseria m
12	2248.5	95.7	594	09JPH8	09jph8 neisseria m
13	2248.5	95.7	594	09JPH7	09jph7 neisseria m
14	2241.5	95.4	592	09JPS9	09jps9 neisseria m
15	2241.5	95.4	592	09JPS0	09jps0 neisseria m
16	2235.5	95.1	598	09JPS0	09jps0 neisseria m

17	2235.5	95.1	598	2	0930Y5	093qy5 neisseria m
18	2235.5	95.1	598	2	09JPT0	09jpt0 neisseria m
19	2207.5	93.9	592	2	0930Y2	093qy2 neisseria m
20	2123.5	90.4	598	2	09JPS8	09jps8 neisseria m
21	2117.5	90.1	598	2	09JPR7	09jpr7 neisseria m
22	2115.5	90.0	595	2	09JPH0	09jph0 neisseria m
23	2089.5	88.9	592	16	09JQW4	09jqw4 neisseria m
24	2081.5	88.6	589	2	09JPI0	09jpi0 neisseria m
25	2075.5	88.3	600	2	09JPS5	09jps5 neisseria m
26	2069.5	88.1	589	2	0930Y1	093qy1 neisseria m
27	901.5	38.4	2353	2	P71401	P71401 haemophilus
28	874	37.2	1098	2	048152	048152 haemophilus
29	868.5	37.0	1096	2	08GM79	08gm79 haemophilus
30	844.5	35.9	1210	2	08GM74	08gm74 haemophilus
31	836.5	35.6	1210	2	08GM75	08gm75 haemophilus
32	835.5	35.6	1204	2	08GM76	08gm76 haemophilus
33	563	24.0	1002	2	08GM78	08gm78 haemophilus
34	561	23.9	1004	2	08GM77	08gm77 haemophilus
35	405	17.2	1299	16	09FX36	09fx36 pasteurella
36	381.5	16.2	2314	2	08KQW8	08kqw8 moraxella c
37	375.5	16.0	2059	16	09PD50	09pd50 xylella fas
38	365	15.5	1588	16	08XD64	08xd64 escherichia
39	360.5	15.3	1190	16	09PC04	09pc04 xylella fas
40	359	15.3	1461	16	08ZL64	08zl64 salmoneilla
41	357	15.2	1107	16	09F2D8	09f2d8 salmoneilla
42	350.5	14.9	1778	16	08RCB2	08rcb2 escherichia
43	346.5	14.7	1964	2	08KQW9	08kqw9 moraxella c
44	341	14.5	2712	16	09FX35	09fx35 pasteurella
45	334.5	14.2	688	2	08RQ60	08rq60 actinobacil

#### ALIGNMENTS

RESULT 1	ID	0930Y3	PRELIMINARY;	PRT;	591 AA.
0930Y3	AC	0930Y3;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)			
DE	NHh outer membrane protein.				
GN	NHhA.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SRRAIN-EG329;				
RA	Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;				
RT	"Identification and characterization of a gene encoding a novel outer				
RT	membrane protein of Neisseria meningitidis."				
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF157606; AAK68867.1; -				
DR	InterPro: IPR005594; Yada.				
DR	Pfam: PF03895; Yada; 1.				
SQ	SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;				
Query Match	99.3%; Score 2333; DB 2; Length 591;				
Best Local Similarity	100.0%; Pred. No. 7.2e-94;				
Matches	458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	4	TDLTSGTEKLSFANGKVNITSPTKGLNFAKETAGTNGDTTVHLNGISLTLDTLANT	63		
DB	134	TDLTSGTEKLSFANGKVNITSPTKGLNFAKETAGTNGDTTVHLNGISLTLDTLANT	193		
OY	64	GATTNTNNDVDEDEKRAASVDVNLAGNINIGVAPGTASNDVDFRYPDVEFLSAD	123		
DB	194	GATTNTNNDVDEDEKRAASVDVNLAGNINIGVAPGTASNDVDFRYPDVEFLSAD	253		
OY	124	TKTTVNVESKDKGKTEVKIGAKTSVIREKDKLVTGKDGKNGSSTDEGEGLVTAKEV	183		

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Db 254 TKTITVNESKDNKKTEVKIGAKTSYKEKDGKLVTKDKGENSSSTDEGEGLTAYKEV 313
QY 184 IDAVKAKGMRKTTTANGOTGOADKEFTVTSCTNTVTFASGKTTATVSKDDOGNTTMYD 243
Db 314 IDAVKAKGMRKTTTANGOTGOADKEFTVTSCTNTVTFASGKTTATVSKDDOGNTTMYD 373
QY 244 VNVGDALVNVOLQNSGMWLDKSAVAGSSGKVIISGVNPSKGMDETVINMAGNNIEITRN 303
Db 374 VNVGDALVNVOLQNSGMWLDKSAVAGSSGKVIISGVNPSKGMDETVINMAGNNIEITRN 433
QY 304 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVDALNVGSKDKNRPVITTNVAPGVKEGDV 363
Db 434 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVDALNVGSKDKNRPVITTNVAPGVKEGDV 493
QY 364 TNVAOLKGVAAQNLNRINDVGNARAGIAQAATAGLVQAVLPGKSMAIGGGTYRGAG 423
Db 494 TNVAOLKGVAAQNLNRINDVGNARAGIAQAATAGLVQAVLPGKSMAIGGGTYRGAG 553
QY 424 YAIQYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 461
Db 554 YAIQYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

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## RESULT 2

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ID Q9JPS7 PRELIMINARY: PRT: 591 AA.
AC Q9JPS7:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -.
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; Yada: 1.
SQ SEQUENCE 591 AA: 62113 MW: 533453CAE5A91EIF CRC64:

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Query Match 99.3%; Score 2333; DB 2; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-94;  
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 TDLTNSVGTSEKLSFSAANGKVNITSDPKGLNFAKKTAGTNGDTYVNLNGISTLTPTLLNT 63
Db 134 TDLTNSVGTSEKLSFSAANGKVNITSDPKGLNFAKKTAGTNGDTYVNLNGISTLTPTLLNT 193
QY 64 GATTNVTNDNTYDDEKRRASVYKVDLNAAGNINIKGVKPGTTASDNDVFTYDTPVELSAD 123
Db 194 GATTNVTNDNTYDDEKRRASVYKVDLNAAGNINIKGVKPGTTASDNDVFTYDTPVELSAD 253
QY 124 TKTITVNESKDNKKTEVKIGAKTSYKEKDGKLVTKDKGENSSSTDEGEGLTAYKEV 183
Db 254 TKTITVNESKDNKKTEVKIGAKTSYKEKDGKLVTKDKGENSSSTDEGEGLTAYKEV 313
QY 184 IDAVKAKGMRKTTTANGOTGOADKEFTVTSCTNTVTFASGKTTATVSKDDOGNTTMYD 243

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Db 314 IDAVKAKGMRKTTTANGOTGOADKEFTVTSCTNTVTFASGKTTATVSKDDOGNTTMYD 373
QY 244 VNVGDALVNVOLQNSGMWLDKSAVAGSSGKVIISGVNPSKGMDETVINMAGNNIEITRN 303
Db 374 VNVGDALVNVOLQNSGMWLDKSAVAGSSGKVIISGVNPSKGMDETVINMAGNNIEITRN 433
QY 304 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVDALNVGSKDKNRPVITTNVAPGVKEGDV 363
Db 434 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVDALNVGSKDKNRPVITTNVAPGVKEGDV 493
QY 364 TNVAOLKGVAAQNLNRINDVGNARAGIAQAATAGLVQAVLPGKSMAIGGGTYRGAG 423
Db 494 TNVAOLKGVAAQNLNRINDVGNARAGIAQAATAGLVQAVLPGKSMAIGGGTYRGAG 553
QY 424 YAIQYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 461
Db 554 YAIQYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

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## RESULT 3

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ID Q9JRI8 PRELIMINARY: PRT: 591 AA.
AC Q9JRI8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992 (Adhesin) (Nhaa outer membrane
DE protein).
GN GMA992 OR NMB0992 OR NHAH.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / Serogroup B, B2169, B283, and H44/76;
RX MEDLINE=20175755; PubMed=10710307;
RA Pizze M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khoui H., Qin H., Yamathevan J.,
RA Gill J., Scarlato V., Masiagnani V., Pizze M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).

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RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF226375; AAF42524.1; -.
DR EMBL: AF226375; AAF42524.1; -.
DR EMBL: AF226367; AAF42516.1; -.

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DR EMBL: AF226367; AAF42516.1; -.

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Db 69 TDLTSVEFEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNIGSTLIDTLLNT 128
Qy 64 GATTNVTNDNTDDEKKRAASVKDYLNAGWNIGVKPGCTASDNDVFEVRYTDVFEELSAD 123
Db 129 GATTNVTNDNTDDEKKRAASVKDYLNAGWNIGVKPGCTASDNDVFEVRYTDVFEELSAD 188
Qy 124 TKTITVNVESKDNKGKTEVKIGAKTSVKEKDGLVTKGKGNGSSSTDEBEGGLTAYEV 183
Db 189 TKTITVNVESKDNKGKTEVKIGAKTSVKEKDGLVTKGKGNGSSSTDEBEGGLTAYEV 248
Qy 184 IDAVKAKGRMKTTTANGOTGADKEFTVTSNTVTFASGKGTATVASKDOGNITVYD 243
Db 249 IDAVKAKGRMKTTTANGOTGADKEFTVTSNTVTFASGKGTATVASKDOGNITVYD 308
Qy 244 VNVGDALVNOLONSGWNLDKRAVAGSSGKVIISGNVSPSKGMDTVINAGNNIEITRN 303
Db 309 VNVGDALVNOLONSGWNLDKRAVAGSSGKVIISGNVSPSKGMDTVINAGNNIEITRN 368
Qy 304 GKNIDIATSMTPPOSSSVSLGAGADAPLTLSVGDALNVSSKDKNRPVRTITNAPGVKEGDV 363
Db 369 GKNIDIATSMTPPOSSSVSLGAGADAPLTLSVGDALNVSSKDKNRPVRTITNAPGVKEGDV 428
Qy 364 TNVAOLKGVAAONLNRRIDNVGDNARAGIAOAIAATGAVOAYLPCKSMMAIGGGTYRGEGAG 423
Db 429 TNVAOLKGVAAONLNRRIDNVGDNARAGIAOAIAATGAVOAYLPCKSMMAIGGGTYRGEGAG 488
Qy 424 YAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYOM 461
Db 489 YAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYOM 526
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## RESULT 6

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QJPS1 PRELIMINARY: PRT; 530 AA.
AC 09JPS1: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;
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Query Match 97.7%; Score 2296; DB 2; Length 530;  
Best Local Similarity 98.5%; Pred. No. 2.6e-92;  
Matches 451; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Qy 4 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNIGSTLIDTLLNT 63
Db 73 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNIGSTLIDTLLNT 132
Qy 64 GATTNVTNDNTDDEKKRAASVKDYLNAGWNIGVKPGCTASDNDVFEVRYTDVFEELSAD 123
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Db 133 GATTNVTNDNTDDEKKRAASVKDYLNAGWNIGVKPGCTASDNDVFEVRYTDVFEELSAD 192
Qy 124 TKTITVNVESKDNKGKTEVKIGAKTSVKEKDGLVTKGKGNGSSSTDEBEGGLTAYEV 183
Db 193 TKTITVNVESKDNKGKTEVKIGAKTSVKEKDGLVTKGKGNGSSSTDEBEGGLTAYEV 252
Qy 184 IDAVKAKGRMKTTTANGOTGADKEFTVTSNTVTFASGKGTATVASKDOGNITVYD 243
Db 253 IDAVKAKGRMKTTTANGOTGADKEFTVTSNTVTFASGKGTATVASKDOGNITVYD 312
Qy 244 VNVGDALVNOLONSGWNLDKRAVAGSSGKVIISGNVSPSKGMDTVINAGNNIEITRN 303
Db 313 VNVGDALVNOLONSGWNLDKRAVAGSSGKVIISGNVSPSKGMDTVINAGNNIEITRN 372
Qy 304 GKNIDIATSMTPPOSSSVSLGAGADAPLTLSVGDALNVSSKDKNRPVRTITNAPGVKEGDV 363
Db 373 GKNIDIATSMTPPOSSSVSLGAGADAPLTLSVGDALNVSSKDKNRPVRTITNAPGVKEGDV 432
Qy 364 TNVAOLKGVAAONLNRRIDNVGDNARAGIAOAIAATGAVOAYLPCKSMMAIGGGTYRGEGAG 423
Db 433 TNVAOLKGVAAONLNRRIDNVGDNARAGIAOAIAATGAVOAYLPCKSMMAIGGGTYRGEGAG 492
Qy 424 YAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYOM 461
Db 493 YAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYOM 530
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## RESULT 7

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QJPS6 PRELIMINARY: PRT; 600 AA.
AC 09JPS6: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;
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Query Match 97.5%; Score 2291; DB 2; Length 600;  
Best Local Similarity 98.5%; Pred. No. 4.9e-92;  
Matches 451; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 4 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNIGSTLIDTLLNT 63
Db 143 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNIGSTLIDTLLNT 202
Qy 64 GATTNVTNDNTDDEKKRAASVKDYLNAGWNIGVKPGCTASDNDVFEVRYTDVFEELSAD 123
Db 203 GATTNVTNDNTDDEKKRAASVKDYLNAGWNIGVKPGCTASDNDVFEVRYTDVFEELSAD 262
Qy 124 TKTITVNVESKDNKGKTEVKIGAKTSVKEKDGLVTKGKGNGSSSTDEBEGGLTAYEV 183
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Db 263 TKTITTVNESKDNKGTTEVIGAKTSYIKKEKDKLVTGKGNGSGSTDEEGGLVTAKEV 322
QY 184 IDAVNKGWRRKTTTANGOTGOADKFETVTSCTVWTFASGKGTATYASKDOGNITWYD 243
Db 323 IDAVNKGWRRKTTTANGOGQADKFETVTSCTVWTFASGKGTATYASKDOGNITWYD 382
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVTSGSNVSPSKGKMDETVINAGNNIETRN 303
Db 383 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVTSGSNVSPSKGKMDETVINAGNNIETRN 442
QY 304 GKNDIATSMTPQPSVSLGAGADAPLTVSDGALNVGSKKDKNKPVRITVAVPGVKEGDV 363
Db 443 GKNDIATSMTPQPSVSLGAGADAPLTVSDGALNVGSKKDKNKPVRITVAVPGVKEGDV 502
QY 364 TVNAQLKGVANLNNRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 423
Db 503 TVNAQLKGVANLNNRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 562
QY 424 YAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 461
Db 563 YAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 600

RESULT 8
Q9JPS3 PRELIMINARY: PRT: 590 AA.
ID 09JPS3 AC 09JPS3
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Piazza M., Scarlito V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanucci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL EMBL: AF226378; AAF42527.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 97.1%; Score 2281.5; DB 2; Length 590;
Best Local Similarity 98.3%; Pred. No. 1.2e-91;
Matches 451; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
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Db 312 IDAVNKGWRRKTTTANGOTGOADKFETVTSCTVWTFASGKGTATYASKDOGNITWYD 371
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVTSGSNVSPSKGKMDETVINAGNNIETRN 303
Db 372 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVTSGSNVSPSKGKMDETVINAGNNIETRN 431
QY 304 GKNDIATSMTPQPSVSLGAGADAPLTVSDG-ALNVGSKKDKNKPVRITVAVPGVEGD 362
Db 432 GKNDIATSMTPQPSVSLGAGADAPLTVSDGEBALNVGSKDANKPVRITVAVPGVEGD 491
QY 363 VTNVAQLKGVANLNNRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 422
Db 492 VTNVAQLKGVANLNNRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 551
QY 423 GYAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 461
Db 552 GYAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 590

RESULT 9
Q93QY4 PRELIMINARY: PRT: 594 AA.
ID 093QY4 AC 093QY4
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Nha outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 594 AA; 62297 MW; 9DD448B04B3A8EA2 CRC64;

Query Match 96.2%; Score 2260.5; DB 2; Length 594;
Best Local Similarity 97.4%; Pred. No. 1e-90;
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
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Db 496 VTNVAQLGVAGNQLNNHIDNDVGNARAGIAQAIAATAGLVOAALPCKSMMAIGGTYRGEA 555
QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 594

RESULT 10
ID 09JPI3 PRELIMINARY; PRT: 594 AA.
AC 09JPI3: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92.
GN GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and B2232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -.
DR EMBL: AF226369; AAF42518.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 96.1%; Score 2257.5; DB 2; Length 594;
Best Local Similarity 97.4%; Pred. No. 1.4e-90;
Matches 447; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSGANGKKNVITSDTKGNLFAKKTAGTNGDTTVHLNGIGSTLTPTLLNT 63
Db 136 TDLTSEVEREKLSFGANGKKNVITSDTKGNLFAKKTAGTNGDTTVHLNGIGSTLTPTLLNT 195
QY 64 GATTNVTNDNVTDDKKRRAASVYKDVNLNAGWNIGVYKPGTTASDNDVFTYDTVEFLSAD 123
Db 196 GATTNVTNDNVTDDKKRRAASVYKDVNLNAGWNIGVYKPGTTASDNDVFTYDTVEFLSAD 255
QY 124 TKTTVNVESKDKNGKRTVEKIGAKTSVIREKDKLVTKGDKGENSSSTDEGEGLVTAKEV 183
Db 256 TKTTVNVESKDKNGKRTVEKIGAKTSVIREKDKLVTKGDKGENSSSTDEGEGLVTAKEV 315
QY 184 IDAVKAKGRMKTATTANGOTGADKFEFVTSCTNTTFASGKTATVSKDDOGNTVYAD 243
Db 316 IDAVKAKGRMKTATTANGOTGADKFEFVTSCTNTTFASGKTATVSKDDOGNTVYAD 375
QY 244 VNVGDALVNNOLONGSNMIDSKAIVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 303
Db 376 VNVGDALVNNOLONGSNMIDSKAIVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 435
QY 304 GNKIDIASMTPOFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 362
Db 436 GNKIDIASMTPOFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 495
QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 VTNVAQLGVAGNQLNNHIDNDVGNARAGIAQAIAATAGLVOAALPCKSMMAIGGTYRGEA 555
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QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 594

RESULT 11
ID 09JPS2 PRELIMINARY; PRT: 594 AA.
AC 09JPS2: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92.
GN GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 96.1%; Score 2257.5; DB 2; Length 594;
Best Local Similarity 97.4%; Pred. No. 1.4e-90;
Matches 447; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSGANGKKNVITSDTKGNLFAKKTAGTNGDTTVHLNGIGSTLTPTLLNT 63
Db 136 TDLTSEVEREKLSFGANGKKNVITSDTKGNLFAKKTAGTNGDTTVHLNGIGSTLTPTLLNT 195
QY 64 GATTNVTNDNVTDDKKRRAASVYKDVNLNAGWNIGVYKPGTTASDNDVFTYDTVEFLSAD 123
Db 196 GATTNVTNDNVTDDKKRRAASVYKDVNLNAGWNIGVYKPGTTASDNDVFTYDTVEFLSAD 255
QY 124 TKTTVNVESKDKNGKRTVEKIGAKTSVIREKDKLVTKGDKGENSSSTDEGEGLVTAKEV 183
Db 256 TKTTVNVESKDKNGKRTVEKIGAKTSVIREKDKLVTKGDKGENSSSTDEGEGLVTAKEV 315
QY 184 IDAVKAKGRMKTATTANGOTGADKFEFVTSCTNTTFASGKTATVSKDDOGNTVYAD 243
Db 316 IDAVKAKGRMKTATTANGOTGADKFEFVTSCTNTTFASGKTATVSKDDOGNTVYAD 375
QY 244 VNVGDALVNNOLONGSNMIDSKAIVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 303
Db 376 VNVGDALVNNOLONGSNMIDSKAIVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 435
QY 304 GNKIDIASMTPOFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 362
Db 436 GNKIDIASMTPOFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 495
QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 594
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RESULT 12
Q9JPR8 PRELIMINARY; PRT; 599 AA.
AC Q9JPR8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Masiagnan V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16BFF53C1970C CRC64;

Query Match 96.1%; Score 2257.5; DB 2; Length 599;
Best Local Similarity 97.4%; Pred. No. 1.4e-90;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSGANGKYNITSDPKGLNPAKETAAGNDTTHVHLNGISLTLDLLNT 63
DB 141 TDLTSGTEKLSFGANGKNVNTSDTKGLNPAKETAAGNDTTHVHLNGISLTLDLLNT 200
QY 64 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTTASDNVDVFRYDVEFLSAD 123
DB 201 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTTASDNVDVFRYDVEFLSAD 260
QY 124 TKTTTVNESKDKNGKTEVKGAKTSYIKERDGLVYTKDGENGSTDEEGELVTAKEV 183
DB 261 TKTTTVNESKDKNGKTEVKGAKTSYIKERDGLVYTKDGENGSTDEEGELVTAKEV 320
QY 184 IDAVNKGWEMKTTTANGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYMD 243
DB 321 IDAVNKGWEMKTTTANGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYMD 380
QY 244 VNVGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSPSKGKDEYNINAGNNEIETRN 303
DB 381 VNVGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSPSKGKDEYNINAGNNEIETRN 440
QY 304 GKNDIATSMTPQFSSVSLGAGADAPTLSDVG--DALNVGSKDKKPKVRIITNVAAGVEGD 362
DB 441 GKNDIATSMTPQFSSVSLGAGADAPTLSDVG--DALNVGSKDKKPKVRIITNVAAGVEGD 500
QY 363 VTNVAOLKGYAONLNNRIDVNDGNARAGIAQAIATAGLVAAYLPGRKSMALIGGTATYGEA 422
DB 501 VTNVAOLKGYAONLNNRIDVNDGNARAGIAQAIATAGLVAAYLPGRKSMALIGGTATYGEA 560
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QY 423 GYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461
DB 561 GYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 13
Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198; and 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Masiagnan V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226368; AAF42517.1; -.
DR EMBL: AF226358; AAF42507.1; -.
DR EMBL: AF157604; AAK68865.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 95.7%; Score 2248.5; DB 2; Length 594;
Best Local Similarity 97.2%; Pred. No. 3.4e-90;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSGANGKYNITSDPKGLNPAKETAAGNDTTHVHLNGISLTLDLLNT 63
DB 136 TDLTSGTEKLSFGANGKNVNTSDTKGLNPAKETAAGNDTTHVHLNGISLTLDLLNT 195
QY 64 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTTASDNVDVFRYDVEFLSAD 123
DB 196 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTTASDNVDVFRYDVEFLSAD 255
QY 124 TKTTTVNESKDKNGKTEVKGAKTSYIKERDGLVYTKDGENGSTDEEGELVTAKEV 183
DB 256 TKTTTVNESKDKNGKTEVKGAKTSYIKERDGLVYTKDGENGSTDEEGELVTAKEV 315
QY 184 IDAVNKGWEMKTTTANGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYMD 243
DB 316 IDAVNKGWEMKTTTANGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYMD 375
QY 244 VNVGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSPSKGKDEYNINAGNNEIETRN 303
DB 376 VNVGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSPSKGKDEYNINAGNNEIETRN 435
QY 304 GKNDIATSMTPQFSSVSLGAGADAPTLSDVG--ALNVGSKDKKPKVRIITNVAAGVEGD 362
DB 436 GKNDIATSMTPQFSSVSLGAGADAPTLSDVG--ALNVGSKDKKPKVRIITNVAAGVEGD 495
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OY 363 VTNAQLKGVAQNLRIDNDGNARAGIAQAIAATAGLVOAYLPKSKMAATGGCTYRGEA 422  
 DB 496 VTNAQLKGVAQNLRIDNDGNARAGIAQAIAATAGLVOAYLPKSKMAATGGCTYRGEA 555  
 OY 423 GYALGYSSISDGGNMIITGTASGNSRGHFGASASVGYOM 461  
 DB 556 GYALGYSSISDGGNMIITGTASGNSRGHFGASASVGYOM 594

RESULT 14

O9UPR9 PRELIMINARY: PRT: 598 AA.  
 AC O9UPR9; 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Outer membrane protein GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NGH36;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226382; AAF42531.1; -.  
 DR InterPro: IPR005594; Yada.  
 DR Pfam: PF03895; Yada; 1.  
 SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 95.7%; Score 2248.5; DB 2; Length 598;  
 Best Local Similarity 97.2%; Pred. No. 3.4e-90;  
 Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

OY 4 TDLTSGTEKLSFSGANGKKNVITSDTKGNFAKETAGTNGDTYVHLNIGSTLTDTLLNT 63  
 DB 140 TDLTSGTEKLSFSGANGKKNVITSDTKGNFAKETAGTNGDTYVHLNIGSTLTDTLLNT 199  
 OY 64 GATTNVTNDNTDDEKRAASVKDYLNAGWNIGVKGPGTTASDNDVFRITDYVEFLSAD 123  
 DB 200 GATTNVTNDNTDDEKRAASVKDYLNAGWNIGVKGPGTTASDNDVFRITDYVEFLSAD 259  
 OY 124 TKTITVNESKDNKGTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 183  
 DB 260 TKTITVNESKDNKGTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 319  
 OY 184 IDAVNKAQWRKKTITANGOTGADKFEETVSTNTFASGKTATFVSKDDOGNTIYWD 243  
 DB 320 IDAVNKAQWRKKTITANGOTGADKFEETVSTNTFASGKTATFVSKDDOGNTIYWD 379  
 OY 244 VNVGALVNQNLONGSNWLDKRAVAGSSGKVTSGNVSPSKGMDVTVINAGNNIEIRN 303  
 DB 380 VNVGALVNQNLONGSNWLDKRAVAGSSGKVTSGNVSPSKGMDVTVINAGNNIEIRN 439  
 OY 304 GKNIDIATSMTPQESSVSLGAGADAPTLSVDG -ALNVGSKKDNKPVRTITNAPGVKRGD 362  
 DB 440 GKNIDIATSMTPQESSVSLGAGADAPTLSVDGALNVGSKKDNKPVRTITNAPGVKRGD 499  
 OY 363 VTNAQLKGVAQNLRIDNDGNARAGIAQAIAATAGLVOAYLPKSKMAATGGCTYRGEA 422  
 DB 500 VTNAQLKGVAQNLRIDNDGNARAGIAQAIAATAGLVOAYLPKSKMAATGGCTYRGEA 559

OY 423 GYALGYSSISDGGNMIITGTASGNSRGHFGASASVGYOM 461  
 DB 560 GYALGYSSISDGGNMIITGTASGNSRGHFGASASVGYOM 598

RESULT 15

O9UPR9 PRELIMINARY: PRT: 592 AA.  
 AC O9UPR9; 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Outer membrane protein GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-860800;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226382; AAF42510.1; -.  
 DR InterPro: IPR005594; Yada.  
 DR Pfam: PF03895; Yada; 1.  
 SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FDD3C879 CRC64;

Query Match 95.4%; Score 2241.5; DB 2; Length 592;  
 Best Local Similarity 96.9%; Pred. No. 6.7e-90;  
 Matches 445; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

OY 4 TDLTSGTEKLSFSGANGKKNVITSDTKGNFAKETAGTNGDTYVHLNIGSTLTDTLLNT 63  
 DB 134 TGLIVETEKLSFSGANGKKNVITSDTKGNFAKETAGTNGDTYVHLNIGSTLTDTLLNT 193  
 OY 64 GATTNVTNDNTDDEKRAASVKDYLNAGWNIGVKGPGTTASDNDVFRITDYVEFLSAD 123  
 DB 194 GATTNVTNDNTDDEKRAASVKDYLNAGWNIGVKGPGTTASDNDVFRITDYVEFLSAD 253  
 OY 124 TKTITVNESKDNKGTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 183  
 DB 254 TKTITVNESKDNKGTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 313  
 OY 184 IDAVNKAQWRKKTITANGOTGADKFEETVSTNTFASGKTATFVSKDDOGNTIYWD 243  
 DB 314 IDAVNKAQWRKKTITANGOTGADKFEETVSTNTFASGKTATFVSKDDOGNTIYWD 373  
 OY 244 VNVGALVNQNLONGSNWLDKRAVAGSSGKVTSGNVSPSKGMDVTVINAGNNIEIRN 303  
 DB 374 VNVGALVNQNLONGSNWLDKRAVAGSSGKVTSGNVSPSKGMDVTVINAGNNIEIRN 433  
 OY 304 GKNIDIATSMTPQESSVSLGAGADAPTLSVDG -DALNVGSKKDNKPVRTITNAPGVKRGD 362  
 DB 434 GKNIDIATSMTPQESSVSLGAGADAPTLSVDGKALNVGSKKDNKPVRTITNAPGVKRGD 493  
 OY 363 VTNAQLKGVAQNLRIDNDGNARAGIAQAIAATAGLVOAYLPKSKMAATGGCTYRGEA 422  
 DB 494 VTNAQLKGVAQNLRIDNDGNARAGIAQAIAATAGLVOAYLPKSKMAATGGCTYRGEA 553  
 OY 423 GYALGYSSISDGGNMIITGTASGNSRGHFGASASVGYOM 461  
 DB 554 GYALGYSSISDGGNMIITGTASGNSRGHFGASASVGYOM 592

Mon Oct 6 12:38:52 2003

us-09-771-382-35.rspt

Page 9

Search completed: October 6, 2003, 09:30:50  
Job time : 35.8588 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.11902 Seconds  
(Without alignments)  
3045.266 Million cell updates/sec

Title: US-09-771-382-35

Perfect score: 2350  
Sequence: 1 NNCTDLTSVGTERTKSFSSANG.....TASGNSRGHGASASVGYOM 461

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190.5	8.1	2003	YDBA_ECOLI	P36666 escherichia
2	181.5	7.7	1039	AG43_ECOLI	P39160 escherichia
3	179.5	7.6	2249	OMPA_RICRI	P15921 rickettsia
4	174	7.4	1577	HLVA_PROMI	P16466 proteus mir
5	170.5	7.3	1953	BIGA_SALTY	P25927 salmonella
6	170	7.2	933	SLAP_CAMEE	P35837 campylobact
7	168	7.1	1608	HLVA_SERMA	P15320 serratia ma
8	166.5	7.1	1654	OMPB_RICRI	Q33047 r outer mem
9	166	7.1	1567	ICEN_XANCT	P18127 xanthomonas
10	166	7.1	1655	OMPB_RICCN	Q9K843 r outer mem
11	165.5	7.0	1645	OMPB_RICTY	P36989 r outer mem
12	163.5	7.0	1025	SLAP_CANCR	P35828 caulobacter
13	163.5	7.0	1569	YPUA_ECOLI	P52143 escherichia
14	162	6.9	737	ALYS_ENTFA	P37710 enterococu
15	161.5	6.9	917	HXA3_HAEIN	P45355 haemophilus
16	161.5	6.9	1007	Y741_CHLMU	O9PJ66 chlamydia m
17	161.5	6.9	1656	OMPB_RICJA	O06533 r outer mem
18	161	6.9	550	FLIC_SHEFL	O08860 shigella fl
19	159.5	6.8	1300	120K_RICRI	P14914 rickettsia
20	158.5	6.7	1148	ICEN_PSESX	Q30611 pseudomonas
21	158	6.7	2021	OMPA_RICCN	O52657 rickettsia
22	156	6.6	497	FLIC_ECOLI	P49494 escherichia
23	155.5	6.6	928	PM10_CHLPN	O9R655 chlamydia p
24	155.5	6.6	1286	ALDA_ECOLI	O03135 escherichia
25	154.5	6.6	918	YMOB_CAREL	P34467 caenorhabdi
26	153.5	6.5	2660	YEBJ_ECO57	O8X877 escherichia
27	152.5	6.5	1196	ICEV_PSESX	O33479 pseudomonas
28	152	6.5	1643	OMPB_RICPR	O53020 r outer mem
29	151	6.4	642	FLIC_CAMEE	O09P66 campylobact
30	150.5	6.4	507	FLIC_SALON	O06974 salmonella
31	150.5	6.4	537	TEEB_STRPY	P18481 streptococ
32	150.5	6.4	954	FLRY_CANCR	P15345 caulobacter
33	149	6.3	367	FLC2_PROMI	P42273 proteus mir

34	149	6.3	928	HXA2_HAEIN	P45354 haemophilus
35	149	6.3	948	HP11_DEIRA	P56867 deinococcus
36	148.5	6.3	507	FLIC_SALBE	O06968 salmonella
37	148.5	6.3	1396	VLTE_BPR5	P13390 bacterioph
38	148.5	6.3	2358	1YEBJ_ECOLI	P76347 escherichia
39	148	6.3	1325	YDEK_ECOLI	P32051 escherichia
40	147.5	6.3	1036	HP12_DEIRA	P13126 deinococcus
41	147.5	6.3	1200	ICEN_PSESY	P06620 pseudomonas
42	147	6.3	1005	Y456_CHLTR	O84462 chlamydia t
43	146.5	6.2	1150	APMU_PIG	P12021 sus scrofa
44	146.5	6.2	1153	PVDB_PLAKN	P50493 plasmodium
45	146.5	6.2	1210	ICEN_PSEFL	P09815 pseudomonas

## ALIGNMENTS

```

RESULT 1
YDBA_ECOLI          STANDARD:      PRT: 2003 AA.
ID YDBA_ECOLI
AC P36666: P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; Pubmed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; Pubmed=9097039;
RA Albal H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kaba H., Kashimoto K., Kimura S., Kitkawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; Pubmed=1665988;
RA Moszer I., Glasner P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S.TYPHIMURUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. THE GENE CODING FOR
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
BETWEEN AMINO ACIDS 839 AND 840.
-----
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CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR Ecocore; EG11307; ydBA.
KM Hypothetical protein; Complete proteome.
FT CONFLICT 489 I -> V (IN REF. 2).
FT CONFLICT 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12CB853220EE CRC64;

Query Match      8.1%; Score 190.5; DB 1; Length 2003;
Best Local Similarity 24.0%; Pred. No. 0.016;
Matches 135; Conservative 66; Mismatches 201; Indels 160; Gaps 31;

QY 1 NNETDITSVCTEKLSSANGKNVNTSDTKGLNFAKETAGTNGDTVHLNG-----IG 53
DB 276 DNKGTTVTDPSMGIOIDGKAIVNNE-----GESTTNGTGTQINGDQATANNNG 328
QY 54 STLTDLTLTGATNTYNTDNTDEKKRAASVADVYNAGMNKGVKPGTTASDNVDFERT 113
DB 329 KTVYDGDSDTGTREINNNKVIOD-----GDLDSGGGHGI-DITGDSATVYDNKGTMY 381
QY 114 YDTVEF-LSADRTTTVNVEESKD-----NGKTEVKIGAKTSVKEKDKLVTG 161
DB 382 TDPESIGIQVDGQAVVNNEGESALTNGGTGQINGDDATANNNGKTV---DGKDSYG 437
QY 162 KD-KGNG-----STDEEGELVTAKE-----VIDA-----VN 188
DB 438 TELAGNNGKVIODGDLDVSGGGHIDITGDSATVDKGTMYTVDPSIGIQIDGQAIYN 497
QY 189 KAGWRKTTTANGOTGOADKFEVTSGLNTVFASGKGTATVYSKD-----CGNITVMD 243
DB 498 NGG---ESTITNGCTG-----TQINGNAT-ANNNGKTVYDGDSDTGTGKINIGI---- 544
QY 244 VNVGDALNV-----NOLONGMN-LDSK-----AVAGSGKVIYSGVSPSKGMDFTVNI 292
DB 545 VNLDSGLTGTGAGHVENIGDNGTVNNKGDIVYSDIGSLVINGEATVYNTGDIVNS- 603
QY 293 NAGNNEITRNKNIDIASM-TPOFS-----SYSLGA-----GADAPLTSLVVG 335
DB 604 NEATGFSITTSNGSKVSLAGSMOYGFSTGVLDLNGNNSVTLAKDLKVVQKATGTINVG 663
QY 336 DALNV---GSKKDNKFPVITNYA---PGV-----KEGDYTNVQOLKGAQN-LNNRI 380
DB 664 DANVTITGNVYLDKTKADNMAEYFPDPSVGINVYGSNNVTLLDKLTVSDSEVTSRQ 723
QY 381 DNV-DGNARAGIAQAIATAGLV-----QAYLPKRSMAIIGGTYRGEAGYAI 426
DB 724 SNLFDGSAE-----KTSGLVYVIGDNTVNMNGELIGEKNALADGQSVTSLRPGYX 776
QY 427 -----GYSSISDGGNMIK 441
DB 777 TSVIVVSGSSVYLNLDGTTISG 798

```

## RESULT 2

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AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P39180; P75614; P7360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RX Henderson I.R., Owen P.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RP GENE NAME.
RX MEDLINE=92757509; PubMed=9103983;
RA Henderson I.R., Meenan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
CC FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -1- SIMILARITY: TO ADHESIN AIDA-I AND TO BORETELLA PERTACTIN.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC
CC EMBL; AE000291; AAC75061.1; ALT_INIT.
CC EMBL; D90838; BAA15825.1; ALT_INIT.
CC EMBL; D90839; BAA15832.1; ALT_INIT.
CC EMBL; U24429; AAB47869.1; -
CC HSSP; P07505; ISRD.
CC Ecocore; EG12686; flu.

```

DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR Pfam: PF03797; Autotransporter; 1.  
DR Pfam: PF03212; Pertactin; 1.  
DR TIGRFAMs: TIGR01414; autotrans\_bar1; 1.  
KW Outer membrane; Signal; Complete proteome.

FT SIGNAL 1 52  
FT CHAIN 53 551  
FT VARIANT 552 1039  
FT VARIANT 2 2  
FT VARIANT 41 42  
FT VARIANT 46 46  
FT VARIANT 157 157  
FT VARIANT 188 188  
FT VARIANT 303 303  
FT VARIANT 320 320  
FT VARIANT 372 372  
FT VARIANT 493 493  
FT VARIANT 497 497  
FT VARIANT 585 585  
FT VARIANT 709 709  
FT VARIANT 721 721  
FT VARIANT 751 753  
FT VARIANT 803 803  
FT VARIANT 815 815  
FT VARIANT 824 824  
FT VARIANT 829 835  
FT VARIANT 845 847  
FT VARIANT 855 855  
FT VARIANT 888 888  
FT VARIANT 1025 1025  
FT CONFLICT 61 63  
SQ SEQUENCE 1039 AA: 106841 MW: 51706478CDEBEO CRC64;  
ANTIGEN 43 ALPHA CHAIN.  
ANTIGEN 43 BETA CHAIN.  
K -> N (IN STRAIN ML 308-225).  
SL -> FE (IN STRAIN ML 308-225).  
T -> K (IN STRAIN ML 308-225).  
W -> L (IN STRAIN ML 308-225).  
V -> F (IN STRAIN ML 308-225).  
ATN -> STI (IN STRAIN ML 308-225).  
A -> T (IN STRAIN ML 308-225).  
N -> Q (IN STRAIN ML 308-225).  
E -> V (IN STRAIN ML 308-225).  
S -> N (IN STRAIN ML 308-225).  
H -> Y (IN STRAIN ML 308-225).  
E -> K (IN STRAIN ML 308-225).  
M -> T (IN STRAIN ML 308-225).  
GHL -> SHF (IN STRAIN ML 308-225).  
S -> P (IN STRAIN ML 308-225).  
A -> V (IN STRAIN ML 308-225).  
C -> S (IN STRAIN ML 308-225).  
LNLVHTS -> MNLITNA (IN STRAIN ML 308-225).  
QGT -> LGA (IN STRAIN ML 308-225).  
S -> T (IN STRAIN ML 308-225).  
Q -> L (IN STRAIN ML 308-225).  
S -> I (IN STRAIN ML 308-225).  
FTV -> TTT (IN REF. 5).  
LNLVHTS -> MNLITNA (IN STRAIN ML 308-225).

Query Match 7.7% Score 181.5; DB 1; Length 1039;  
Best Local Similarity 24.7%; Pred. No. 0.022;  
Matches 112; Conservative 63; Mismatches 146; Indels 133; Gaps 30;

QY 37 ETAGNDTTHLNGI-----GSTLDTLNTGATTVN---TNDNTTDEK---KRAAS 84  
DB 105 QDGTAKNTTYTSGGLRVNPGSGVSDTVASGGOSLOGRAVNTTLNGSGOMNHEGAI 164  
QY 85 VKDVLN-AGWNKIKVKGDTTASDNVDFRT-----YDYEPISADTKKTTVNES 133  
DB 165 TGTIYNDRKMOY--VKFGYATDTY--VNTGAEGRPAENGDTGFQFRGDAVRTTN--- 217  
QY 134 KDNCKTEVKIG-AKTSVIEKKDKLVTKDKGENSGSTDE---GEGLV---TAKSVI 184  
DB 218 -KNGRQIVRAEGTANTTVV-----YAGGDQTVGHNLDTTLNGVQYVANGSTASDTV 269  
QY 185 DAVKAKGRM-----KTTTANGQTGADKFEVTVSGTNTVPSG---KGTATVYSKD 233  
DB 270 --VNSDMQIVKKNQVAGNTTVN-QKGR-L-QVDAGTATNTVTLQGGALVYSTAATV-- 323  
QY 234 DQG-NITVMDVNVGDLNVLNQNLNSGWNLSKRAVSSSGVSSGVSPEKSKKNDERYNI 292  
DB 324 --GINRLGAFSVYCKADNV-VLENGC-RLD-----VLGHRTN-----TRV 362  
QY 293 NAGNNIEITRNGKNIDATSMTPOFSSVSLGAGADAPLTVSDGALNVGSKKDKRPVRI 352  
DB 363 DDGGTLDV-RNG-----GTATV-----VSMNGC---VILLADSGAAVSGTRSDK----- 403  
QY 353 NVAPGVEGDTVNTAQLKVAQNINNRIDNVGNARAGIAQALITAGLVQAYLPDKSMA 412  
DB 404 --AFSISGGQADALMLKSGSFTLN-----AGDPTATDT----- 435  
QY 413 IGGGTVEAGVAYGYSISDPGMMITKGTASGN 446  
DB 436 VNGSLFTARGSTLAGTTTLNNGALITLSGKTVNN 469

RESULT 3  
ID OMPA\_RICRI STANDARD: PRT: 2249 AA.  
AC P15921;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=783;  
RM [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90354033; PubMed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990).  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PM: GLYCOSYLATED (PROBABLY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPA FAMILY.  
CC -----  
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CC -----  
DR EMBL: M31227; AAA26380.1; -.  
DR PIR: A41477; A41477.  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR Pfam: PF03797; Autotransporter; 1.  
DR TIGRFAMs: TIGR01414; autotrans\_bar1; 3.  
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28  
FT CHAIN 29 2249  
FT DOMAIN 212 1180  
FT REPEAT 212 286  
FT REPEAT 287 358  
FT REPEAT 359 430  
FT REPEAT 431 505  
FT REPEAT 506 577  
FT REPEAT 578 652  
FT REPEAT 653 724  
FT REPEAT 725 799  
FT REPEAT 800 874  
FT REPEAT 875 949  
FT REPEAT 950 1021  
FT REPEAT 1022 1093  
FT REPEAT 1094 1165  
FT REPEAT 1166 1180  
SQ SEQUENCE 2249 AA: 224333 MW: A9D6646C089DF087 CRC64;  
Query Match 7.6% Score 179.5; DB 1; Length 2249;  
Best Local Similarity 24.4%; Pred. No. 0.067;  
Matches 138; Conservative 45; Mismatches 201; Indels 181; Gaps 28;

QY 1 NNETDLISVGTREKISFSANGKRVITSD---TKGLNFAKETAGTN-----CDTTHL 50  
DB 776 DNTTGDNVGVNLN-----NGALSOVYTGIDIGNTSLATISVAGTATIGAVYKATTTKLT 831  
QY 51 GIGSTLDTDTLNL---TGATTNVT-NDNV----- 74  
DB 832 NAASVLTLLTNANAVLTGAVDNTTGGDNVGLNLGALSOVYTGIDIGNTSLATISVAGTAT 891

QY 75 -----TDEKKRAASVKDVLNAGMNIKGVPCPTASDNDVDFRYDVEFLSADTK 125  
 DB 892 TLGAVAKATTTKLTNAASVLTLTNANAVLTGADIDNTGDDNVGLNMGALSOVTDIG 951  
 QY 126 TTTVAVESDNGKKTPEVKIGAKTSYKEKDGKLVYCKDKGENSSDDEBGLVTAKEVID 185  
 DB 952 NT-----NSLAT-ISVAGATATL-----GGAIVATATT 978  
 QY 186 AVNKAQMRKTTTANGOTGADKFEVTGTFNVTFASGKTATVATSKDQGNITVAVDN 245  
 DB 979 KLTDAASAVKFTNPVYVTAIDNTGNANNGI-VTFGNSSTVGNV-----GNTNALTATN 1032  
 QY 246 VEDALNVNOLNSGMNLDKAVAGSSGKVISGNVSPSKKMDETVINAG-----NNIEI 300  
 DB 1033 VGAGL--LQVGGGVVAKANTINLTNDASAVTFNPVYVTAIDNTGNANNGIYVTFGNSSTV 1090  
 QY 301 TENGKRIIDATSMTPQFSSVSLGAGADAPTLSDYDAL--NGSKDN-KPRAITVAVG 357  
 DB 1091 TGNVGN-----TNALATVAVGAG-----LLOVGGGVVAKANTINLTNDASAVTFN--PV 1137  
 QY 358 VKEGDTVNAOLKGVANQNLNRIDNVGNARA-----GIAQATAT--AGL-VQAVLPKG 408  
 DB 1138 VVTGALDNTG-----NANNGVYTFGNSSTVYGDIGNTNALTATVAVGAGITLQA--GG 1187  
 QY 409 SMA-----IGGTYRGEAGVAGIY--SSISDGNMIIK-----440  
 DB 1188 SLAANNIDFGARSTLEFNGPLDGG-----GKAIPYFKGALANGNALLNVTKLTAS 1241  
 QY 441 ----GTSAGNSRGH--FGASASVG 458  
 DB 1242 HLTIGTVAEINIGAGLFTIDASVG 1266

RESULT 4  
 ID HLXA\_PROMI STANDARD; PRT; 1577 AA.  
 AC P16466;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Hemolysin precursor.  
 GN HPMA.  
 OS Proteus mirabilis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Proteus.  
 OX NCBI\_TaxID=584;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.  
 RC STRAIN-ISOLATE 477-12;  
 RX MEDLINE=90170827; PubMed=2407716;  
 RA Uphoff T.S., Welch R.A.;  
 RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";  
 RT J. Bacteriol. 172:1206-1216(1990).  
 RL J. Bacteriol. 172:1206-1216(1990).  
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.  
 CC -FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.  
 CC -SUBCELLULAR LOCATION: Outer membrane.  
 CC -MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.  
 CC -SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).  
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 CC EMBL: M30186; AA25657.1; -.  
 DR PIR: A35140; A35140.  
 KW Hemolysis; Toxin; Outer membrane; Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 1577 HEMOLYSIN.  
 SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924BD9 CRC64;  
 Query Match 7.4%; Score 174; DB 1; Length 1577;  
 Best Local Similarity 21.4%; Pred No. 0.085;  
 Matches 126; Conservative 79; Mismatches 171; Indels 214; Gaps 32;  
 QY 7 TSVGEKLSFSANGKNTSDTKGLNFA-----KETAGT-----N 42  
 DB 710 TSTETQANSTISGANVLDQAN-KDVTFAFGSDLKTAGNASTIGDVAVFSTENKKQTON 768  
 QY 43 GDTTVH-----LNGIS-----TLDTLLNTGATTNTVND-----72  
 DB 769 TPTTISGFSYTGVDKVGSKADFOYDKQHTQTEVTKRNGSQTEVAGDILLITANKDLHE 828  
 QY 73 -----NVTDEKKRAASVKDVLNAGMNI-----KGKPG- 101  
 DB 829 GASHVEGRKQESGENIQLAVNDSETSKTDSLNVGIDGVNLDSGYTRPKKALIEDGV 888  
 QY 102 --TTASDNDV--VFYDVEFLS--ADTKTTVNE-----SKDNGKTEVKI 144  
 DB 889 NNTKPGNNTDLTKRYTARDAIANLANLSNLEFPNVGEVGIKGGSGQSOTDSQAVSTSI 948  
 QY 145 GAKTSYIKKDKGLYTRKDKGENSSDDEBGLVTAKEVIDA-VNKAQMRKTTTANGOT 203  
 DB 949 MNGKIDI-DSNNKL--HDGTHYSTQGGISLTANTHTSEATLKHQTFHEHETKGGGDI 1004  
 QY 204 GOADKEFEVTSCTNVTFE-SGKQTPA-----TVSKDQGNITVAVVAVGALNVQLQ 256  
 DB 1005 GVSTK-----TGSIDIVALKGEQTTDNALMETKAGSOFPSNGDISINVE-----NAH 1054  
 QY 257 NSGWNLDKRAVAGSSGKVISGNVSPSKKMDETVINAGNIIETR-----NG 304  
 DB 1055 YEGAGFDAG-----KGR--TV-INAGDILLAQATDTHSESGSNVNG 1093  
 QY 305 K-NIDATSMTPQFSSVSLGAGADAPTL--SYDGDALNVGSKDKKPAVITVAVPVKKG 361  
 DB 1094 SANLKVGT--TPE--SKDYGGGFGNAGTTTHSKKQTTAKVCTTSGGIELNMGHNLTLTG 1149  
 QY 362 DVTNVAOLKGVANQNLNRID-----NVGDNARAGIAQ-----ATAAGLYQA 403  
 DB 1150 --THLSBEDIALNATNKYDLOSASSEHTEKGNLSGVOAGGKMKTTDDASSVNGL-----1204  
 QY 404 YLPKKSMAIG-----GGTYRGEAGVAGIYSSISDGNMIIKGT 443  
 DB 1205 ---GSAQFAIGKODEKSVSREGT-----INNSGNLTJNGNS 1238

RESULT 5  
 ID BIGA\_SALTY STANDARD; PRT; 1953 AA.  
 AC P25927; P25928; Q9XCQ3;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative surface-exposed virulence protein bigA precursor.  
 GN BIGA OR STM3478.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14028;  
 RA Stojiljkovic I., Valentine P., Hefron F.;  
 RT "Salmonella typhimurium rhs homolog.":  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE-21534948; PubMed-11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 Courtney L., Potwolik S., All J., Dante M., Du F., Hou S., Layman D.,  
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,  
 Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 IT2.";  
 RL Nature 413:852-856(2001).  
 RN [3]  
 RP SEQUENCE OF 1-765 FROM N.A.  
 RC STRAIN-IT2;  
 RX MEDLINE-91100301; PubMed-1987123;  
 RA Wu J.Y., Siegel L.M., Kredich N.M.;  
 RT "High-level expression of *Escherichia coli* MADPH-sulfite reductase:  
 requirement for a cloned cysC plasmid to overcome limiting streptococcal  
 cofactor.";  
 RT J. Bacteriol. 173:325-333(1991).  
 RL -! CAUTION: Ref.13 sequence differs from that shown due to frameshifts  
 in positions 414 and 732.  
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 CC  
 DR EMBL; AF133696; AAD9458.1; -  
 DR EMBL; AE008859; AAL22340.1; -  
 DR EMBL; M64605; AAA27042.1; ALT\_FRAME.  
 DR EMBL; M64606; AAA27043.1; ALT\_FRAME.  
 DR StGene; SG10437; b19a.1  
 KW Virulence; Repeat; Signal; Complete proteome.  
 FT SIGNAL 1 27  
 FT CHAIN 28 1953  
 FT  
 FT DOMAIN 101 252  
 FT REPEAT 101 103  
 FT REPEAT 104 113  
 FT REPEAT 114 122  
 FT REPEAT 123 133  
 FT REPEAT 134 144  
 FT REPEAT 145 155  
 FT REPEAT 156 166  
 FT REPEAT 167 177  
 FT REPEAT 178 188  
 FT REPEAT 189 199  
 FT REPEAT 200 210  
 FT REPEAT 211 221  
 FT REPEAT 222 232  
 FT REPEAT 233 243  
 FT REPEAT 244 252  
 FT REPEAT 207 207  
 FT CONFLICT 514 514  
 FT CONFLICT 1698 1698  
 FT CONFLICT 1795 1798  
 FT CONFLICT 1836 1837  
 SQ SEQUENCE 1953 AA; 200150 MM; 611B3F1C954D9D1AE CMC64;  
 Query Match 7.38; Score 170.5; DB 1; Length 1953;  
 Best Local Similarity 23.18; Pred. No. 0.17;  
 Matches 124; Conservative 60; Mismatches 199; Indels 154; Gaps 28;  
 QY 17 SANGNVTITSDPKGLNFAKTAGT-----NGDT-----TVHLNGGSLT----- 57  
 DB 422 SGNSTTTTACG-----IAVSGGTGTAITIDGDNATIKNTGSDISGAGSTGTVIDGNAR 476  
 QY 58 -----DTLNTGATTNVTNDNTV-DDEKRRASVKD-----VLNAG-WNIKG 97

Db 477 VNNDGDWITIDGGGHHITGDNVVIDNAGSTTVSAGADAFALYIEGDNALVINENQITSG 536  
 QY 98 VKRGTTASDNVDVRYTVDYEFISADPKTTTVNVESDNKKEVTKGATSVYKENDGK 157  
 Db 537 GAVGTIRIDG-----DAHTNTGDIADVAGASAIVII----- 568  
 QY 158 LVTGKRGKSGSSSTDEGEGLVT--AKRVI--DAVNKRGMRKTTTANGOTGADKFEFTV 213  
 Db 569 -----NGDMSLTQAGDLVTDGAMGIIITGNGNEA-----KRTGATYRADSDVGFV 617  
 QY 214 SGTNVTF-----ASGKGTATVSKDDGNITVYVDVNVGDALNVQNLNSGMNLDLSKA 266  
 Db 618 AGEKRTFKNGKGDIDVSLNGTGALYS-GDMSQVTLDDGIIV--VSVDGSKGVFSSANGVS 673  
 QY 267 VAGSGSKV-ISCNVSPS-----KGKDEVTYNINAGNNIETTRNGK-NI--DIATS 312  
 Db 674 VSGDSNAVDITGVNINISADYGGODDLAAGAPPLGVVGVGNGNTVTLGALNIDNDLSAT 733  
 QY 313 MTFQFSSVSLGAGADAPTLSDVDGALNVGSKDKKPVRTNVAGVKEGDTVYVQOLKGV 372  
 Db 734 GGOYLDVYGLSVGGDDNDVEIDG-GINTHSED--PLDGTIS-----ADITGISVSGNS 783  
 QY 373 AONLNRIDNVGDNARAG-----IAQATATAGLV-----QAYLP-----GKSMMA 412  
 Db 784 TVTLNGH-STIDNTTVGHHVVLARVNNGSLILIGDSSVDVNVSYIPTGYTYNALMA 842  
 QY 413 IGGGTYRGEG-----YAI-----GYSSISDGCNMIIKKTGASNSGKHGASASVG 458  
 Db 843 DGEOSTIENKGDITSHGVSIVIRADNGSEVNSGDIIVATYSNSSEDRAIYFRASG 899  
 RESULT 6  
 SLAP\_CAME  
 ID SLAP\_CAME STANDARD; PRT; 933 AA.  
 AC P35827;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE S-layer protein (Surface array protein) (SAP).  
 GN SAP.  
 OS Campylobacter fetus.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=196;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
 RC STRAIN-84-32 / 23D;  
 RX MEDLINE-90354448; PubMed-2387868;  
 RA Blaser M.J., Gotschlich E.C.;  
 RT "Surface array protein of *Campylobacter* fetus. Cloning and gene  
 structure.";  
 RT J. Biol. Chem. 265:14529-14535(1990).  
 RN [2]  
 RP ERRATUM.  
 RX MEDLINE-91035477; PubMed-2229082;  
 RA Blaser M.J., Gotschlich E.C.;  
 RL J. Biol. Chem. 265:19372-19372(1990).  
 CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
 CC CRITICAL FOR VIRULENCE.  
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC  
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 CC  
 DR EMBL; J05577; AAA23032.1; -

KW Cell wall; S-layer.  
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4B5B1E9 CRC64;  
Query Match 7.2%; Score 170; DB 1; Length 933;  
Best Local Similarity 22.4%; Pred. No. 0.075;  
Matches 126; Conservative 64; Mismatches 217; Indels 156; Gaps 27;  
OY 5 DLTSGTEKLSFSANGNKVNITSD-TKGLNFAKETAGT----- 41  
DB 288 DEVENGEYKGVENGLDIVSPATDASKSVN--ETTGTITTAFTAGTGKVDVACKISAL 345  
OY 42 --NGDTYHLNGIGSTLIDTLNLTGATNTVINDNTD-----DEKKRA----- 83  
DB 346 TADSTSVNLATNTITLTSAMATSVNLKORQAKDATITSAMOQKYNRRNRRIATITTS 405  
OY 84 -----SVKDYLNAGNNIKGVKPGCTASNDVFEFTDVEFLSADTKTTTVN--VEKSD 135  
DB 406 ATAVENLTVKHATNALNGMDKLATVTLDNAALTAIDI-----KSASTLNLINSSV 458  
OY 136 NG-----KRTVEYKIGAKTSVIREK-----DGKLVTKGDKGNGSSSTD 172  
DB 459 NGPKHLYSKRRCYKFRKRAAKVKLNTAATDQVTLKANATDNLDFDSATAKTSTVTA 518  
OY 173 EGEG---LYTAKEVIDAVNKKAGMKTTAN-----GQTGQADKFETVTSCTVNTAS 222  
DB 519 SSGGFTLVKGAEEVETLVN-----IDTTFANALOSVSEKGTGGGKRF-SVKGTGDDKIE 572  
OY 223 GKGTATVYSK--DDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAG---SSGKVISG 277  
DB 573 FVGTTLTGSGVIDAGNNTIAMSALTSANFTMIKNIEENVAISDAVATADLSSSAFKNS 632  
OY 278 NVSPSKGMDETVNNINANNIEITRNGN-----IDATSMTPQSSS 319  
DB 633 VIITTKKADPTTLTKNDQVINFPAADAGSVKLTVKLNQVATAMIVKIVLDAAKDTN 692  
OY 320 VSLGAGAPPLTSVDG--DALNVS-KKDNKPVRTTNVAPGVKEDVTNV---AQL--- 369  
DB 693 IALGTAADKALVLDITGETIETNITSLVATSPETTANV-NAKLVDVSIITIDGQITLG 751  
OY 370 -KGVANQNLNRIIDVNDGNA-RAGI---AQAIATAGLVQAYLPGKSMAIGGTYGGEAGY 424  
DB 752 HAGTAGTDYSKVSMIDALAKAGLTFDASAI-TLG-----ANATIKGS----- 794  
OY 425 AIGTSSIS-DGANNIITKGTASGN 446  
DB 795 --GADSIYVKGGINVVDLVAGGD 815  
RESULT 7  
HLTA\_SERMA STANDARD: PRT; 1608 AA.  
AC P15320;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Hemolysin precursor.  
GN SHLA.  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_Taxid=615;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
RC STRAIN=SN8;  
RX MEDLINE=88257037; PubMed=3290200;  
RA Poole K., Schiebel E., Braun V.;  
RT "Molecular characterization of the hemolysin determinant of Serratia  
marcescens.";  
RL J. Bacteriol. 170:3177-3188(1988).  
CC -i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
CELL MEMBRANS AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
CC DEFINED.  
CC -i- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM

CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
CC REQUIRES SHLB FUNCTION.  
CC -i- SUBCELLULAR LOCATION: Outer membrane.  
CC -i- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HEMA).  
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CC  
DR EMBL; M2618; AAA50323.1; -  
DR PIR; A28182; A28182.  
KW Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 1608 HEMOLYSIN.  
SQ SEQUENCE 1608 AA; 165078 MW; D65B476FE7DAD51 CRC64;  
Query Match 7.1%; Score 168; DB 1; Length 1608;  
Best Local Similarity 22.3%; Pred. No. 0.18;  
Matches 125; Conservative 73; Mismatches 207; Indels 156; Gaps 27;  
OY 1 NNEEDLISVTEKLSFSANGNK-VNIT-SDTKGLNFAKETAGTNGDTVHLNGIGSTLTD 58  
DB 558 SHASELTSGTGLRL-----NGOQGVITTSKARGQKGEVTA-TTGGLRLID-NALETVYDK 611  
OY 59 TLLNLTGATNTVINDVNDDEKKRAASVKNVNLNAGNNIGVAPGTTASNDVDFRIVDYVE 118  
DB 612 IDARTGFANITSSHKADNSYOSTASSEL-----KSDTNLTVLSHKDADV 657  
OY 119 F-----LSADTKTTTVNVE----- 132  
DB 658 IGSQVASGSELSEKTCGINNVKAAERQONIDEOKTALTIVNGYAKKAGDKOYRAGLRTEH 717  
OY 133 SKDNCKTEVYKIGAKTSVIREKDGKLVTKGDKGNGSS--TDESGELVTAKEV--IDAVN 188  
DB 718 TRDSEKTYRTENSA--SSLSGSVYKLAKEAKVTEFGSKLVADKGVASVGNKVSFLADD 775  
OY 189 KAGWEMKTTTANG--OTGOADKFETVTSCTNVTPFASGKTATVYSK-----DDOGNIT 239  
DB 776 KTASNTDQTKIGGCGYTGIDK--LGSYVAGYEENK-TQOSSKAITSGSDYKQMLT 831  
OY 240 VMYDVNVDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGMDETVNNINANNIE 299  
DB 832 ----INARDKLQOQASHGAVGQENAGVDHLAADPTASTTTTKTDVGVNI----- 880  
OY 300 ITRNGKNIDTASMTPOSSVSLG-----GADAPTLSDGDALNVSCK--D 345  
DB 881 ----GANVDYSAVTRPVERAVGAKAKLDATGVIINDIGIGAPNVLGIDGAGGSSSEKRS 936  
OY 346 NKPVRTTNVAPGV-----KEGV---TNVAOLKGVANLUN-----NRIDVNDGNA 387  
DB 937 SQAAYSSVQAGSIDINAKGEYRROGTQYQASKG-AVNLTLDSHRSSEANRQDROSDYT 995  
OY 388 RAGIAQAIATAGLVQAYLPGKSMAIG---GTYRGEAGYAIGTSSISDGNW----- 437  
DB 996 R-----GSAG-VRYVTTTSDTLVDKAGEGTORSNSASQAVTGSIDAANGINNVK 1047  
OY 438 ---IITGTAAGNSRKHFGASA 455  
DB 1048 KDAILYGTALNGRGKTAVNA 1068  
RESULT 8  
OMP\_RICRI STANDARD: PRT; 1654 AA.  
AC O53047;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)

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DE (surface protein antigen) (Cell surface antigen 5) (Scas) (ompB)
DE (omp B) [contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN ompB
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OC NCBI_Taxid=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R.
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (omp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor."
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN-R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii."
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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DR EMBL, X16353; CA34403.1; -.
DR PIR, S18227; S18227.
DR InterPro: IPR006315; Autotransport.
DR Pfam: IPR005545; Autotransporter.
DR TrEMBL: TIGR01414; autotransporter, 1.
DR TrEMBL: TIGR01414; autotransporter, 2.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT DOMAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;
Query Match 7.18; Score 166.5; DB 1; Length 1654;
Best Local Similarity 22.14; Pred. No. 0.22;
Matches 114; Conservative 59; Mismatches 214; Indels 129; Gaps 24;
QY 19 NGKKNVITSTKGLNFAKTAGTNGDTTV-HLNCIGSTLDTLTLNCAATNVTNDN--VT 75
DB 340 NGVAVATIDGOVYAKMDYQSANATGQVNRHIVDVGCTTAETKASAKVTITQDSNFGN 399
QY 76 DDEKRAASYK--DVLAAGNINIK--VKPGTASDNDVFEVTD--TVEFLSADTETTT 128
DB 400 TDGGNLAQIKVKNATILNFTGDSNPGNTAG----VITPDANTLESASADNAVAV 454
QY 129 VN---VESKNG-----KTEVKIGATSVIKEDGLVYGGDK-----GENGSST 171
DB 455 TNNITATEAGAGVYQVLSGTHAEELRLGNAGSIFKLADGVINGKVMQTLVYGALAACT 514
QY 172 DEBGLVTAKEVIDAVNKKAGRMKTTTANAGTQGAOKFEVTV--SGTVTFASG----- 223
DB 515 ITLDGSAFTITGDIAGNAGGAAALORTLTAN-----DAKKTLTJLGAGNIAGAGGTTDLQA 568
QY 224 KGTATATVSKDQGNITVYMDV-----NVGDALNVQLNSGWN-----LDSKAVA- 268

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DB 569 NGGITKLT-STQNNIVDFDLATIDGTGVVDASSLTNAOTLTINIGTIGANNNKTLGQ 627
QY 269 ---GSSGKVIS-GNV-----SSKRMDETVINNGNN 297
DB 628 FNIGSSKTVYLSNGVAINELVIGNDGAVOFAHDYTLTRTTNAGOGKILFNPVYNNGT 687
QY 298 IEITRNCKNIDATSMTPQFSSVSLGAGADAPLTVGDALNVGSKKDNKPVRT-----N 353
DB 688 LAA---GTNIGSATNPPLAEINFGSKGVNVDI-----VLNVEGYNLATNTITTDAN 736
QY 354 VAPGVKEGDYTNVAOLKGVANLNMRIDYDGNARAGIAQAIATVAGLVQVLPKSMMAI 413
DB 737 VGSFVFVAGGNINIVS-GTVGGQGNKFNVT-----ALENGTVYKFL 776
QY 414 GGGTYRGEAGYALCYSSIDSGMNIITGTSAGNSRG 449
DB 777 GNATFNGNTTIAN-STLQIGGNTYADCVASADTGC 811
RESULT 9
ICEN_XANCT STANDARD; PRT; 1567 AA.
ID ICEN_XANCT
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_Taxid=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X565;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
RT Xanthomonas campestris pv. translucens."
RL Mol. Genet. 223:163-166(1990).
CC -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CC CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -1- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
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CC -----
DR EMBL: X52970; CA37140.1; -.
DR HSSP: P06620; IINA.
DR InterPro: IPR000258; Ice_nucleatn.
DR Pfam: PF00818; Ice_nucleation; 81.
DR PRINTS: PR00327; ICENUCLEATN.
DR PROSITE: PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
Query Match 7.18; Score 166; DB 1; Length 1567;
Best Local Similarity 20.94; Pred. No. 0.22;
Matches 100; Conservative 69; Mismatches 222; Indels 88; Gaps 18;

```

```
OY 15 SEFANGNKVNITSDTKGLNFAKE-----TACTNEDTVHLNGISLT--DTLLN 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 832 STQTSQSGSDTAGYGTQTAAREGSDVYTAGYSTAGADSTLLISGYSTQTAGSDSSLT 891
OY 63 TGATNNVNDVTDDEKKRAASVKNVYLAAGMKVKGKGTTSDBVDFVRYTDYEFLLSA 122
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 892 AGYGTQTAARKSD-----VTAGYGSTG---TAGADSTLLAGYGSTQTAGS 934
OY 123 DTKTTTVAVESKDNKQTEVKIGAKTSYIKEDKGLVYTKDKGNGSSTDEGEGLVPAKE 182
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 935 DSSLTAGYGTQTAARKSDMTAGYSTGTAGADSTLLING-----YGSTQTAGS----- 982
OY 133 VIDAVNKAQWRMKTTTANGQGTQADKFEYVSGTAVTASGSGGTTATVSKDDQGNITVWY 242
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 983 --DSSLTAGYGTQTAAREGSDVYTAGYGTGTAGADSTLLAGYGSTQTAGSD--SSLTAGY 1038
OY 243 DVNVDALNVNQLONGMNLDSKAVAGSSGKVIISGNVSPSKKMETVINAGNNEIIR 302
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1039 -----GSTOTARQSGSYTAGYGTGTAGADSTLLIAGYGTQTAGSDSSLTAGYGT--QTAR 1093
OY 303 NGKNIDIASMTPOFSSVSLGAGADAPTLVVDGDLNMGSKKDNKPVRTTNYAPGV--- 358
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1094 QGSDI-----TAGYGTGT--AGADSSLTAGYGSTQTAGYD-----SNLTAGYGTQ 1138
OY 359 ---KGGDYTNVAQLKGVAKONLNRIIDVNDGNARAGIAQAIATPA--GLVQAYLPKSKMAIG 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1139 TAREDSLTAGYGTSTAGHSSSLTAGYGTQTAGYNSILITGYSTQTAGRESSSLTAGY 1198
OY 415 GGTYSGEAGY---AIGYSSISDGG--NMILIGTAGSGNSRGH-----FGASASVGYQ 460
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1199 GST--STAGYDSTLTAGYGTGTAGYKSTLTLAGYGSNSTAGHSSSLTAGYGTQTAGYE 1255

RESULT 10
OMP. RICC. STANDARD: PRT: 1655 AA.
ID OMP. RICC. STANDARD: PRT: 1655 AA.
AC Q9KKA3; Q9KKA9; Q9XC45;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (ompB)
DE (Romp B) [Contains: 120 kDa surface-exposed protein (surface protein
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RCI085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OY NCBI_TaxId=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RT Science 293:2093-2098 (2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rompB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
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CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP. FAMILY.
CC -----
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CC -----
DR EMBL: AE008659; AAL03623.1; -
DR EMBL: AF123721; AAF34124.1; -
DR EMBL: AF123726; AAF34129.1; -
DR EMBL: AF149110; AAD39533.1; -
DR PIR: E97835; E97835.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005346; Autotransporter.
DR Pfam: PF03797; Autotransporter.1.
DR TIGRPFAM: TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1..1334 120 kDa SURFACE-EXPOSED PROTEIN.
FT 1335..1655 32 kDa BETA PEPTIDE.
FT VARIANT 61..61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75..75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78..78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251..251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413..413 I -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959..959 N -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988..988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139..1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139..1139 R -> GH (IN REF. 3).
FT CONFLICT 353..354 KD -> S (IN REF. 3).
FT CONFLICT 776..776 E -> S (IN REF. 3).
FT CONFLICT 1159..1159 F -> D (IN REF. 3).
FT CONFLICT 1177..1177 G -> S (IN REF. 3).
FT CONFLICT 1492..1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E9377D5FCB37 CRC64;

Query Match 7.1%; Score 166; DB 1; Length 1655;
Best Local Similarity 23.6%; Pred. No. 0.23;
Matches 118; Conservative 57; Mismatches 230; Indels 94; Gaps 23;

OY 19 NGKNVNITSDTKGLNFAKEGTAGTNGDTT-----VHLNGISLTLDTLTGATTVNTDNV 74
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 340 NGKVATLIGQVYAKDMVLOSANAVGVNFRHIVDGTGTGTAFAKTAASVATLTONSNGQT 399
OY 75 TDDEKKRAASVND---VINAGNINIGVPCGTASNDVDFVRYD---TYEFLSADTKTTTY 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 400 TDFGNLAQIIVPNTMTLLNGNTGDASNGNTAG-----VTFEDNGTLTASASADANAV 454
OY 129 VN-----VESKDNQ-----KTEVKIGAKTSYIKEDKGLVYTKGDKG-----ENG 169
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 455 TNNITAIENSAGVVOVLSGTHAELRLNAGSVFELADGTIVNGKVNQALVGAALAGT 514
OY 170 STDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQGTQADKFEYV-----SGTNVTF 220
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 515 ILLDSASATITG---DIGNAG-----AALQGITLLANDATKTLTGGANIIGANGTINF 566
OY 221 ASGKTATATVAKDDQGNITVMYDV-----NVGALNVNQLONGMNLDSKAVAGSSSK 273
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 567 QANGGTIKITF--TNNIVVDLAIADQGTGVASSLTNQLTLTKIGITGVANNKT 624
OY 274 VISGNVSPSKGM--DETVIN--AGNN--LEIFNGKNIDIASMTPO---FSSV--- 320
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 625 LGQFNIGSKVLSGDAVAINELVIGNNGAVFAINTYLTITFTNAAGGKIIFNPVYNN 684
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RT      crescentus paracrystalline surface layer protein.";
RL      Can. J. Microbiol. 38:193-202(1992).
RN      [2]
RP      REVISIONS TO 376: 636 AND 842-843.
RA      Awram P.;
RL      Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Bingle W.H., Awram P.A., Nornellind J.F., Smit J.K.;
RT      "The secretion signal of c. crescentus S-layer protein is located in
RT      the C-terminal 82 amino acids of the molecule.";
RL      Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RA      MEDLINE-21173698; PubMed-11295647;
RC      STRAIN-ATCC 19089 / CB15;
RX      MEDLINE-21173698; PubMed-11295647;
RA      Nieman W.C., Feldblyum T.V., Land M.T., Paulsen I.T., Nelson K.E.,
RA      Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA      Porocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA      Debroy R.T., Dodson R.J., Durkin A.S., Gynn M.L., Haft D.H.,
RA      Kolonay J.F., Smit J., Craen M.B., Khouri H., Shetty J., Berry K.,
RA      Utterberg S.L., Venter J.C., Wolf A., Yamachyan J., Ermolava M., White O.,
RA      Salzman T.L., Venter J.C., Shapiro L., Fraser C.M.;
RT      "Complete genome sequence of Caulobacter crescentus.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN      [5]
RP      SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RC      STRAIN-ATCC 19089 / CB15;
RX      MEDLINE-89008089; PubMed-3049545;
RA      Fisher J.A., Smit J.K., Agabian N.;
RT      "Transcriptional analysis of the major surface array gene of
RT      Caulobacter crescentus.";
RL      J. Bacteriol. 170:4706-4713(1988).
RN      [6]
RP      CHARACTERIZATION.
RC      STRAIN-ATCC 19089 / CB15;
RX      MEDLINE-98292737; PubMed-9620954;
RA      Awram P., Smit J.K.;
RT      "The Caulobacter crescentus paracrystalline S-layer protein is
RT      secreted by an ABC transporter (type I) secretion apparatus.";
RL      J. Bacteriol. 180:3062-3069(1998).
RN      [7]
RP      FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
RC      OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
CC      PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
CC      -1 SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC      LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
CC      (TYPE I) SECRETION APPARATUS.
CC      -1 MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
CC      SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
CC      SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
CC      -----
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CC      -----
DR      EMBL; AF062345; AAC38665.2; -
DR      EMBL; AF193063; AAF19365.1; -
DR      EMBL; AE005779; AAK22991.1; ALT_INIT.
DR      PIR; A48995; A48995.
DR      HSSP; P22629; ISMC.
DR      TIGR; CC1007; -
DR      InterPro; IPR001343; HemlYsn_Ca_bind.
DR      Pfam; PF00353; hemolysinCbind; 3.
DR      PRINTS; PR00313; CABDNCRPT.
KW      Cell wall, S-layer, Calcium-binding; Complete proteome.
FT      INT. MET.
SQ      SEQUENCE 1025 AA; 98001 MW; AD7A326E1363DBAC CRC64;

```

	Query Match	7.0%; Score 163.5; DB 1; Length 1025;
	Best Local Similarity 23.8%; Pred. No. 0.18;	
	Matches 129; Conservative 63; Mismatches 199; Indels 153; Gaps 26	
QY	8 SVGTETKLSFSAN-----GKNVITSDPTKGLNFAKETAGTNGDTTVHLN 50	
DB	254 TTGDTDLTGTANNNDTFVAGEVAGATLTVGDTLSCGACTDVLNWWQAALVTLPTGVITIS 313	
QY	51 GI-----GSTLT-----DTLNT---GATTNT---NDNVTDEKKRAASVDV 88	
DB	314 GIEIMNVYSGAIIYTLNNTSSGVGTGLTALNTNTSGAAQYTAGAGOMLTPTTAAQAN-NVA 372	
QY	89 LNAQMNI-----KGYKPGFTASDNDVDFVDTYDFEFLSDTKTNTVNSKDKNGKTEVKI 144	
DB	373 VDGANAVTVASTGVTSGIT-----TVGANSASAGTIVSVANSSTTTGAILAV 420	
QY	145 GAKTSV-IKEKDKLV---TGKDKGENSSTDG-----EGLVTAKEVIDAVNK 189	
DB	421 TGGTAIVYAYQAGANAVNTLTQADVYTVNGSSTTAVTVTQPAATAGATVAGRVGAVT- 479	
QY	190 AGFMKTKTTANGQTGQADKFETVTSG-----TNYTFASGKTTATVSKDDGDN 237	
DB	480 -----ITDSSAASATTKGKIATVTLGSGAATIDSSALTTVNL-SGTSISLIGR---GA 530	
QY	238 ITWYDVVVGALVNWQNLQNSGMNIDSKAAVAGS-----SGKVISGVNVPSPKMGMDVY 290	
DB	531 LTAAPTAT-LTLVNVNGLTGTGALTDSPAADDGFTTININGSTASSTIASLVAADATLL 589	
QY	291 NINAGNNIEITRN-----GKNI--DIATSMTPQFSSVSGAGADAPTLSDV 334	
DB	590 NISGDARTIISHRAALTGITVNSVSGATLGAELATGLV--FTG---GAGADSLILGAT 644	
QY	335 GDALVSGSKDKNKPVRITNVAPG--VKEGDTVNAQLKGVAONLNRIQNDV----- 384	
DB	645 TKAIYMGAGDDTVTVSSATLGAAGSGVANGDGTDV-----LVANVSGSSFSADPAFGFET 699	
QY	385 ----GNRAG-----IAQAITAGLVQ----AYLPQKSMALAGGTYRGEACATGY 428	
DB	700 LRVAGAAAGGSNANGFTALDLAGATAGTFTTNVAVNVGLTVLAAPGTFTVTLANAGT 759	
QY	429 SSI 431	
DB	760 SDV 762	
RESULT 13		
YPJA_ECOLI STANDARD: PRT: 1569 AA.		
ID	YPJA_ECOLI	STANDARD: PRT: 1569 AA.
AC	P52143; P76610; P77017; P77019;	
DT	01-OCT-1996 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Hypothetical outer membrane protein ypjA.	
GN	YPJA OR B2647..	
OS	Escherichia coli.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC	Enterobacteriaceae; Escherichia.	
OX	NCBI_TaxID=562;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-K12 / MG1655;	
RA	MEDLINE=9742617; PubMed=9278503;	
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,	
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,	
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,	
RA	Mau B., Shao Y.;	
RT	"The complete genome sequence of Escherichia coli K-12.";	
RL	Science 277:1453-1474(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-K12;	
RA	MEDLINE=9249980; PubMed=9205837;	
RA	Yanamoto Y., Alda H., Baba T., Hayashi K., Inada T., Isono K.,	

RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,  
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,  
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
RA Yamagata S., Horuchi T.;  
RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli*  
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and  
RT analysis of its sequence features.";  
RL DNA Res. 4:91-113(1997).  
CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).  
CC -1- SIMILARITY: STRONG, TO BORDETELLA PERTACIN.  
CC -----  
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DR EMBL: U36840; AAA79815.1; ALT\_SEQ.  
DR EMBL: AE000350; AAC75695.1; -.  
DR EMBL: D90889; BAA16514.1; ALT\_INIT.  
DR EMBL: D90890; BAA16518.1; ALT\_INIT.  
DR PIR: A65044; A65044.  
DR Ecocore: EG13213; YPJA.  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR InterPro: IPR004899; Pertactin.  
DR InterPro: IPR003991; Pertactin\_C.  
DR Pfam: PF03797; Autotransporter; 1.  
DR Pfam: PF03212; Pertactin; 1.  
DR PRINTS: PR01484; PERTACTIN.FAM.  
DR TRIGRAMS: TRIGR01414; autotrans. bar1; 2.  
DR Hypothetical protein. Outer membrane. Complete proteome.  
KW SEQUENCE 1569 AA; 162774 MW; DD006A9A32154596 CRC64;  
SQ  
Query Match 7.0%; Score 163.5; DB 1; Length 1569;  
Best Local Similarity 19.8%; Pred. No. 0.29;  
Matches 95; Conservative 86; Mismatches 235; Indels 63; Gaps 17;  
QY 1 NNETDLTSVTEKLSANGKNVNTSDPKGLNFAKETAGTNGDTVHLNG----- 51  
DB 410 NNTNTLNGTQNNINNYGATGTGNTNGSTQNIK-----SGRADTIISSGSQVYKDG 464  
QY 52 --IGSTLT--DTLNTGATNTNTNDVNDDEKKRAASKVDLNAQMNK--YKPGT 103  
DB 465 TAIQNTISAGSLIVTGGIAHGVN-----QETGSALVANT-GAETDIEGYNKLSHFTI 517  
QY 104 ASDNVDFTVTEFLSADTKTTFVNVESKDNKGKTEVKGAKTSVIREKDKLTGTD 163  
DB 518 TGGEANYVYLEMNGE-LTVVAKTSAKNT-TIDTGGGLIYQKEKKTSTFLNNGVLEVD 575  
QY 164 KEBNGSDEBEGLV---TAKEVIDAVNKAQ--WRMKTTFANGQTQADKEFTVSGTN 217  
DB 576 GGEAKHVEQSGGALASTTSGLTLEGTSYGAPEFIRNSSEAKNVYLENAGSLTVYTGSR 635  
QY 218 V--TPASGKTATVSKD-----DQGNITVMDVNVGDLANNOLONSMNDLSKRVAS 270  
DB 636 AVDTIINANGKADYIGKDGIVLNSAGTQTTIASATSDANIKGGQIVYGLATEENIES 695  
QY 271 SGRVTSIGNVSPSKKMDFTVINAGNNIEITRNGKNIDTATSTPQSSVSLGAGADAPT 330  
DB 696 GEGQIVDGGST-----EKTHINGNQ-IVQNYGKAIN--TIDVSLQOIMANGTREGSI 745  
QY 331 LSYDGDALNVGSKDKNRPRTINVAPEVGEQVTVNAQLKGYAQNINRINDVNGNARAG 390  
DB 746 INGGQVNVGGLAENSIVLNDGTLDRKSGSTGIGQSSGALVATPATRTVYTRAG 805  
QY 391 IQAATATAGLVQAYLPGRSMMAIGGTFVGEAGVAYGVSISDGGWII--IGTASGNS 447  
DB 806 VAFSTIEGQ-----ANNILANGCVLTVESDTSDDKTQVNMGGREIVKTRATATGTT 857

RESULT 14  
ALYS\_ENTFEA STANDARD; PRT; 737 AA.  
AC P37710;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Autolysin precursor (EC 3.2.1.1) (Peptidoglycan hydrolase)  
DE (Beta-glycosidase).  
GN EF0799.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91358349; PubMed=1679432;  
RA Bellevue C., Potvin C., Trudel J., Asselin A., Bellemare G.;  
RT "Cloning, sequencing, and expression in *Escherichia coli* of a  
RT Streptococcus faecalis autolysin.";  
RL J. Bacteriol. 173:5619-5623(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=V583 / ATCC 700802;  
RX MEDLINE=22550857; PubMed=12663927;  
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,  
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,  
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,  
RA Vamathevan J., Tian B., Upton J., Hansen T., Shetty J., Khouri H.,  
RA Ulteback T., Radue D., Ketchum K.A., Dougherty B.A., Fraser C.M.;  
RT "Role of mobile DNA in the evolution of vancomycin-resistant  
RT Enterococcus faecalis.";  
RL Science 299:2071-2074(2003).  
CC -1- FUNCTION: Hydrolyzes the cell wall of *E. faecalis* and  
CC M. lysodeikticus. May play an important role in cell wall growth  
CC and cell separation.  
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -1- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDGLYCAN  
CC BINDING.  
CC -1- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.  
CC -1- SIMILARITY: Contains 6 LysM repeats.  
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CC -----  
DR EMBL: M58002; AAA67325.1; -.  
DR EMBL: AE016949; AAO80613.1; -.  
DR PIR: A38109; A38109.  
DR TIGR: EF0799;  
DR InterPro: IPR002901; Amidase\_4.  
DR InterPro: IPR002482; LysM.  
DR Pfam: PF01832; Amidase\_4; 1.  
DR Pfam: PF01476; LysM; 5.  
DR SMART: SM00257; LysM; 6.  
DR SMART: SM00047; Lys2; 1.  
DR Hydrolase: Glycosidase; Bacteriolytic enzyme; Cell wall;  
KW Cell division; Septation; Repeat; Signal.  
FT SIGNAL 1 53  
FT CHAIN 54 737  
FT REPEAT 363 405  
FT REPEAT 431 473  
FT REPEAT 499 541  
FT REPEAT 567 609  
FT REPEAT 633 675  
FT REPEAT 695 737  
FT REPEAT 85 85  
FT CONFLICT 118 118  
A -> V (IN REF. 1).  
T -> I (IN REF. 1).  
A -> V (IN REF. 1).



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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 13.1962 Seconds  
(without alignments)  
3359.577 Million cell updates/sec

Title: US-09-771-382-35  
Perfect score: 2350  
Sequence: 1 NNEFDLTSVTEKLSFSGANG.....TASGNSNGHFGASASVGYQW 461

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_76:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2333	99.3	591	2	G81133	adhesin NMB0992 (i
2	2089.5	88.9	592	2	A81888	probable surface f
3	393.5	16.7	298	2	I64138	adhesin homolog HI
4	375.5	16.0	2059	2	D82671	surface protein XF
5	365	15.5	1588	2	A86036	probable adhesin Z
6	360.5	15.3	1190	2	H91188	probable adhesin F
7	357	15.2	1107	2	A82615	surface protein XF
8	328.5	14.0	658	2	AC0976	probable autotrans
9	205	8.7	1536	2	A43855	probable surface p
10	195	8.3	585	2	F90961	high-molecular-we
11	195	8.3	585	2	F85809	flagellin (importe
12	194.5	8.3	4919	2	T31105	hypothetical prote
13	194	8.3	936	2	I40711	hypothetical prote
14	192.5	8.2	1910	2	AF0394	sepb protein - Cam
15	192.5	8.1	1004	2	C82672	surface-exposed ou
16	190.5	8.1	2020	2	C48339	ABC-type transport
17	190.5	8.1	2020	2	C48339	cell surface prote
18	185	7.9	365	2	AB3486	high-molecular-we
19	184	7.8	1477	2	B43855	surface-array prot
20	182.5	7.8	1109	2	A56143	hypothetical prote
21	182.5	7.8	3029	2	S76109	hypothetical prote
22	181.5	7.7	1091	2	G64964	adhesin/invasin, p
23	181	7.7	364	2	A81019	flagellin - Escher
24	180.5	7.7	584	2	C48658	hypothetical prote
25	180.5	7.7	2551	2	B98047	probable autotrans
26	180	7.6	3705	2	AD0123	190K surface antiq
27	179.5	7.6	2249	2	A41477	probable flagellin
28	177	7.5	980	2	H90681	probable structura
29	177	7.5	980	2	D85532	

30	177	7.5	2232	2	T34434	hypothetical prote
31	176.5	7.5	5188	2	B85547	probable RTX faml
32	176	7.5	1461	2	E90696	hypothetical prote
33	175.5	7.5	1428	2	AC2224	hypothetical prote
34	175.5	7.5	2273	2	T09083	hemagglutinin/hemo
35	175.5	7.5	2468	2	A83412	hypothetical prote
36	175.5	7.5	3013	2	AB0480	probable invasin Y
37	174.5	7.4	5291	2	F90696	hypothetical prote
38	174	7.4	1577	2	A35140	hemolysin A precu
39	173.5	7.4	1651	2	JC1340	outer membrane pro
40	173	7.4	1430	2	AF0351	probable autotrans
41	172.5	7.3	4152	2	T31102	filamentous hemag
42	172	7.3	1461	2	A85547	hypothetical prote
43	171.5	7.3	1635	2	A10452	hemolysin (importe
44	170	7.2	893	2	A37284	surface-array prot
45	169	7.2	883	2	AC2444	hypothetical prote

ALIGNMENTS

RESULT 1						
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)						
C:Species: Neisseria meningitidis						
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001						
C:Accession: G81133						
R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizzato, M. Science 287, 1809-1815, 2000						
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175753; PMID:10710307						
A:Accession: G81133						
A:Status: Preliminary						
A:Molecule type: DNA						
A:Residues: 1-591 <TEF>						
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AA41395.1; PID:g722						
A:Experimental source: serogroup B, strain MC58						
C:Genetics:						
A:Gene: NMB0992						
Query Match						
Best Local Similarity 99.3%; Score 2333; DB 2; Length 591;						
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	4	TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKFTAGTNGDPTVHLNGIGSTLDTLLNT	63			
DB	134	TDLTSVTEKLSFSGANGKVNITSDTKGLNFAKFTAGTNGDPTVHLNGIGSTLDTLLNT	193			
QY	64	GATTNTNDNTVDEKKRAASVKDVLNAGWNIKGVKPGTTASDNDVFRIVYEPLSAD	123			
DB	194	GATTNTNDNTVDEKKRAASVKDVLNAGWNIKGVKPGTTASDNDVFRIVYEPLSAD	253			
QY	124	TKTTTVNESKDNCKTEVKIGAKTSYIKEDGLVYKDGKNGSGSSDDEEGVYTKEV	183			
DB	254	TKTTTVNESKDNCKTEVKIGAKTSYIKEDGLVYKDGKNGSGSSDDEEGVYTKEV	313			
QY	184	IDAVNKGWRKTTTANGOTGQADKFTETVSGTIVTFASGKTATATYKSDOGNITWYD	243			
DB	314	IDAVNKGWRKTTTANGOTGQADKFTETVSGTIVTFASGKTATATYKSDOGNITWYD	373			
QY	244	VNVGDALNVNOLQNSGWNLDKSAVAGSSGKVISGVNSVBSKGMDEYVINAANNIEITRN	303			
DB	374	VNVGDALNVNOLQNSGWNLDKSAVAGSSGKVISGVNSVBSKGMDEYVINAANNIEITRN	433			
QY	304	GKNIDVATSMPPQSSVSLGAGADAPTLVSVDGLNLSKDKNDKPVRTTNVAPGVKGDV	363			
DB	434	GKNIDVATSMPPQSSVSLGAGADAPTLVSVDGLNLSKDKNDKPVRTTNVAPGVKGDV	493			
QY	364	TNVAQLGVAQNLNRIDNDVGNARAGIAQAIATAGVQAVALPKSKMAATGCGTYRGEAG	423			

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Db          494 TNVAOLKGYAQNINNDVGNARAGIAQAIATAGLVAATYLPFGKSMMAIGGTYGKNG 553
Oy          424 YAIYSSISDGGWMIITKTASGNSRGHFGASASVGYOW 461
          |||
          554 YAIYSSISDGGWMIITKTASGNSRGHFGASASVGYOW 591

RESULT 2
A:1888
A:probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
R.; Holtz, S.; Jørgensen, K.; Leather, S.; Mouton, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MIMD:20222556; PMID:10761919
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CA84461.1; PID:9737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match          88.9%; Score 2089.5; DB 2; Length 592;
Best Local Similarity 91.1%; Pred. No. 6.4e-104;
Matches 420; Conservative 10; Mismatches 26; Indels 5; Gaps 3;

Oy          4 TDLTSTGTEKLSFSGANGKRVNTSDTKGLNFAKETAGTNGDTVHLNGISLTDTLLMT 63
          |||
          134 TGLINTEKLSFGANGKRVNTSDTKGLNFAKETAGTNGDTVHLNGISLTDTLLMT 193
          |||
          64 GATTNTNNTVDEDEKRRASVYKDVNAGMNTKGVKPGTAA--SDVAVDVRVRYDPEFLS 121
          |||
          194 SASHDAGNOST--HYTRAATKIDVNLNAGMNTKGVKPGTAA--SDVAVDVRVRYDPEFLS 251
          |||
          Oy          122 ADRTTNTVNESKDNKKTETVIGAKTSYIKERDGLVTKDGENGSSSTDEGEGLVTK 181
          |||
          Db          252 ADRTTNTVNESKDNKKTETVIGAKTSYIKERDGLVTKDGENGSSSTDEGEGLVTK 311
          |||
          Oy          182 EYIDAVNKAAGMKRTTANGOTGQADKFEYTVSGTNTVTSAGKGTATVSKDDQNTVW 241
          |||
          Db          312 EYIDAVNKAAGMKRTTANGOTGQADKFEYTVSGTNTVTSAGKGTATVSKDDQNTVW 371
          |||
          Oy          242 YDVNVDALNVNOLONGNLSKAYAGSSGVISGNSPSKGMDETNNINAGNIEIT 301
          |||
          Db          372 YDVNVDALNVNOLONGNLSKAYAGSSGVISGNSPSKGMDETNNINAGNIEIT 431
          |||
          Oy          302 RGNKNIDATSMTPQPSVSLGAGADAPLTSYDGD--ALNVGSKDKMPRTVTVAGVKE 360
          |||
          Db          432 RGNKNIDATSMTPQPSVSLGAGADAPLTSYDGDALNVGSKDKMPRTVTVAGVKE 491
          |||
          Oy          361 GGVTVNVAOLKGYAQNINNDVGNARAGIAQAIATAGLVAATYLPFGKSMMAIGGTYGK 420
          |||
          Db          492 GGVTVNVAOLKGYAQNINNDVGNARAGIAQAIATAGLVAATYLPFGKSMMAIGGTYGK 551
          |||
          Oy          421 EAGYATGYSSISDGGWMIITKTASGNSRGHFGASASVGYOW 461
          |||
          Db          552 EAGYATGYSSISDGGWMIITKTASGNSRGHFGASASVGYOW 592
          |||

RESULT 3
A:16138
A:adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Fejlschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
A.; Goehyne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glöck, A.; Kelley, J.M.; Weidman,
J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
```

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Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MIMD:95350630; PMID:7542800
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:LA2023; NID:91574598; PID:91574589; TIGR:H11732

Query Match          16.7%; Score 393.5; DB 2; Length 298;
Best Local Similarity 50.6%; Pred. No. 3.7e-14;
Matches 91; Conservative 23; Mismatches 49; Indels 17; Gaps 5;

Oy          9 VGTETKLS--FSANGN-----KVNITSDTKGLNFAKETAGTNGDTVHLNGISLTDT 57
          |||
          Db          116 VETAKVSDTLTIGGNTPAAGATPKVSTSTADGLKAK--GTNDFTVHLNGLASTLP 172
          |||
          Oy          58 DTLLNTGATTNTYNDNVTDDEKRRASVYKDVNAGMNTKGVKPGTAA--SDVAVDVRVRYDPEFLS 117
          |||
          Db          173 DVTNTGASTSVT--FSPSDIEKTRATIDVNLNAGMNTKGVKPGTAA--SDVAVDVRVRYDPEFLS 231
          |||
          Oy          118 EFLSADTKTTNTVNESKDNKKTETVIGAKTSYIKERDGLVTKD--KGENGSSSTDEGEGLVTK 175
          |||
          Db          232 EFLTGDKNLTVVLTAKENKKTETVIGAKTSYIKERDGLVTKD--KGENGSSSTDEGEGLVTK 291
          |||

RESULT 4
A:82671
A:surface protein XFI529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MIMD:20365717; PMID:10910347
A:Note: For a complete list of authors see reference number A59328 below
A:Accession: D82671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2059 <STM>
A:Cross-references: GB:AE003982; GB:AE003849; NID:9106554; PIDN:AAF84338.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Brites, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fr
J.D.; Duneira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chdo, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.V.; Sawa
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahov, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XFI529

Query Match          16.0%; Score 375.5; DB 2; Length 2059;
Best Local Similarity 25.4%; Pred. No. 3.7e-12;
Matches 155; Conservative 76; Mismatches 183; Indels 197; Gaps 26;

Oy          1 NNETDITS-VGTETKLSFSGANG-----KVNITSDTKGLNFAKETAGTNGDTVHLNGI--- 52
          |||
          Db          1496 SNELVITSHSTSSVYTLNNGSVVNRVTNNGD-----GVNIDVVVYVNDLGLS 1544
          |||
          Oy          53 ---GSLTDTLLNTGCA--TNTVT-----NDVNTDDEKRRASVYKDVNAGMNT----- 95
          |||
          Db          1545 IYVGASLTLTSGINAGSHKKTITVYAGTGTEDVAVNFSOLK---SVSEAVDVGKMTLTSANGANG 1601
          |||
```











Oy	85	YKDV-----	LNAGNNIKGVPRGTTASDNVDF-----	VRDYVEFL--	SADT	124
Db	616	VKNVTLNNDSELANNL	SLNASHNVTPLNNKSKLSAOKADIKAVNLT	TLNDTTELTAKNLDI		675
Oy	125	KTTTVNVESKONGKRT	EVKIGAKTSVIREKDKL-----	YNGKD		163
Db	676	NSTTIT-----	NGGTLAGITANITTEKLNKREKLLI	AEONLFTVNGSHYENKGDIVSKD		731
Oy	164	K-----	GENGSSTDEGEGLVTAKEVIDAVAKAGMRKMTT	TANGOTGQADFEVYTSGTNY		218
Db	732	KATVFEKNSDFTSNGSK	LVMAQN-----	QLKVNNNFTTISGD--	DITLLGNV	778
Oy	219	TF-ASGKGTATVSKD	QGNITVYMDVNVGDALNVQLQN----	SGMNLDSKAVAGSSGK		273
Db	779	TLNAGTFT-----	NSGNLFTVTKTLVDGIDQNF	TWKGMLTVGEDLHKISKRTITNDGK		831
Oy	274	VIS-----	GN-----	VSPSKGKMD		288
Db	832	LISIKNLNISSEADFI	NNGTLLGIEALKIATKCNFTNKEKALLIASN	SLDLSVAGEK--K		889
Oy	289	TVN-----	INAGNNIEITRNK--	NIDATSMT-QQFSVSIGAGADAPTL	SVGDALNVGS	342
Db	890	TFNNOTIEGKMLNIT	NTGCAFLVNDATIRSEVLNITTS	IGVNSNNITL-ISNRLNITS		948
Oy	343	KKDNKPRVITNVA	PG-----	VKEGDVTN-----	VAQLKGVAQNLNRRIDNV	383
Db	949	-----	AANFTNESNGTVMSNGLLNITAKQGNIT	NNKMLIASRQQLNTFAVADNITN----		998
Oy	384	DGNARAGTQAATATAG	LV-----	QAYLPG-----	KSMMAIGGTTY	418
Db	999	DSNISNKTA-VLHSL	ONISLNSKQOYVNLGEIYAGNNISVKAHQLKNDV	KLMGDIITTKTK		1057
Oy	419	RCGAGYAIGYSISD	GGNMWIKGTASGNSRGHFGASASVGY			459
Db	1058	EGQASTKYLQAS-----	NGHFGNDSSSG			1082

RESULT 14

I40711

sapB protein - Campylobacter fetus

C.Species: Campylobacter fetus

C.Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 08-Oct-1999

C.Accession: I40711

R: Dworkin, J.; Tummuru, M. K.; Blaser, M. J.

J. Biol. Chem. 270, 15093-15101, 1995

A.Title: Segmental conservation of sapA sequences in type B Campylobacter fetus cells.

A.Reference number: A56999; MUID:95318069; PMID:7797493

A.Status: preliminary

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-936 <RES>

A.Cross-References: EMBL:U25133; NID:g801999; PIDN:AAA79683.1; PID:g802000

C:Genetics: sapB

Query Match	8.3%	Score 194;	DB 2;	Length 936;
Best Local Similarity	23.0%;	Pred. No. 0.0061;		
Matches	118;	Conservative	66;	Mismatches 223; Indels 106; Gaps 22
QY	4	TDLTSVGTGKLSF-----	SANKNKVITSDTGLNFAKCTAGTGTGVLNGI	52
		I : I : I :	I : I : I :	I : I :
DB	325	TAFATAGTGKVDVAGKITALTALDASGTSVNLATNDITLTSA-----	NAATSVNLKTS	378
QY	53	GSTLTDLTNGCATNTVND-----	NYDDEKRAASKVDYLNACGNIKGVAPGTTASLN	107
		I : I : I : I : I :	I : I : I :	I :
DB	379	GAAKSATITTSANAAANITITDAGVAAYTSAPRAVENILTVKHATNTVTLAGMMDKLAVTLDN		438
QY	108	VDF-----	VRTYVEFLSADTKTTTVNVEKSD-----	NGKKEVYKIG A-----
		I : I : I : I :	I : I : I :	I : I :
DB	439	AALTAIAIDIKSASTLNLINSSVGNHISITPAADVTVHLHSGSAAKVKLNTATDQTVTLK		498
QY	153	EK--GCKLVLTGCKDKENKSSDDEGG-----	LVTAKEVIDAVNKAQRMKTTTN-----	200

```

Db      499 ANATDNLSLEFDGTAKTITSVTASGSGKTLVIGAEVETLVN-----IDTTFAGADYVS 553
QY      201 GGTGGADPFETVYTSCTNTNTFASGKGTATVSK--DDQGNIFYWYDVNVGDALNVOLNS 258
Db      554 GKDAOSGKRF-SVKTGTGDGKIEFVGTTLLEGSVIGAGADDTIAMKSAALTISANFTMIKN 612
QY      259 GWNL---GSKAAGSGSGKVISGNSVSPSKCKMDETVINAGNNIEIR-----302
Db      613 E-NVAISDAVATADLSSAFKNIIITTKRAADTTLTLLINKDQYINFAADRGSKVLTKL 671
QY      303 ---NGKN--IDTATMTPOFSSVSIGAGADAPPLSYDG--DALNVS--KKDKPVARITNV 354
Db      672 NDVYTGANVYVKIVLDDAAKADASIALGTEATIDKALVYIDTETIINTISLVKATSPENTANT 731
QY      355 APGVKEGVDTNVAOLKGVANQNLNNRIDVNGNARAGIAQAIATAGVQVAILPKSMAIG 414
Db      732 V-NAKLTYTSTII-----IDGPAKITLGHNA-GTAGDYSKVSIMIDRAL- 773
QY      415 GGTYYGAGYAIGYSSISDGGWIIITKGTASGNS 447
Db      774 -----KAGLTFDASATITLGANATYTKGSGGADS 800

```

RESULT 15  
AF0394  
Probable adhesin *hmwa* [Imported] - *Yersinia pestis* (strain CO92)  
C:Species: *Yersinia pestis*  
C:Date: 02-Nov-2001 #sequence.revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AF0394  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Farrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586350  
A:Accession: AF0394  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 11910 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:q15981183; GSPDB:GND0175  
C:Genetics:  
A:Gene: *hmwa*

```

Query Match      8.2%; Score 192.5; DB 2; Length 1910;
Best Local Similarity 23.5%; Pred. No. 0.019;
Matches 118; Conservative 62; Mismatches 159; Indels 163; Gaps 26.

QY      13 KLSFANKNKNVITS-----DTKGLFAFAETAGT-----NGDPTVHLNGI-GS-- 54
      11 : : : : | | | | : : | | | | | | : : : : | |
DB      837 KISGSSSSNNVNTTNGHISLAVNGKEIGSTVSVDYANIITAKGDELNTITGKKSPE 896
      11 : : : : | | | | : : | | | | | | : : : : | |
QY      55 -TLPTLLNTGATVNT--NDNV--TDDEKKRAASVDVLNAGMNTKGV---KPGSTASD 106
      11 : : : : | | | | : : | | | | : : | | : : | | : :
DB      897 NNATITANNISNGIITANDAVLMTNITFLTAGDIDKTDLTS--PKGLMFRONGMTTAA 954
      11 : : : : | | | | : : | | | | : : | | : : | | : :
QY      107 NVDFVRYDYVEFLSADTKTTTVNESKDNCKRTEVKIGAKTSVIKEKDGKLVTKSDGE 166
      11 : : : : | | | | : : | | | | : : | | : : | | : :
DB      955 NILVAN-----STSGSEYTKINSSN-----KNITAGKDISIIAGNSKTA 997
      11 : : : : | | | | : : | | | | : : | | : : | | : :
QY      167 NGSSTDEGEGLTAKEVIDAVNAKGMRAKKT---TANGQIGQADKFEVYSGTVNT--- 219
      11 : : : : | | | | : : | | | | : : | | : : | | : :
DB      998 TGFNTN-----IENVN-----IETNNGNFTNGIT-----STWLSGVNVSANG 1033
      11 : : : : | | | | : : | | | | : : | | : : | | : :
QY      220 --FAAGSKGTATVSKDDGNTIVMTDVNV-----GDALVNVLONLQSGMWLDSKAVNG 269
      11 : : : : | | | | : : | | | | : : | | : : | | : :
DB      1036 VDTTSNSTGTGIVLDNTNIIITTVGDINTIYTNSSGKGIMIKSNSTLNS--NKDITTEGV 1093
      11 : : : : | | | | : : | | | | : : | | : : | | : :
QY      270 SSGK-----VISGNSPSKGMKDEYNI-----NAGN-----NIETFRNGKNIDIA 310
      11 : : : : | | | | : : | | | | : : | | : : | | : :
DB      1094 SAGNGEGYIIQSSSASKRNNISAGCNTITLIGMGNGSOHLLINLGNVSTISGKNRIDN 1155
      11 : : : : | | | | : : | | | | : : | | : : | | : :
QY      311 TSMPTQFSSVSIAGACADAPTLSDGALNVGSKDKNKPVRTTNVAPGVKEGDTVNAOLK 370
      11 : : : : | | | | : : | | | | : : | | : : | | : :

```

Db	1154	GS-----SAGTG-----	DYFTNVELNATAGNVSIYAETK	1183
QY	371	GVAQNINNRIDNVNGN----	ARAGIAQAIAATAGLVOAYLPGKSMMAIGGGTYRGEAGYAI	426
Db	1184	TALSTSLNAYVLSIGGNNSIKAONG-----	WLIKKA-----FWTTOGAGI	1222
QY	427	GY---SSIDGGMWIKGTASG	445	
Db	1223	GFRANSSLSVDGNILKGETEG	1244	

Search completed: October 6, 2003, 09:33:34  
Job time : 15.1962 secs

PN WO200155182-A1.  
XX  
XX 02-AUG-2001.  
PD  
PF 25-JAN-2001; 2001WO-AU00069  
PF  
XX 25-JAN-2000; 2000US-0177917  
XX  
PR

PA (UYOU ) UNITV QUEENSLAND.  
 XX  
 XX Peak IRA, Jennings MP;  
 XX  
 XX MPI: 2001-488774/53.  
 DR N-PSDB; AAS09124.  
 XX  
 XX New Nhba surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 XX  
 PS Claim 12; Fig 5; 91pp: English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhba  
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhba deletion mutant #1.  
 CC  
 XX  
 SQ Sequence 512 AA;

Query Match 100.0%; Score 2600; DB 22; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-154;  
 Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIRIILNSALNMVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 60  
 DB 1 MNKIRIILNSALNMVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 60  
 QY 61 GTEKISFSANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGISLTPTLTLTGATTV 120  
 DB 61 GTEKISFSANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGISLTPTLTLTGATTV 120  
 QY 121 TNDNVTDEKRRASAVKVDLNMGNIKGVKPGTTASDNDVFATYTVFEFLSADTFTTV 180  
 DB 121 TNDNVTDEKRRASAVKVDLNMGNIKGVKPGTTASDNDVFATYTVFEFLSADTFTTV 180  
 QY 181 NVESKDNKGKTEVKIGAKTSVIRKDKLVTKDKGENSSSTDEGEGLVTAKEVIDAVNK 240  
 DB 181 NVESKDNKGKTEVKIGAKTSVIRKDKLVTKDKGENSSSTDEGEGLVTAKEVIDAVNK 240  
 QY 241 AGMRKMTTANOTGQADKFEYVTSCTNTPASGKTTATVSKDDOGNTTAVTDVAVGA 300  
 DB 241 AGMRKMTTANOTGQADKFEYVTSCTNTPASGKTTATVSKDDOGNTTAVTDVAVGA 300  
 QY 301 LNVNOLONGSMNIDSKAVAGSSGKVTSGNVSPSKGMDFTVININAGNNIEITRNGKNIDI 360  
 DB 301 LNVNOLONGSMNIDSKAVAGSSGKVTSGNVSPSKGMDFTVININAGNNIEITRNGKNIDI 360  
 QY 361 AFSMTPOFSSSVLSIGAGADAPTLISVDGDLNVGSKDKNKEPVRTTNVAPVKEGDTVNAOL 420  
 DB 361 AFSMTPOFSSSVLSIGAGADAPTLISVDGDLNVGSKDKNKEPVRTTNVAPVKEGDTVNAOL 420  
 QY 421 KQVACLNLNRINDVGNAGNARAQAATATAGLVQAYIRPGSSMAIGGCTRGEGVAGIS 480  
 DB 421 KQVACLNLNRINDVGNAGNARAQAATATAGLVQAYIRPGSSMAIGGCTRGEGVAGIS 480  
 QY 481 SISDGNMTIKGTASGNSRGHFGASASVGYQW 512  
 DB 481 SISDGNMTIKGTASGNSRGHFGASASVGYQW 512

RESULT 2  
 AAY27202  
 ID AAY27202 standard; Protein; 591 AA.  
 XX

AC AAY27202;  
 XX  
 XX 24-SEP-1999 (first entry)  
 XX  
 XX Amino acid sequence of N. meningitidis protein ORF40-1.  
 DE  
 XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
 KW bacterial infection; treatment.  
 XX  
 XX Neisseria meningitidis.  
 OS  
 XX WO936544-A2.  
 PN  
 XX 22-JUL-1999.  
 PD  
 XX 14-JAN-1999; 99WO-1B00103.  
 PF  
 XX 09-OCT-1998; 98GB-0022143.  
 PR 14-JAN-1998; 98GB-0000760.  
 PR 01-SEP-1998; 98GB-0019015.  
 XX  
 XX (CHIR-) CHIRON SPA.  
 PA  
 XX Grandi G, Massignani V, Piazza M, Rappuoli R, Scarlato V;  
 PI  
 XX MPI: 1999-444400/37.  
 DR  
 XX N-PSDB; AAX99124.  
 DR  
 XX  
 PT New protein and its nucleotide sequence, useful in vaccines or  
 PT diagnostic compositions for treating and/or preventing Neisseria  
 PT meningitidis infections  
 XX  
 XX Claim 1; Page 62; 123pp; English.\*  
 PS  
 XX The invention provides proteins (AAY27201-245) from Neisseria  
 CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
 CC encoding the proteins. Compositions comprising the protein, nucleic acid  
 CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
 CC vaccine composition or a diagnostic composition. The composition is also  
 CC useful for treating or preventing an infection due to Neisseria  
 CC bacteria, especially Neisseria meningitidis.  
 CC  
 XX  
 SQ Sequence 591 AA;

Query Match 98.1%; Score 2550.5; DB 20; Length 591;  
 Best Local Similarity 86.6%; Pred. No. 1.1e-150;  
 Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIRIILNSALNMVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 54  
 DB 1 MNKIRIILNSALNMVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 60  
 QY 55 -----TDLTSVTEKELSFASANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 101-  
 DB 55 -----TDLTSVTEKELSFASANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 101-  
 QY 121 NGTNFTSVLSKDETDLTSVTEKELSFASANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
 DB 121 NGTNFTSVLSKDETDLTSVTEKELSFASANGKVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
 QY 102 GIGSTLTPTLLNTGATNTNTNNDVDEKRRASAVSDVNLNAGNNIKGVKPGTTASDNDVF 161  
 DB 102 GIGSTLTPTLLNTGATNTNTNNDVDEKRRASAVSDVNLNAGNNIKGVKPGTTASDNDVF 161  
 QY 181 GIGSTLTPTLLNTGATNTNTNNDVDEKRRASAVSDVNLNAGNNIKGVKPGTTASDNDVF 240  
 DB 181 GIGSTLTPTLLNTGATNTNTNNDVDEKRRASAVSDVNLNAGNNIKGVKPGTTASDNDVF 240  
 QY 241 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIRKDKLVTKDKGENSS 221  
 DB 241 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIRKDKLVTKDKGENSS 221  
 QY 222 TDEGEGLVTAKEVIDAVNKAQMRKMTTANOTGQADKFEYVTSCTNTPASGKTTATV 281  
 DB 222 TDEGEGLVTAKEVIDAVNKAQMRKMTTANOTGQADKFEYVTSCTNTPASGKTTATV 281  
 QY 301 TDEGEGLVTAKEVIDAVNKAQMRKMTTANOTGQADKFEYVTSCTNTPASGKTTATV 360  
 DB 301 TDEGEGLVTAKEVIDAVNKAQMRKMTTANOTGQADKFEYVTSCTNTPASGKTTATV 360  
 QY 282 SKDDOGNTTAVTDVAVGDLNVLNOLONGSMNIDSKAVAGSSGKVTSGNVSPSKGMDFTVIN 341

```
Db      361 SKDDGNTITVMYDVNVDALNVQNLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETV 420
QY      342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPPR 401
Db      421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPPR 480
QY      402 ITNVAPVKEGDVTNVAQLKGVANLNRIIDNVGNARAGIAOAIATAGLVQAYLPKSKM 461
Db      481 ITNVAPVKEGDVTNVAQLKGVANLNRIIDNVGNARAGIAOAIATAGLVQAYLPKSKM 540
QY      462 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 512
Db      541 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 591

RESULT 3
AA23746
ID      AA23746 standard; Protein; 591 AA.
XX
AC      AA23746;
XX
DT      08-SEP-1999 (first entry)
XX
DE      A surface protein of Neisseria meningitidis.
XX
KM      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX
OS      Neisseria meningitidis.
XX
PN      W09931132-A1.
XX
PD      24-JUN-1999.
XX
PF      14-DEC-1998; 98WO-AU01031.
XX
PR      12-DEC-1997; 97GB-0026398.
XX
PA      (ISTS-) ISTS INNOVATION LTD.
XX      (UYOU ) UNIV QUEENSLAND.
XX
PI      Jennings MP, Moxon ER, Peak IRA;
XX
DR      MPI: 1999-418754/35.
XX      DR N-PSDB; AAX85798.
XX
PT      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX
PS      Claim 1; Page 127-128; 132pp; English.
XX
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX
SQ      Sequence 591 AA;

Query Match      98.1%; Score 2550.5; DB 20; Length 591;
Best Local Similarity 86.6%; Pred. No. 1.1e-150;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY      1 MKKIVITINSALNAVYVSELTRNHTKRASATVKTAVLATLTFATVOASANNE----- 54
Db      1 MKKIVITINSALNAVYVSELTRNHTKRASATVKTAVLATLTFATVOASANNEQEDDL 60
QY      55 ----- 54
```

```
Db      61 YLDPVORTAVAILVNSDKECTGCKEKEENSQMAVYFNEKGVLTAREITLKAGDNLKIQ 120
QY      55 -----TDLTSVGETEKLSPSANGKNKNTISDRKGLNFAKETACTNDQTYHLN 101
Db      121 NGTNFTYSLKRDLDLTLDSVGETEKLSPSANGKNKNTISDRKGLNFAKETACTNDQTYHLN 180
QY      102 GIGSTLTDLTLNGATTNTVNDVNDVDEKRRASAVDVLNAGNNINGVKRGCTTASDVDF 161
Db      181 GIGSTLTDLTLNGATTNTVNDVNDVDEKRRASAVDVLNAGNNINGVKRGCTTASDVDF 240
QY      162 VRTYDVEFLSADTKTTTNNVESKDNKGKTEVKGAKTSYIKERDKLYTGKDKGENGSS 221
Db      241 VRTYDVEFLSADTKTTTNNVESKDNKGKTEVKGAKTSYIKERDKLYTGKDKGENGSS 300
QY      222 TDEGEGLVTAKVEYDAVNKAQFMKTTTANGOTGQADKFEETVTSGTNVTFASGKGTATV 281
Db      301 TDEGEGLVTAKVEYDAVNKAQFMKTTTANGOTGQADKFEETVTSGTNVTFASGKGTATV 360
QY      282 SKDDGNTITVMYDVNVDALNVQNLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETV 341
Db      361 SKDDGNTITVMYDVNVDALNVQNLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETV 420
QY      342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPPR 401
Db      421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPPR 480
QY      402 ITNVAPVKEGDVTNVAQLKGVANLNRIIDNVGNARAGIAOAIATAGLVQAYLPKSKM 461
Db      481 ITNVAPVKEGDVTNVAQLKGVANLNRIIDNVGNARAGIAOAIATAGLVQAYLPKSKM 540
QY      462 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 512
Db      541 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 591

RESULT 4
AAU06171
ID      AAU06171 standard; Protein; 591 AA.
XX
AC      AAU06171;
XX
DT      24-OCT-2001 (first entry)
XX
DE      N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
XX
KM      Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
OS      Neisseria meningitidis strain PMC21.
XX
PH      key
XX      Location/Qualifiers
XX      1..51
XX      /label= Signal_peptide
XX      1..50
XX      /label= C1
XX      /note= "Conserved region 1"
XX      51..108
XX      /label= V1
XX      /note= "Variable region 1"
XX      52..591
XX      /label= Mature_NhhA
XX      /note= "predicted mature protein, specifically
XX      claimed in claim 12"
XX
FT      109..120
FT      /label= C2
FT      /note= "Conserved region 2"
FT      121..124
FT      /label= V2
FT      /note= "Variable region 2"
FT      125..188
FT      /label= C3
FT      /note= "Conserved region 3"
FT      189..210

Region
Region
Region
Region
```

```

FT      /label= V3
FT      /note= "Variable region 3"
FT      211..229
FT      Region
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      Region
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..591
FT      /label= C5
FT      /note= "Conserved region 5"
XX
XX      WO20015182-A1.
XX
XX      02-AUG-2001.
XX
XX      25-JAN-2001; 2001WO-AU00069.
XX
XX      25-JAN-2000; 2000US-0177917.
XX
XX      (UYQU ) UNIV QUEENSLAND.
XX
XX      Peak IRA, Jennings MP;
XX
XX      WPI; 2001-488774/53.
XX      N-PSDB; AAS09161.
XX
XX      New Nhha surface antigen polypeptides and polynucleotides from
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      preventing broad spectrum of Neisseria meningitidis .
XX
XX      Claim 9; Fig 1; 91pp; English.
XX
XX      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Nhha
XX      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX      characterized by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      medicaments. The mutant proteins when used as a vaccine can effectively
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      would be expected from a corresponding wild-type surface antigen.
XX      CC The present sequence representing the wild type surface antigen Nhha
XX      from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
XX
XX      Sequence 591 AA:
SQ
Query Match      98.1%; Score 2550.5; DB 22; Length 591;
Best Local Similarity 86.6%; Pred. No. 1.1e-150;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
QY      1 MNKIVRIIWSNLSALNMAVYSELTRNHTKRASATVTAVALATLLFAFVQASANNE----- 54
DB      1 MNKIVRIIWSNLSALNMAVYSELTRNHTKRASATVTAVALATLLFAFVQASANNEQEDL 60
QY      55 ----- 54
DB      61 YLDPVQRTVAVLIVNSDEKTEGKEKEVEENSDMAVYFNEKGVLPAREITLAKGDNLIKIQ 120
QY      55 ----- 101
DB      121 NGTNFTYSIKKDLTDLTSTVTEKLSFSANGNKVNITSDTKGNFAKETAGTNGDTVHLN 180
QY      102 GIGSTLTPTLNTGATNTVNDNVTDDEKRAASVYKVDVLAAGWNLKGVKPGTTASDNVDF 161
DB      181 GIGSTLTPTLNTGATNTVNDNVTDDEKRAASVYKVDVLAAGWNLKGVKPGTTASDNVDF 240
QY      162 VRTYTVTEFLSADTITTYVNVSKNGKKTEYKIKAKTSVIEKKGKLVTKGDKGENSS 221
DB      241 VRTYTVTEFLSADTITTYVNVSKNGKKTEYKIKAKTSVIEKKGKLVTKGDKGENSS 300

```

```

QY      222 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEETVTSSTNTVFSAGKGTATV 281
DB      301 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEETVTSSTNTVFSAGKGTATV 360
QY      282 SKDDGNTITVYDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKVIISGVNPSKGMDETV 341
DB      361 SKDDGNTITVYDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKVIISGVNPSKGMDETV 420
QY      342 NINAGNNIEITRNKGNIDTATSMTPQFSSVSLGAGADAPTISVDDDALNVSKKDNKPYR 401
DB      421 NINAGNNIEITRNKGNIDTATSMTPQFSSVSLGAGADAPTISVDDDALNVSKKDNKPYR 480
QY      402 ITNVAPEGKEDVTVNAQLKGYAQNLRNIDNVGNARAGIAQAIATAGLYOAYLPGKSM 461
DB      481 ITNVAPEGKEDVTVNAQLKGYAQNLRNIDNVGNARAGIAQAIATAGLYOAYLPGKSM 540
QY      462 MAIGGTYRGEAGYAIYSSISDGGNWIITKGTASNSRGRHFGASASVGYOW 512
DB      541 MAIGGTYRGEAGYAIYSSISDGGNWIITKGTASNSRGRHFGASASVGYOW 591

RESULT 5
AAV23737
ID      AAV23737 standard; Protein: 592 AA.
XX
XX      AAV23737;
XX
XX      08-SEP-1999 (first entry)
XX
XX      A surface protein of Neisseria meningitidis.
XX
XX      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX
XX      Neisseria meningitidis.
XX
XX      WO9931132-A1.
XX
XX      24-JUN-1999.
XX
XX      14-DEC-1998; 98WO-AU01031.
XX
XX      12-DEC-1997; 97GB-0026398.
XX
XX      (ISTS-) ISIS INNOVATION LTD.
XX      (UYQU ) UNIV QUEENSLAND.
XX
XX      Jennings MP, Moxon ER, Peak IRA;
XX
XX      WPI; 1999-418754/35.
XX      N-PSDB; AAX85788.
XX
XX      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX
XX      Claim 1; Page 86-87; 132pp; English.
XX
XX      The present sequence represents a surface protein of Neisseria
XX      meningitidis which is approximately 62 kDa. The N. meningitidis
XX      surface glycoproteins, nucleic acids, the primers and optionally
XX      a thermostable polymerase, or antibodies are useful in a kit for
XX      the detection or diagnosis of N. meningitidis infection in humans.
XX      CC The N. meningitidis surface glycoproteins can also be used to
XX      prevent or treat N. meningitidis infection in humans, especially
XX      in the form of vaccines. The proteins and antibodies can also
XX      be used to identify immunoreactive peptides.
XX
XX      Sequence 592 AA:
SQ
Query Match      97.9%; Score 2546; DB 20; Length 592;
Best Local Similarity 86.3%; Pred. No. 2.1e-150;
Matches 511; Conservative 0; Mismatches 1; Indels 80; Gaps 1;

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```
QY 1 MNKIRIIMNSALNAAWVVSSELTNRNHTKRASATYKTAVALTLLEFATYQASANNE----- 54
   |||||||
Db 1 MNKIRIIMNSALNAAWVVSSELTNRNHTKRASATYKTAVALTLLEFATYQASANNEPRKKD 60
   |||||||
QY 55 ----- 54
   |||||||
Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVVEFNEKGVLTAREITLKAGDNLKIK 120
   |||||||
QY 55 -----TDLTSVGEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 100
   |||||||
Db 121 QNGTNFTYSLKKDLTDLTSVGEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180
   |||||||
QY 101 NGIGSTLDLTLLNTGATTNTNDVNTDEKKRAASVADVNLNAGNINIGVAPGTASPNVD 160
   |||||||
Db 181 NGIGSTLDLTLLNTGATTNTNDVNTDEKKRAASVADVNLNAGNINIGVAPGTASPNVD 240
   |||||||
QY 161 FVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 220
   |||||||
Db 241 FVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 300
   |||||||
QY 221 STDEGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFTVTSCTNVTFASGKGTAT 280
   |||||||
Db 301 STDEGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFTVTSCTNVTFASGKGTAT 360
   |||||||
QY 281 VSKDQGNITVMDVNVGDLNVNQLQNSGNLDSKAVASGSGKVISGNTSPSKGKMDT 340
   |||||||
Db 361 VSKDQGNITVMDVNVGDLNVNQLQNSGNLDSKAVASGSGKVISGNTSPSKGKMDT 420
   |||||||
QY 341 VNINAGNNIEITRNGKNIDIAITSMTPQSSVSLGAGADAPTLSDGDALNVGSKDKNPV 400
   |||||||
Db 421 VNINAGNNIEITRNGKNIDIAITSMTPQSSVSLGAGADAPTLSDGDALNVGSKDKNPV 480
   |||||||
QY 401 RITNVAGVVEGDTNTNAQLKGVANLNRRIDNVDAAGARAGIAQAITAGLYQAYLYDKGS 460
   |||||||
Db 481 RITNVAGVVEGDTNTNAQLKGVANLNRRIDNVDAAGARAGIAQAITAGLYQAYLYDKGS 540
   |||||||
QY 461 MMAIGSGTYGEGAGYGAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 512
   |||||||
Db 541 MMAIGSGTYGEGAGYGAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 592
   |||||||

RESULT 6
AAV57045
ID AAV57045 standard; Protein; 591 AA.
XX
AC AAV57045;
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KM BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KM Infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AAC"
FT Misc-difference 123 /note= "Encoded by AATC"
FT Misc-difference 133 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX
```

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PN WO958683-A2.
XX
PD 18-NOV-1999.
XX
PE 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
XX WPI: 2000-053103/04.
XX N-PDSB: AA239865.
XX
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
XX
PS Claim 4; Fig 2; 74pp; English.
XX
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 591 AA;
XX
Query Match 97.8%; Score 2543.5; DB 21; Length 591;
Best Local Similarity 86.3%; Pred. No. 3e-150;
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;
QY 1 MNKIRIIMNSALNAAWVVSSELTNRNHTKRASATYKTAVALTLLEFATYQASANNE----- 54
   |||||||
Db 1 MNKIRIIMNSALNAAWVVSSELTNRNHTKRASATYKTAVALTLLEFATYQASANNEQGEEDL 60
   |||||||
QY 55 ----- 54
   |||||||
Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVVEFNEKGVLTAREITLKAGDNLKIK 120
   |||||||
QY 55 -----TDLTSVGEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 101
   |||||||
Db 121 NGSNFTYSLKKDLTDLTSVGEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180
   |||||||
QY 102 GIGSTLDLTLLNTGATTNTNDVNTDEKKRAASVADVNLNAGNINIGVAPGTASPNVD 161
   |||||||
Db 181 GIGSTLDLTLLNTGATTNTNDVNTDEKKRAASVADVNLNAGNINIGVAPGTASPNVD 240
   |||||||
QY 162 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 221
   |||||||
Db 241 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 300
   |||||||
QY 222 TDEGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFTVTSCTNVTFASGKGTATV 281
   |||||||
Db 301 TDEGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFTVTSCTNVTFASGKGTATV 360
   |||||||
QY 282 SKDQGNITVMDVNVGDLNVNQLQNSGNLDSKAVASGSGKVISGNTSPSKGKMDT 341
   |||||||
```

Db 361 SKDDGNTITVMYDVNVGDALNVNQLONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDTV 420  
 QY 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 401  
 Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 480  
 QY 402 ITNVAPGVEGDVTNVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKSKM 461  
 Db 481 ITNVAPGVEGDVTNVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKSKM 540  
 QY 462 MAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGSRGHFGASASVGYQW 512  
 Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGSRGHFGASASVGYQW 591

RESULT 7  
 AAY23741  
 ID AAY23741 standard; Protein; 591 AA.  
 XX  
 AC AAY23741;  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX

DE A surface protein of Neisseria meningitidis.  
 XX  
 KM Surface protein; surface glycoprotein; infection; vaccine;  
 KM Immunoreactive peptide.  
 XX  
 OS Neisseria meningitidis.

XX WO931132-A1.  
 PN 24-JUN-1999.  
 PD  
 XX 14-DEC-1998; 98MO-AU01031.  
 PF  
 XX 12-DEC-1997; 97GB-0026398.  
 PR  
 XX (ISIS-) ISIS INNOVATION LTD.  
 PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA;  
 XX  
 DR WPI; 1999-418754/35.  
 DR N-PSDB; AAX85793.  
 XX

XX Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 104-106; 132pp; English.

CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 97.6%; Score 2538.5; DB 20; Length 591;  
 Best Local Similarity 86.3%; Pred. No. 6,2e-150;  
 Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;

QY 1 MNKRYRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNE----- 54  
 Db 1 MNEIIRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60  
 QY 55 ----- 54

Db 61 YLDDPLRTAVAVILVNSDKEGTGEKEVEENSQWAVYFNEKGVLTAAREITLKAGDNLKIKO 120  
 QY 55 -----TDLTSVGTETKLSFANGKNVINTSDTKGLNFAKETAGTNGDTVHLN 101  
 Db 121 NGTNFTYSLKKDLTDLTSTGETKLSFANGKNVINTSDTKGLNFAKETAGTNGDTVHLN 180  
 QY 102 GIGSTLTDLTLLNTGATTTNTDNTDEKKRAASVYKDVNLNAGNNIKGVKPGTTASDNVDF 161  
 Db 181 GIGSTLTDLTLLNTGATTTNTDNTDEKKRAASVYKDVNLNAGNNIKGVKPGTTASDNVDF 240  
 QY 162 VRTYDVEEPLSADTKTTTNNVESKDKGKTEYKIGAKTSVIREKDKLVTGDKGNGSS 221  
 Db 241 VRTYDVEEPLSADTKTTTNNVESKDKGKTEYKIGAKTSVIREKDKLVTGDKGNGSS 300  
 QY 222 TDEGEGLYTAKEVIDAVNKRAGMRKTTTANGGTGADKFEYTSCTNNTFASGKGTATV 281  
 Db 301 TDEGEGLYTAKEVIDAVNKRAGMRKTTTANGGTGADKFEYTSCTNNTFASGKGTATV 360  
 QY 282 SKDDGNTITVMYDVNVGDALNVNQLONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDTV 341  
 Db 361 SKDDGNTITVMYDVNVGDALNVNQLONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDTV 420  
 QY 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 401  
 Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 480  
 QY 402 ITNVAPGVEGDVTNVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKSKM 461  
 Db 481 ITNVAPGVEGDVTNVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKSKM 540  
 QY 462 MAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGSRGHFGASASVGYQW 512  
 Db 541 MAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGSRGHFGASASVGYQW 591

RESULT 8  
 AAU06175  
 ID AAU06175 standard; Protein; 591 AA.  
 XX  
 AC AAU06175;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis EG329 surface antigen NhaA polypeptide sequence.  
 XX  
 KM Surface antigen NhaA; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain EG329.  
 XX  
 FH Key  
 FT Location/Qualifiers  
 FT 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT  
 FT Region  
 FT 51..108  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT  
 FT Region  
 FT 109..120  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT  
 FT Region  
 FT 121..124  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT  
 FT Region  
 FT 125..188  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT  
 FT Region  
 FT 189..210  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT  
 FT Region  
 FT 211..229  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT  
 FT Region  
 FT 230..236  
 FT /label= V4

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FT      /note="Variable region 4"
FT      Region      237..591
FT      /label=C5
FT      /note="Conserved region 5"
XX      WO200155182-A1.
XX
XX      02-AUG-2001.
XX
XX      25-JAN-2001; 2001WO-AU00069.
XX
XX      25-JAN-2000; 2000US-0177917.
XX
XX      (UYOU ) UNIV QUEENSLAND.
XX
XX      Peak IRA, Jennings MP;
XX
XX      WPI; 2001-488774/53.
XX
XX      N-PSDB; AAS09165.
XX
XX      New Nhba surface antigen polypeptides and polynucleotides from
XX      PT Neisseria meningitidis, useful in producing vaccines for treating or
XX      PT preventing broad spectrum of Neisseria meningitidis -
XX
XX      Claim 9; Fig 1; 91pp; English.
XX
XX      The present invention relates to the isolation of novel Neisseria
XX      CC meningitidis mutant polypeptides of the surface antigen Nhba
XX      CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
XX      CC characterised by deletions of non-conserved amino acids, particularly
XX      CC the deletion of variable regions. The deletion mutants are useful in
XX      CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC spectrum of N. meningitidis, and in designing and/or screening of
XX      CC medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC immunise against a broader spectrum of N. meningitidis strains than
XX      CC would be expected from a corresponding wild-type surface antigen.
XX      CC The present sequence representing the wild type surface antigen Nhba
XX      CC from N. meningitidis strain EG329 is 1 of 10 Nhba polypeptide sequences
XX      CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      CC the present invention.
XX
XX      Sequence 591 AA;
SQ
Query Match      97.6%; Score 2538.5; DB 22; Length 591;
Best Local Similarity 86.3%; Pred. No 6.2e-150;
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;
QY      1 MNKIRIIVNSALNANWVVELTRNHTKRASATVKTAVLATLLFATVQASANNE----- 54
DB      1 MNEILRIIVNSALNANWVVELTRNHTKRASATVKTAVLATLLFATVQASANNEGEDEL 60
QY      55 ----- 54
DB      61 YLDPVLTAVLIVNSDEKGTGEKEVENSMDAVFENEKGVLTAREITLKAGDNLIKQ 120
QY      55 -----TDLTSVGTETKLSFGANGKNVITSDFGLNPAKTAGTNGDTVHLN 101
DB      121 NGTNTYSLKKDLTDLTSVGTETKLSFGANGKNVITSDFGLNPAKTAGTNGDTVHLN 180
QY      102 GIGSTLTDLTLLNGATTNVTNDVTDDEKRRASVSKVDLNAWNINIKVKGRTASDNVDF 161
DB      181 GIGSTLTDLTLLNGATTNVTNDVTDDEKRRASVSKVDLNAWNINIKVKGRTASDNVDF 240
QY      162 VRTYDYVEFISADTKTTTAVVESKDNKKTVEKIGATSVYIKEDGKLVYGGKDEGENSS 221
DB      241 VRTYDYVEFISADTKTTTAVVESKDNKKTVEKIGATSVYIKEDGKLVYGGKDEGENSS 300
QY      222 TDEGEGLVTAKEVIDAVNKAQMKRTTANGOTGOADKFEVTSCTNVTFASGKTATV 281
DB      301 TDEGEGLVTAKEVIDAVNKAQMKRTTANGOTGOADKFEVTSCTNVTFASGKTATV 360
QY      282 SKDDGNTVWYDVNVDALNVNQLONGSNGLDSKAVAGSSGKVISGNVSPSKGMDTV 341

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DB      361 SKDDGNTVWYDVNVDALNVNQLONGSNGLDSKAVAGSSGKVISGNVSPSKGMDTV 420
QY      342 NINAGNNIEITRBNKNIDTATSMPPQSSVSLGAGAPTLISVDGALNYSKRNKRPVR 401
DB      421 NINAGNNIEITRBNKNIDTATSMPPQSSVSLGAGAPTLISVDGALNYSKRNKRPVR 480
QY      402 ITVWAPGVKRGADVTNVNQLKGVNQLNNRINDVNDGNARAGIAQAIATAGLVQATLPCKSM 461
DB      481 ITVWAPGVKRGADVTNVNQLKGVNQLNNRINDVNDGNARAGIAQAIATAGLVQATLPCKSM 540
QY      462 MAIGGTYRGEAGYAISSISDGNWIIKGTASGNSRGRHFGASASVGYOM 512
DB      541 MAIGGTYRGEAGYAISSISDGNWIIKGTASGNSRGRHFGASASVGYOM 591

RESULT 9
AAU06183
ID      AAU06183 standard; Protein; 513 AA.
XX
XX      AAU06183;
AC      XX
XX      24-OCT-2001 (first entry)
DT      XX
XX      N. meningitidis H41 Nhba deletion mutant.
DE      XX
XX      Surface antigen Nhba; meningococcal disease; meningitis vaccine;
XX      KW mutant; muteln.
OS      Neisseria meningitidis strain H41.
XX      OS synthetic.
FH      Key      Location/Qualifiers
FT      Peptide      1..51
FT      Protein      /label=Signal-peptide
FT      /label=52..513
FT      /note="Mature_Nhba_deletion_mutant
FT      /note="Predicted mature protein, specifically
XX      claimed in claim 12"
XX      PN      WO200155182-A1.
XX      PD      02-AUG-2001.
XX      PE      25-JAN-2001; 2001WO-AU00069.
XX      PR      25-JAN-2000; 2000US-0177917.
XX      PA      (UYOU ) UNIV QUEENSLAND.
XX      PI      Peak IRA, Jennings MP;
XX      WPI; 2001-488774/53.
XX      N-PSDB; AAS09173.
XX
XX      New Nhba surface antigen polypeptides and polynucleotides from
XX      PT Neisseria meningitidis, useful in producing vaccines for treating or
XX      PT preventing broad spectrum of Neisseria meningitidis -
XX
XX      Claim 12; Fig 6; 91pp; English.
XX
XX      The present invention relates to the isolation of novel Neisseria
XX      CC meningitidis mutant polypeptides of the surface antigen Nhba
XX      CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
XX      CC characterised by deletions of non-conserved amino acids, particularly
XX      CC the deletion of variable regions. The deletion mutants are useful in
XX      CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC spectrum of N. meningitidis, and in designing and/or screening of
XX      CC medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC immunise against a broader spectrum of N. meningitidis strains than
XX      CC would be expected from a corresponding wild-type surface antigen.
XX      CC The present sequence represents N. meningitidis strain H41 surface
XX      CC antigen Nhba deletion mutant.

```

SQ Sequence 513 AA;  
Query Match 94.5%; Score 2456.5; DB 22; Length 513;  
Best Local Similarity 95.3%; Pred. No. 6 6e-145;  
Matches 489; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKKIRIINNSALNMAVAVSELTRNHTKRAATVAVATLTLFAVQASANNEDLTSV 60  
DB 1 MKKIRIINNSALNMAVAVSELTRNHTKRAATVAVATLTLFAVQANATDEDEEL 60  
QY 61 GTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTYVHLNGISLTTLMLNTGATTYV 120  
DB 61 ETEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTYVHLNGISLTTLMLNTGATTYV 120  
QY 121 TNDNTYDDEKRRASVAVKDVNLNAGWNKGVKPGTTASDNDVFRYTYDVEFLSADTKTTV 180  
DB 121 TNDNTYDDEKRRASVAVKDVNLNAGWNKGVKPGTTASDNDVFRYTYDVEFLSADTKTTV 180  
QY 181 NVESKDNKGKTEVKIGAKTSVIEKDKLVTKGDKGNGSSYDEGEGLVTAKEVIDAVNK 240  
DB 181 NVESKDNKGKTEVKIGAKTSVIEKDKLVTKGDKGNGSSYDEGEGLVTAKEVIDAVNK 240  
QY 241 AGRMKTATTANOTGADKFEYVTSNTNTPASGKTATVSKDOGNTTAVTDVAVGA 300  
DB 241 AGRMKTATTANOTGADKFEYVTSNTNTPASGKTATVSKDOGNTTAVTDVAVGA 300  
QY 301 LNVNOLONGSMNLDKRAVAGSSGKVTSGNVSPSKGMDETVNIAGNNIEITPANGKNDI 360  
DB 301 LNVNOLONGSMNLDKRAVAGSSGKVTSGNVSPSKGMDETVNIAGNNIEITPANGKNDI 360  
QY 361 AFSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKDNKPVRTTNVAPGVKEGDTVNAQ 419  
DB 361 AFSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTTNVAPGVKEGDTVNAQ 420  
QY 420 LKGVNOLNRRIDNDVGNARAGIAQAIATAGLVQAVLPKSMMAIGCGTYRGAGAIQY 479  
DB 421 LKGVNOLNRRIDNDVGNARAGIAQAIATAGLVQAVLPKSMMAIGCGTYRGAGAIQY 480  
QY 480 SSISDGNMIIRKTASGNSRGHFASASVGYOM 512  
DB 481 SSISDGNMIIRKTASGNSRGHFASASVGYOM 513

RESULT 10  
AA23743  
ID AA23743 standard; Protein; 599 AA.  
XX  
XX AA23743;  
AC  
DT 08-SEP-1999 (first entry)  
XX  
XX A surface protein of Neisseria meningitidis.  
DE  
XX  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW Immunoreactive peptide.  
XX  
XX Neisseria meningitidis.  
OS  
XX  
XX MO9931132-A1.  
PN  
XX  
XX 24-JUN-1999.  
PD  
XX  
XX 14-DEC-1998; 98WO-AU01031.  
PF  
XX  
XX 12-DEC-1997; 97GB-0026398.  
PR  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU) UNIV QUEENSLAND.  
XX  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
PI  
XX  
XX WPI; 1999-418754/35.  
DR N-PSDB; AAX85795.

XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX  
PS Claim 1; Page 114-115; 132pp; English.

CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

SQ Sequence 599 AA;  
Query Match 94.4%; Score 2453.5; DB 20; Length 599;  
Best Local Similarity 83.0%; Pred. No. 1.2e-144;  
Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

QY 1 MKKIRIINNSALNMAVAVSELTRNHTKRAATVAVATLTLFAVQASANNE----- 54  
DB 1 MKKIRIINNSALNMAVAVSELTRNHTKRAATVAVATLTLFAVQANATDEDEEEL 60  
QY 55 ----- 54  
DB 61 EPPVNSALVLPQIMIDKEGNGENESTGNTGMSIYYDNHNTLHGATVTLKAGDLKIKONTN 120  
QY 55 -----TDLTSVGETKLSFSANGKVNITSDTKGLNFAKETAAGTNG 94  
DB 121 KMTNENTNDSSEYTSLSKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAAGTNG 180  
QY 95 DPTVHLNGISLTTLTLNTGATTNTNNDVNDDEKRRASVAVKDVNLNAGWNKGVKPGTT 154  
DB 181 DPTVHLNGISLTTLTLNTGATTNTNNDVNDDEKRRASVAVKDVNLNAGWNKGVKPGTT 240  
QY 155 ASDNDVFRYTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVIEKDKLVTKGKD 214  
DB 241 ASDNDVFRYTYDVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVIEKDKLVTKGKD 300  
QY 215 KGEENGSSYDEGEGLVTAKEVIDAVNKAGRMKTATTANOTGADKFEYVTSNTNTPASG 274  
DB 301 KGEENGSSYDEGEGLVTAKEVIDAVNKAGRMKTATTANOTGADKFEYVTSNTNTPASG 360  
QY 275 KGTATTAVSKDDGNTTAVTDVAVGALNVLNOLONGSMNLDKRAVAGSSGKVTSGNVSPSK 334  
DB 361 KGTATTAVSKDDGNTTAVTDVAVGALNVLNOLONGSMNLDKRAVAGSSGKVTSGNVSPSK 420  
QY 335 GRMDETVNIAGNNIEITPANGKNDIATSMTPQFSSVSLGAGADAPTLSDVDG-DALNVGS 393  
DB 421 GRMDETVNIAGNNIEITPANGKNDIATSMTPQFSSVSLGAGADAPTLSDVDGKALNVGS 480  
QY 394 KRDNKPVRTTNVAPGVKEGDTVNAQOLKVAONLNNRIDNDVGNARAGIAQAIATAGLVQ 453  
DB 481 KRDNKPVRTTNVAPGVKEGDTVNAQOLKVAONLNNRIDNDVGNARAGIAQAIATAGLVQ 540  
QY 454 AYLPGKSMMAIGCGTYRGAGAIQYSSISDGNMIIRKTASGNSRGHFASASVGYOM 512  
DB 541 AYLPGKSMMAIGCGTYRGAGAIQYSSISDGNMIIRKTASGNSRGHFASASVGYOM 599

RESULT 11  
AAU06176  
ID AAU06176 standard; Protein; 599 AA.  
XX  
XX AAU06176;  
AC  
XX  
XX 24-OCT-2001 (first entry)  
DT  
XX  
XX N. meningitidis H38 surface antigen NhaA polypeptide sequence.  
DE  
XX







DB 541 KSMMAIGGTYRGEAGYAI GYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 15  
ID AAY23739 standard; Protein; 594 AA.  
AC AAY23739;  
XX 08-SEP-1999 (first entry)  
DE A surface protein of Neisseria meningitidis.  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KM immunoreactive peptide.  
XX Neisseria meningitidis.  
OS Neisseria meningitidis.  
PN WO9931132-A1.  
PD 24-JUN-1999.  
PF 14-DEC-1998; 98WO-AU01031.  
PR 12-DEC-1997; 97GB-0026398.  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU) UNITV QUEENSLAND.  
PI Jennings MP, Moxon ER, Peak IRA;  
DR WPI; 1999-418754/35.  
XX N-PSDB; AAX85791.  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PS Claim 1; Page 95-97; 132pp; English.  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
SQ Sequence 594 AA:

Query Match 93.9%; Score 2442; DB 20; Length 594;  
Best Local Similarity 83.3%; Pred. No. 6.3e-144;  
Matches 495; Conservative 4; Mismatches 13; Indels 82; Gaps 2;

OY 1 MNKIRIIMNSALNMVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNE----- 54  
DB 1 MNKIRIIMNSALNMVWVSELTRNHTKRASATVKTAVLATLLFATVQANATDDDDLYLE 60  
OY 55 ----- 54  
DB 61 PVQRTAVVLSFRSDEKTEGTEGTEDSNMVYFDEKRVLKAGAITLKAQDNLIKONTNE 120  
OY 55 -----TDLTSVTEKLSFSGANGKNVNTSDTKGINPAKETAGTNGDPTVH 99  
DB 121 NTNDSFTYSLKKDLTDLTSVTEKLSFSGANGKNVNTSDTKGINPAKETAGTNGDPTVH 180  
OY 100 LKNGISSTLTDTLLNTGATNTVNDVYTDDEKRAASVSKDYLNAGWNINIKGPKGTASDNV 159  
DB 181 LKNGISSTLTDTLLNTGATNTVNDVYTDDEKRAASVSKDYLNAGWNINIKGPKGTASDNV 240  
OY 160 DFVRTYDVEFLSADTKTTTVNVEESKDNKTEVKIGAKTSVIEKDKGLVTGDKGENG 219

DB 241 DFVRTYDVEFLSADTKTTTVNVEESKDNKTEVKIGAKTSVIEKDKGLVTGDKGENG 300  
OY 220 SSTDEGEGLYTAKEVIDAVNRAGWNRKTTTANGOTGQADKFEYVSGTNTFASGKGT 279  
DB 301 SSTDEGEGLYTAKEVIDAVNRAGWNRKTTTANGOTGQADKFEYVSGTNTFASGKGT 360  
OY 280 TVSKDDGNITVMDVNVGDLNVLNQLNSGWNLDKRAVAGSSGKVISGNSPSKGMDE 339  
DB 361 TVSKDDGNITVMDVNVGDLNVLNQLNSGWNLDKRAVAGSSGKVISGNSPSKGMDE 420  
OY 340 TVNINAGNNIETTRNGKNIDTATSWTPFSSVSIGAGADAPTLVSVDG-ALNVGSKKNK 398  
DB 421 TVNINAGNNIETTRNGKNIDTATSWTPFSSVSIGAGADAPTLVSVDGALNVGSKKNK 480  
OY 399 PVRTINAVPGYKESGDTNVAOLKGYAONLNNRIDVNDNARAGIAQAATAGLYOAYLP 458  
DB 481 PVRTINAVPGYKESGDTNVAOLKGYAONLNNRIDVNDNARAGIAQAATAGLYOAYLP 540  
OY 459 KSMMAIGGTYRGEAGYAI GYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512  
DB 541 KSMMAIGGTYRGEAGYAI GYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

Search completed: October 6, 2003, 09:22:25  
Job time : 46.9684 secs





Db	301	I DEEGGLTAKEVIDAVKAKGMRKMTTANQGTQADKREIYWSGNTNVPASCKGTTAYV	360
QY	282	SKDDOGNTITVMADVAGDALNVOIIONSGMNLDSKRVAGSSGKVIISGNVSPSKGKDETV	341
Db	361	SKDDOGNTITVMADVAGDALNVOIIONSGMNLDSKRVAGSSGKVIISGNVSPSKGKDETV	420
QY	342	NINAGNNIETIRFNGKNIDITATSMTPPOFSSVSLGAGADATPLSYDGBALNVGSKDKNPVR	401
Db	421	NINAGNNIETIRFNGKNIDITATSMTPPOFSSVSLGAGADATPLSYDGBALNVGSKDKNPVR	480
QY	402	ITTNVAPGVKEGDDVTNVAOLKGYAQNILNBRIDNVVGNARAGIAQAIITAGLVAAYLEPKSM	461
Db	481	ITTNVAPGVKEGDDVTNVAOLKGYAQNILNBRIDNVVGNARAGIAQAIITAGLVAAYLEPKSM	540
QY	462	MAIIGGCTRGEGVYAIGYSSISDGGWIIITKGTASGNSRHHFGASASVGVOM	512
Db	541	MAIIGGCTRGEGVYAIGYSSISDGGWIIITKGTASGNSRHHFGASASVGVOM	591

```

: RESULT 2
: US-09-669-974-21
: Sequence 21, Application US/09669974
: Patent No. 6333173
: GENERAL INFORMATION:
: APPLICANT: PEAR, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 21
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
: US-09-669-974-21

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[illegible]

QY	282	KKDDCGNTTVMYDVVVGADLANTNOLONGSMNIDSKRVACSSGCVIGSNVSPSKGKDETV	34.1
Db	361	SKDDGNTTVMYDVVVGADLANTNOLONGSMNIDSKRVACSSGCVIGSNVSPSKGKDETV	42.0
QY	342	NINACNNIETITPNKGRNIDATSMTPQFSSVSLGAGADPTLSYDGDALNVGSKKDKPVR	40.1
Db	421	NINACNNIETITPNKGRNIDATSMTPQFSSVSLGAGADPTLSYDGDALNVGSKKDKPVR	48.0
QY	402	ITTVAPGYKEGDVTVAQLKGYAQNINRINDVNGNARAGIAOAITPAGLVQAYLPGRSM	46.1
Db	481	ITTVAPGYKEGDVTVAQLKGYAQNINRINDVNGNARAGIAOAITPAGLVQAYLPGRSM	54.0
QY	482	MAIGCGTTRGEAGYALGVSSISDGGWIIITKGTASGSRCHFGASASAVGVOM	51.2
Db	541	MAIGCGTTRGEAGYALGVSSISDGGWIIITKGTASGSRCHFGASASAVGVOM	59.1

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: RESULT 3
: US-09-377-155-2
: Sequence 2, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-10
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
: US-09-377-155-2

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Query Match	Similarity	97.9%	Score 2546:	DB 3:	Length 592:
Best Local	Similarity	86.3%:	Pred. No. 5.4e-197:		
Matches	511:	Conservative	0:	Mismatches 1:	Indels 80: Gaps 1:
QY	1	MNKRIIRIIMNSALNMAVYVSELTNRHTRKASATVTAVALATLLEFATVOASANNE-----	54		
DB	1	MNKRIIRIIMNSALNMAVYVSELTNRHTRKASATVTAVALATLLEFATVOASANNEPRKKD	60		
QY	55	-----	54		
DB	61	LYLDFVORTVAVLIVNSDKEGTGEKEVEENSMAVYFNEKGVLTAREITTLKAGDNLIK	120		
QY	55	-----TDLTSVGTPEKLSFSGANKVNIITSDTKGLNFAKETAGTNGDTVYHL	100		
DB	121	QNGTTFYSLIKKDLDTLTSVGTPEKLSFSGANKVNIITSDTKGLNFAKETAGTNGDTVYHL	180		
QY	101	NGISGTLTDLTLNTGATTNVTDNDVTDDEKKRAASVKDVLNAGNIKGVKPGCTASDVID	160		
DB	181	NGISGTLTDLTLNTGATTNVTDNDVTDDEKKRAASVKDVLNAGNIKGVKPGCTASDVID	240		
QY	161	FVRTDVEPLSADIKRTTIVNESKDNGKKTPEVKIGARTSVYKEKDGKLYTKDKGENGS	220		
DB	241	FVRTDVEPLSADIKRTTIVNESKDNGKKTPEVKIGARTSVYKEKDGKLYTKDKGENGS	300		
QY	221	STDEGEGLVTAKEVIDAANKAGMRKTTTANGCTGOADKFEVTVSGTNVTFASGKGTAT	280		
DB	301	STDEGEGLVTAKEVIDAANKAGMRKTTTANGCTGOADKFEVTVSGTNVTFASGKGTAT	360		
QY	281	VSKDQGNITVYDVNVGDALNVNOLONGMGLDSKAAVSGSGKVIISGVNPSRKGKMET	340		
DB	361	VSKDQGNITVYDVNVGDALNVNOLONGMGLDSKAAVSGSGKVIISGVNPSRKGKMET	420		

OY	341	NNNANGNNIEITRRNKNKNDIATSMTPQESSVSLGAGADAPTLVSODALNVGSKKNKPPV	400
Db	421	NNNANGNNIEITRRNKNKNDIATSMTPQESSVSLGAGADAPTLVSODALNVGSKKNKPPV	480
OY	401	RITNAPPVKKEGDVNNVAOLKGVANLNRRIDNVGNNARAGIAQATATAGIYVAYLPGRKS	460
Db	481	RITNAPPVKKEGDVNNVAOLKGVANLNRRIDNVGNNARAGIAQATATAGIYVAYLPGRKS	540
OY	461	MMAIIGGGRGREGAGYAIGYSSISDGGNNWIKGTASGNSRGHGASASVYGW	512
Db	541	MMAIIGGGRGREGAGYAIGYSSISDGGNNWIKGTASGNSRGHGASASVYGW	592

RESULT 4  
 US-09-669-974-2  
 ; Sequence 2, Application US/09669974  
 ; Patent No. 633173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/669, 974  
 ; CURRENT FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US 09/377,155  
 ; PRIOR FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/A098/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 592  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria meningitidis  
 US-09-669-974-2

[illegible]

Db 421 VNINAGNNIEITRRNCKNIDDIATSMTPQFSVSILGAGADAPLTLSVDDGALNVSCKRKNRPV 480

Qy 401 RITNAPCPVKBEDDYNNAVLKCAVQNLNRRINDNNGNAAGATQALATATGIVQATYLPGRS 460

Db 481 RITNAPCPVKBEDDYNNAVLKCAVQNLNRRINDNNGNAAGATQALATATGIVQATYLPGRS 540

Qy 461 MMAIGGGYTRGAGAYALGYSSTISDGGNWIITKGTASGNSKGFHGASASVYGQW 512

Db 541 MMAIGGGYTRGAGAYALGYSSTISDGGNWIITKGTASGNSKGFHGASASVYGQW 592

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RESULT 5
US-09-377-155-11
: Sequence 11, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-11

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Query Match	Similarity	Score	2538	5	DB	3	Length	591					
Best Local	Similarity	86.3%	Pred	No.	2.2e-196								
Matches	510	Conservative	1	Mismatches	1	Indels	79	Gaps					
QY	1	MNKTYRIIWN	SALN	AMVVS	SELT	RNHT	RASATV	TAVALATL	LFATV	QASANNE	-----	54	
	1	1	1	1	1	1	1	1	1	1	1	1	
Db	1	MNEILRIIWN	SALN	AMVVS	SELT	RNHT	RASATV	TAVALATL	LFATV	QASANNE	QEDDL	60	
QY	55	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	54	
Db	61	YLDPEYLT	AVL	IYNSD	EGTE	GEKE	KEVE	NSDM	AVYFNE	KGYLT	AREITL	LKAGD	MLKIQ
QY	55	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	101	
Db	121	NGTNP	YSLK	KD	LD	LD	LD	LD	LD	LD	LD	LD	LD
QY	102	GIGST	LD	LD	LD	LD	LD	LD	LD	LD	LD	LD	LD
Db	181	GIGST	LD	LD	LD	LD	LD	LD	LD	LD	LD	LD	LD
QY	162	VRFTD	YVE	FL	SAD	RT	TV	TV	TV	TV	TV	TV	TV
Db	241	VRFTD	YVE	FL	SAD	RT	TV	TV	TV	TV	TV	TV	TV
QY	222	TDEGE	GL	YTA	KE	YDA	VN	KAG	MR	KTT	TANG	OT	GO
Db	301	TDEGE	GL	YTA	KE	YDA	VN	KAG	MR	KTT	TANG	OT	GO
QY	282	SKDDO	GN	TT	YV	AV	GD	AL	VN	OL	NS	GM	LD
Db	361	SKDDO	GN	TT	YV	AV	GD	AL	VN	OL	NS	GM	LD
QY	342	NINAG	NN	ET	IR	NG	KN	ID	IAT	SMT	PO	FSS	VL
Db	421	NINAG	NN	ET	IR	NG	KN	ID	IAT	SMT	PO	FSS	VL
QY	402	ITN	VA	PG	VE	BD	TV	VA	OL	K	GV	AO	LN
	402	ITN	VA	PG	VE	BD	TV	VA	OL	K	GV	AO	LN

Db 481 ITNAPGVKGGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPGRSM 540  
QY 462 MAIGGGTYRGEAGYAIIGYSSISDGGNMIIKTGASGNSRGHFGASASVGYOW 512  
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Db 541 MAIGGGTYRGEAGYAIIGYSSISDGGNMIIKTGASGNSRGHFGASASVGYOW 591

RESULT 6  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRN  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 97.6%; Score 2538.5; DB 4; Length 591;  
Best Local Similarity 86.3%; Pred. No. 2.2e-196;  
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;

QY 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVTAVALTLTLPFAVQASANNE----- 54  
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Db 1 MNEILRIIWSALNMAVYSELTRNHTKRASATVTAVALTLTLPFAVQASANNEDEEDL 60  
|||||  
QY 55 ----- 54  
Db 61 YLDPVLRVAVLIVNSDEGTEGKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
QY 55 -----TDLTSVGTREKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTBLN 101  
|||||  
Db 121 NGTNTYSLKQDLTDLTSVGTREKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTBLN 180  
|||||  
QY 102 GIGSTLPTLNTGATTVNTNDVTDDEKKRAASVYKDVNLNAGWNIKGVKPGTTASDNDF 161  
|||||  
Db 181 GIGSTLPTLNTGATTVNTNDVTDDEKKRAASVYKDVNLNAGWNIKGVKPGTTASDNDF 240  
|||||  
QY 162 VRTYTVFELISADTETTVNVNVEKNGKTEYKIGAKTSVIEKEKGKLVTKGDKENGSS 221  
|||||  
Db 241 VRTYTVFELISADTETTVNVNVEKNGKTEYKIGAKTSVIEKEKGKLVTKGDKENGSS 300  
|||||  
QY 222 TDEGGLVTAKEVIDAVNKAQGRMKTTPANGOTGADKFEYVTSCTNVTFAAGKGTATV 281  
|||||  
Db 301 TDEGGLVTAKEVIDAVNKAQGRMKTTPANGOTGADKFEYVTSCTNVTFAAGKGTATV 360  
|||||  
QY 282 SKDDOGNTVMTDVNVGDLNVLONSGWNIDSKRAVAGSSGKVISGNVSPSKGMDTV 341  
|||||  
Db 361 SKDDOGNTVMTDVNVGDLNVLONSGWNIDSKRAVAGSSGKVISGNVSPSKGMDTV 420  
|||||  
QY 342 NINAGNNIETFRNGKNIDIASMTPOFSSVSLGAGADAPTLTSDVDALNAGSKKDKPPR 401  
|||||  
Db 401 NINAGNNIETFRNGKNIDIASMTPOFSSVSLGAGADAPTLTSDVDALNAGSKKDKPPR 480  
|||||  
QY 402 ITNAPGVKGGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPGRSM 461  
|||||  
Db 481 ITNAPGVKGGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPGRSM 540

QY 462 MAIGGGTYRGEAGYAIIGYSSISDGGNMIIKTGASGNSRGHFGASASVGYOW 512  
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Db 541 MAIGGGTYRGEAGYAIIGYSSISDGGNMIIKTGASGNSRGHFGASASVGYOW 591

RESULT 7  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRN  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 94.4%; Score 2453.5; DB 3; Length 599;  
Best Local Similarity 83.0%; Pred. No. 1.6e-189;  
Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

QY 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVTAVALTLTLPFAVQASANNE----- 54  
|||||  
Db 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVTAVALTLTLPFAVQANADEDEEDL 60  
|||||  
QY 55 ----- 54  
Db 61 EPPVASALVLOEMIDKEGNGENESTGNGMSIYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
|||||  
QY 55 -----TDLTSVGTREKLSFSANGKNVNTSDTKGLNFAKETAGTNG 94  
|||||  
Db 121 KNTNENTNDSSFTYSLKQDLTDLTSVGTREKLSFSANGKNVNTSDTKGLNFAKETAGTNG 180  
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QY 95 DTTVHLNGIGSTLPTLNTGATTVNTNDVTDDEKKRAASVYKDVNLNAGWNIKGVKPGTT 154  
|||||  
Db 181 DTTVHLNGIGSTLPTLNTGATTVNTNDVTDDEKKRAASVYKDVNLNAGWNIKGVKPGTT 240  
|||||  
QY 155 ASDNDFVRYTVFELISADTETTVNVNVEKNGKTEYKIGAKTSVIEKEKGKLVTKGD 214  
|||||  
Db 241 ASDNDFVRYTVFELISADTETTVNVNVEKNGKTEYKIGAKTSVIEKEKGKLVTKGD 300  
|||||  
QY 215 KGENSSDDEGGLVTAKEVIDAVNKAQGRMKTTPANGOTGADKFEYVTSCTNVTFAAG 274  
|||||  
Db 301 KGENSSDDEGGLVTAKEVIDAVNKAQGRMKTTPANGOTGADKFEYVTSCTNVTFAAG 360  
|||||  
QY 275 KGTATVSKDDOGNTVMTDVNVGDLNVLONSGWNIDSKRAVAGSSGKVISGNVSPSK 334  
|||||  
Db 361 KGTATVSKDDOGNTVMTDVNVGDLNVLONSGWNIDSKRAVAGSSGKVISGNVSPSK 420  
|||||  
QY 335 GKMDTVNINAGNNIETFRNGKNIDIASMTPOFSSVSLGAGADAPTLTSDVDG-DALNAGS 393  
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Db 421 GKMDTVNINAGNNIETFRNGKNIDIASMTPOFSSVSLGAGADAPTLTSDVDG-DALNAGS 480  
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QY 394 KQDNKPPVRLTNNAPGVKGGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIAATAGLVQ 453  
|||||  
Db 481 KQDNKPPVRLTNNAPGVKGGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIAATAGLVQ 540  
|||||  
QY 454 ATLPGKSMALIGGGTYRGEAGYAIIGYSSISDGGNMIIKTGASGNSRGHFGASASVGYOW 512  
|||||  
Db 541 ATLPGKSMALIGGGTYRGEAGYAIIGYSSISDGGNMIIKTGASGNSRGHFGASASVGYOW 599

RESULT 8  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 94.4%; Score 2453.5; DB 4; Length 599;  
Best Local Similarity 83.0%; Pred. No. 1.6e-189;  
Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

QY 1 MNKIYRIWNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASANNE----- 54  
DB 1 MNKIYRIWNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASANNEDEEEL 60  
QY 55 ----- 54  
DB 61 EPVRSALVLOFMIDKEGNGENESTGNIGMSIYYDNHNLHGATVTLKAGDNLKIKONTN 120  
QY 55 ----- 54  
DB 121 KNTNENTNDSFTYSLKRDLTDLTJVSGETKLSFGANGKNVNTSDTKGLNFAETAGTNG 180  
QY 95 DFTVHLNGIGSTLDTLTLNTGATTNTNDNTDEKKRAASVADVNLNAGNIGVKGPTT 154  
DB 181 DTTVHLNGIGSTLDTLTLNTGATTNTNDNTDEKKRAASVADVNLNAGNIGVKGPTT 240  
QY 155 ASDNVDVFRYDVEFLSADTKTTTVNVESEKDKGKTEVKGAKTSVKEKDKLVTKGD 214  
DB 241 ASDNVDVFRYDVEFLSADTKTTTVNVESEKDKGKTEVKGAKTSVKEKDKLVTKGK 300  
QY 215 KEGNGSTDEGEBLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEYVSGTNVTFASG 274  
DB 301 KEGNGSTDEGEBLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEYVSGTNVTFASG 360  
QY 275 KGTATVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSK 334  
DB 361 KGTATVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSK 420  
QY 335 GKMDFTVNIAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDG-DALNVGS 393  
DB 421 GKMDFTVNIAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDG-DALNVGS 480  
QY 394 KDNKRVRTTNVAPVKEGVDYTNVAOLKGYAQNMLNRRIDNVNOCNARAQIAIATAGLVQ 453  
DB 481 KDNKRVRTTNVAPVKEGVDYTNVAOLKGYAQNMLNRRIDNVNOCNARAQIAIATAGLVQ 540  
QY 454 AYLPKSKMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512  
DB 541 AYLPKSKMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 9

US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 94.2%; Score 2449; DB 3; Length 594;  
Best Local Similarity 83.3%; Pred. No. 3.6e-189;  
Matches 495; Conservative 6; Mismatches 11; Indels 82; Gaps 2;

QY 1 MNKIYRIWNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASANNE----- 54  
DB 1 MNKIYRIWNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASTDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVORTAVVLSFRSDKESTGEKEVTEDSNMGVYEDDKCVLTAGITTLKAGDNLKIKONTNE 120  
QY 55 ----- 54  
DB 121 NTNASSFTYSLKRDLTDLTJVSGETKLSFGANGKNVNTSDTKGLNFAETAGTNGDTTVH 180  
QY 100 LNIIGSTLDTLTLNTGATTNTNDNTDEKKRAASVADVNLNAGNIGVKGPTTASDNV 159  
DB 181 LNIIGSTLDTLTLNTGATTNTNDNTDEKKRAASVADVNLNAGNIGVKGPTTASDNV 240  
QY 160 DFTVRYDVEFLSADTKTTTVNVESEKDKGKTEVKGAKTSVKEKDKLVTKGDKENG 219  
DB 241 DFTVRYDVEFLSADTKTTTVNVESEKDKGKTEVKGAKTSVKEKDKLVTKGDKEND 300  
QY 220 SSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEYVSGTNVTFASGKTGA 279  
DB 301 SSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEYVSGTNVTFASGKTGA 360  
QY 280 TVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSKGKMD 339  
DB 361 TVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSKGKMD 420  
QY 340 TVNINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDG-DALNVGS 398  
DB 421 TVNINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDG-DALNVGS 480  
QY 399 PVRITVNPVKEGVDYTNVAOLKGYAQNMLNRRIDNVNOCNARAQIAIATAGLVQAVLP 458  
DB 481 PVRITVNPVKEGVDYTNVAOLKGYAQNMLNRRIDNVNOCNARAQIAIATAGLVQAVLP 540  
QY 459 KSMMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512  
DB 541 KSMMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 10  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:

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1  APPLICANT: PEAK, Ian Richard Ansell
2  APPLICANT: JENNINGS, Michael Paul
3  APPLICANT: MOXON, E. Richard
4  TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
5  FILE REFERENCE: 065064/0128
6  CURRENT APPLICATION NUMBER: US/09/669,974
7  CURRENT FILING DATE: 2000-09-26
8  PRIOR APPLICATION NUMBER: US 09/377,155
9  PRIOR FILING DATE: 1999-08-19
10 PRIOR APPLICATION NUMBER: PCT/A098/01031
11 PRIOR FILING DATE: 1998-12-14
12 PRIOR APPLICATION NUMBER: GB 9726398.2
13 PRIOR FILING DATE: 1997-12-12
14 NUMBER OF SEQ ID NOS: 33
15 SOFTWARE: PatentIn Ver. 2.0
16 SEQ ID NO 9
17 LENGTH: 594
18 TYPE: prt
19 ORGANISM: Neisseria meningitidis
20 US-09-669,974-9

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Query Match	94.28;	Score 2449;	DB 4;	Length 594;
Best Local Similarity	83.38;	Pred. No. 3.6e-189;		
Matches 495;	Conservative	6;	Mismatches 11;	Indels 82;
				Gaps 2

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QY 1 MNKVIIRIIMNSALNMVWVSELTNRHNRKASQVTVATVATLLEFAVQASANNE----- 54
Db 1 MNKVIIRIIMNSALNMVWVSELTNRHNRKASQVTVATVATLLEFAVQASSTDDDDLLYLE 60
QY 55 ----- 54
Db 61 PVQRTAVVLSPRDEKGEKTEVEDSDSMGVYFDKKGVLTAGHITLKAGDNLKIKQNTNE 120
QY 55 -----TDLTISVGTSEKLSPSANCKNINITSDTGILNPAKETAGNGTYYH 99
Db 121 NTFNASSFTYSKKKDLTDLTSVGTSEKLSFESANCKNINITSDTGILNPAKETAGNGTYYH 180
QY 100 LNLGISTLTDLTLNLTGATTNTVNDVNTDDEKRAASVKNVLANGMNKKCYKPETTASDVN 159
Db 181 LNLGISTLTDLTLNLTGATTNTVNDVNTDDEKRAASVKNVLANGMNKKCYKPETTASDVN 240
QY 160 DEVRTYDIVEELASDPTKTTTVYNVESKDNKGKTEVAKIGATSVYKEKDGKLVYTKDGKENG 219
Db 241 DEVRTYDIVEELASDPTKTTTVYNVESKDNKGKTEVAKIGATSVYKEKDGKLVYTKDGKENG 300
QY 220 SSTBEGBELVTAKEYIDA>VNKRAGMRKTTTANGQGGADKFEYTVSGTVNTPRASKGTTA 279
Db 301 SSTBEGBELVTAKEYIDA>VNKRAGMRKTTTANGQGGADKFEYTVSGTVNTPRASKGTTA 360
QY 280 TVSDDDGDNITVMYVNVGDLNLVNOLONSGNLNLKSAAVAGSSGKVISGNVSPSKKKME 339
Db 361 TVSKDDGDNITVMYVNVGDLNLVNOLONSGNLNLKSAAVAGSSGKVISGNVSPSKKKME 420
QY 340 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPLTSYVDG-ALNVGSKRKDK 398
Db 421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPLTSYVDEBALNVGSKRKDK 480
QY 399 PVRITTNVAPGYKEGDYTNVAOLIKGYAONLNBRIDNVGNARAGIAQAIATAGLVQAYLPD 458
Db 481 PVRITTNVAPGYKEGDYTNVAOLIKGYAONLNHIDVWGNARAGIAQAIATAGLVQAYLPD 540
QY 459 KSMALIGGCTYRGEAGYALGVSSISDGGWMIITKGTASGNSRHFAGSASVGVOM 512
Db 541 KSMALIGGCTYRGEAGYALGVSSISDGGWMIITKGTASGNSRHFAGSASVGVOM 594

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RESULT11  
US-09-377-155-7  
: Sequence 7, Application US/09377155  
: Patent No. 6197312  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: JENNINGS, Michael Paul  
: APPLICANT:

```

1  APPLICANT:  MOXON, E. Richard
2  TITLE OF INVENTION:  NOVEL SURFACE ANTIGEN
3  FILE REFERENCE:  065064/0128
4  CURRENT APPLICATION NUMBER:  US/09/377,155
5  PRIORITY FILING DATE:  1999-08-19
6  PRIOR APPLICATION NUMBER:  PCT/AU99/01031
7  PRIOR FILING DATE:  1998-12-14
8  .PRIOR APPLICATION NUMBER:  GB 9726398.2
9  PRIOR FILING DATE:  1997-12-12
10 NUMBER OF SEQ ID NOS:  33
11 SOFTWARE:  PatentIn Ver. 2.0
12
13 SEQ ID NO 7
14
15     LENGTH:  594
16     TYPE:  DMT
17
18     ORGANISM:  Neisseria meningitidis
19
20 OS-09-377-155-7

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Query Match	93.98;	Score 2442;	DB 3;	Length 594;
Best Local Similarity	83.38;	Pred. No. 1.3e-188;		
Matches 495;	Conservative 4;	Mismatches 13;	Indels 82;	Gaps 2

QY	1	MNKYIILNNSLNMWVVSSELTNRHTRKASATVKAATLAFLEPATYQASANE	-----	54
Db	1	MNKYIILNNSLNMWVVSSELTNRHTRKASATVKAATLAFLEPATYQASANE	-----	54
QY	55	-----	54	
Db	61	PVGRATAVLSPRSDKEGTEGEDSDSMWAVYPDEKRYLKAGATTLKAGDNLIKONTNE	120	
QY	55	-----	54	
Db	121	NTNDSSFTYSLKRLDLDLTSLVETKLSGANGNKKNITSDTKGNLFAKETAGNGCPYHA	180	
QY	100	LNGIGSTLDTLLNTGATTNVNDVNDVDEDEKRAASYKVDYLNAAWNLKGVKPGTTASDNV	159	
Db	181	LNGIGSTLDTLLNTGATTNVNDVNDVDEDEKRAASYKVDYLNAAWNLKGVKPGTTASDNV	240	
QY	160	DFPRTDYEPFLSADTKTTTVNVESEKDGKKTVEYIGAKTSVIEKDGKLVTSKDKGENG	219	
Db	241	DFPRTDYEPFLSADTKTTTVNVESEKDGKKTVEYIGAKTSVIEKDGKLVTSKDKGENG	300	
QY	220	SSTDEBEGVLTAKEYIDAVNKAQRMKTTTANGOTGQADKEFYVTSCTNVTFASGKGTTA	279	
Db	301	SSTDEBEGVLTAKEYIDAVNKAQRMKTTTANGOTGQADKEFYVTSCTNVTFASGKGTTA	360	
QY	280	TVSKDDOGNITVYDVNNGDALNVQNLNDSGNLDSKRVAGSSGKTVSGWVSPSKGMBE	339	
Db	361	TVSKDDOGNITVYDVNNGDALNVQNLNDSGNLDSKRVAGSSGKTVSGWVSPSKGMBE	420	
QY	340	TVVINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLTSDVD -ALVANGSKKDNK	398	
Db	421	TVVINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLTSDVD -ALVANGSKKDNK	480	
QY	399	PVRITTVAPGVKEGDVTYNAQLKGYAQNLMNRIDNVGNARAGIAQALATAGLVQAYLPG	458	
Db	481	PVRITTVAPGVKEGDVTYNAQLKGYAQNLMNRIDNVGNARAGIAQALATAGLVQAYLPG	540	
QY	459	KSMNALGGGTGGEAGYALGVSSISDGGNMTIITKGASNSNGHGAASASYGOW	512	
Db	541	KSMNALGGGTGGEAGYALGVSSISDGGNMTIITKGASNSNGHGAASASYGOW	594	

RESULT 12  
US-09-669-974-7  
Sequence 7, Application US/09669974  
Patent No. 6333173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/018  
CURRENT APPLICATION NUMBER: US/09/669, 974







GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 37.6045 Seconds  
(without alignments)  
3513.485 Million cell updates/sec

Title: US-09-771-382-23

Perfect score: 2600  
Sequence: 1 MNKIRYRINMSALNAMYVS.....TASGNSNGHGCASAVCYQW 512

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_23:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2590.5	98.1	591	09JRI8	09JRI8 neisseria m
2	2546.5	97.9	591	09JPS7	09JPS7 neisseria m
3	2546.5	97.9	592	09AOP0	09AOP0 neisseria m
4	2538.5	97.6	591	093QY3	093QY3 neisseria m
5	2488	95.7	600	09JPS6	09JPS6 neisseria m
6	2474	95.2	590	09JPS3	09JPS3 neisseria m
7	2453.5	94.4	599	09JPS8	09JPS8 neisseria m
8	2450	94.2	594	09JPS2	09JPS2 neisseria m
9	2449	94.2	594	093QY4	093QY4 neisseria m
10	2446	94.1	594	09JPI3	09JPI3 neisseria m
11	2442	93.9	592	09JPI7	09JPI7 neisseria m
12	2441	93.9	592	09JPS9	09JPS9 neisseria m
13	2440	93.8	596	09JPS9	09JPS9 neisseria m
14	2427	93.3	598	09JPS0	09JPS0 neisseria m
15	2427	93.3	598	09JPI0	09JPI0 neisseria m
16	2418	93.0	598	093QY5	093QY5 neisseria m

17	2407	92.6	592	093QY2	093QY2 neisseria m
18	2308.5	88.8	595	09JPI0	09JPI0 neisseria m
19	2305.5	88.7	595	09JPS8	09JPS8 neisseria m
20	2304	88.6	598	09JPI7	09JPI7 neisseria m
21	2296	88.3	526	09JPS4	09JPS4 neisseria m
22	2296	88.3	530	09JPS1	09JPS1 neisseria m
23	2289	88.0	592	09JQW4	09JQW4 neisseria m
24	2266.5	87.2	589	09JPI0	09JPI0 neisseria m
25	2256	86.8	600	09JPS5	09JPS5 neisseria m
26	2254.5	86.7	589	093QY1	093QY1 neisseria m
27	991	38.1	1098	048152	048152 haemophilus
28	990	38.1	1096	08GM79	08GM79 haemophilus
29	954.5	36.7	2353	P71401	P71401 haemophilus
30	902	34.7	1204	08GM76	08GM76 haemophilus
31	893	34.3	1210	08GM74	08GM74 haemophilus
32	885	34.0	1210	08GM75	08GM75 haemophilus
33	702	27.0	1004	08GM77	08GM77 haemophilus
34	681	26.2	1002	08GM78	08GM78 haemophilus
35	423.5	16.3	1299	09F3X6	09F3X6 pasteurella
36	364.5	14.8	2314	08KQW8	08KQW8 moraxella c
37	378	14.5	2059	09PD50	09PD50 xylella fas
38	372.5	14.3	1190	09PC04	09PC04 xylella fas
39	371.5	14.3	1107	09F2D8	09F2D8 salmonella
40	370.5	14.2	1588	08XD64	08XD64 escherichia
41	368.5	14.2	1461	08ZL64	08ZL64 salmonella
42	360	13.8	1964	08KQW9	08KQW9 moraxella c
43	358.5	13.8	1778	08FCB2	08FCB2 escherichia
44	343	13.2	2712	09F3X5	09F3X5 pasteurella
45	339.5	13.1	688	08R060	08R060 actinobacil

## ALIGNMENTS

RESULT 1  
09JRI8 PRELIMINARY; PRT: 591 AA.  
ID 09JRI8  
AC 09JRI8:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992 (Adhesin) (NMHA outer membrane protein).  
GN GNA992 OR NM80992 OR NMHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B, B2169, B283, and H44/76;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baidi L., Bartoloni E., Capechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Cioeko A., Parksey D.S., Blair E., Cillone H., Clark E.B., Cotton M.D., Uitterback T.R., Khouli H., Qin H., Vamathevan J.,

RA Gill J., Scarlato V., Mastignani V., Piazza M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
RT MC58";  
RL Science 287:1809-1815(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226375; AAF42524.1; -  
DR EMBL: AE002450; AAF41395.1; -  
DR EMBL: AF226367; AAF42516.1; -  
DR EMBL: AF226370; AAF42519.1; -  
DR EMBL: AF226374; AAF42523.1; -  
DR EMBL: AF157611; AAK68872.1; -  
DR TIGR: NMB0992; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
KM Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 98.1%; Score 2550.5; DB 16; Length 591;  
Best Local Similarity 86.6%; Pred. No. 1.7e-100;  
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIRIIMNSALANAWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNE----- 54  
DB 1 MNKIRIIMNSALANAWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNEDEEDL 60  
QY 55 ----- 54  
DB 61 YLDPVORTAVLIVNSDKEGTGEKEVEENSDWAVYFENEKGVLTAREITLKAGDNLIKIQ 120  
QY 55 ----- 54  
DB 61 YLDPVORTAVLIVNSDKEGTGEKEVEENSDWAVYFENEKGVLTAREITLKAGDNLIKIQ 120  
QY 55 ----- 54  
DB 121 NGTNFTYSLKKDLTDLTSVTEKLSFSAKGNKYNITSDTKGLNFAKETAGTNDTTHLN 180  
QY 102 GIGSTLDTLLNGATTNVTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 161  
DB 181 GIGSTLDTLLNGATTNVTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 240  
QY 162 VRTYDVEEFLSADTKTTTVNVESEKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 221  
DB 241 VRTYDVEEFLSADTKTTTVNVESEKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 300  
QY 222 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 281  
DB 301 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 360  
QY 282 SKDDGQNTITMYDVNVDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDYV 341  
DB 361 SKDDGQNTITMYDVNVDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDYV 420  
QY 342 NINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 401  
DB 421 NINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 480  
QY 402 ITTVAGVKEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIATAGLVQAYLPKSK 461  
DB 481 ITTVAGVKEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIATAGLVQAYLPKSK 540  
QY 462 MAIGGTYRGEAGYTAIGSYISIDGNNIITKGTASGNSRGHFGASASVGYOM 512  
DB 541 MAIGGTYRGEAGYTAIGSYISIDGNNIITKGTASGNSRGHFGASASVGYOM 591

RESULT 2  
Q9JPS7  
ID Q9JPS7  
AC Q9JPS7;  
PRELIMINARY; PRT; 591 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA92.  
GN GNA92.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scarlato V., Mastignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 97.9%; Score 2546.5; DB 2; Length 591;  
Best Local Similarity 86.5%; Pred. No. 2.5e-100;  
Matches 511; Conservative 1; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIRIIMNSALANAWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNE----- 54  
DB 1 MNKIRIIMNSALANAWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNEDEEDL 60  
QY 55 ----- 54  
DB 61 YLDPVORTAVLIVNSDKEGTGEKEVEENSDWAVYFENEKGVLTAREITLKAGDNLIKIQ 120  
QY 55 ----- 54  
DB 121 NGTNFTYSLKKDLTDLTSVTEKLSFSAKGNKYNITSDTKGLNFAKETAGTNDTTHLN 180  
QY 102 GIGSTLDTLLNGATTNVTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 161  
DB 181 GIGSTLDTLLNGATTNVTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 240  
QY 162 VRTYDVEEFLSADTKTTTVNVESEKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 221  
DB 241 VRTYDVEEFLSADTKTTTVNVESEKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 300  
QY 222 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 281  
DB 301 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 360  
QY 282 SKDDGQNTITMYDVNVDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDYV 341  
DB 361 SKDDGQNTITMYDVNVDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDYV 420  
QY 342 NINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 401  
DB 421 NINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 480  
QY 402 ITTVAGVKEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIATAGLVQAYLPKSK 461  
DB 481 ITTVAGVKEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIATAGLVQAYLPKSK 540  
QY 462 MAIGGTYRGEAGYTAIGSYISIDGNNIITKGTASGNSRGHFGASASVGYOM 512  
DB 541 MAIGGTYRGEAGYTAIGSYISIDGNNIITKGTASGNSRGHFGASASVGYOM 591

RESULT 3  
Q9AOF0 PRELIMINARY; PRT; 592 AA.  
AC Q9AOF0: 01-DEC-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE Outer membrane protein.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
CX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF125375; AAK09243.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
DR PIR; P03895; Yada; 1.  
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;  
Query Match 97.9%; Score 2546; DB 2; Length 592;  
Best Local Similarity 86.3%; Pred. No. 2.6e-100;  
Matches 511; Conservative 0; Mismatches 1; Indels 80; Gaps 1;  
QY 1 MNKIRIIMNSALNAWVVSSELTNRHTRKASATVKTAVLATLLEFATVQASANNE----- 54  
DB 1 MNKIRIIMNSALNAWVVSSELTNRHTRKASATVKTAVLATLLEFATVQASANNEPRKKD 60  
QY 55 ----- 54  
DB 61 LYLDVORTVAVLIVNSDKETGEGEKEVEENSDMAVYFNEKGLTAREITLAKGDNLIK 120  
QY 55 -----TDLTSVTEKLSFSANGKNVITSDPTKGLNFAKETAGTNGDTVHLN 100  
DB 121 QNGNTFTYSLKDLTDLTSVTEKLSFSANGKNVITSDPTKGLNFAKETAGTNGDTVHLN 180  
QY 101 NGIGSTLDTLLNTGATTNTNDVTDDEKKRAASVKKDVLNAGWNKGVKPGTTASDNVD 160  
DB 181 NGIGSTLDTLLNTGATTNTNDVTDDEKKRAASVKKDVLNAGWNKGVKPGTTASDNVD 240  
QY 161 FVRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKERDGLVTKDKGENSS 220  
DB 241 FVRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKERDGLVTKDKGENSS 300  
QY 221 TDEGEGLVTAKEVIDAVNKAQWRRKTTTANGOTQADKFEFVTSNTVTFASGKTATV 280  
DB 301 TDEGEGLVTAKEVIDAVNKAQWRRKTTTANGOTQADKFEFVTSNTVTFASGKTATV 360  
QY 281 VSKDQGNITVYDVNVGALVNVQNLQNSGNMLDSKAVAGSSGKVIISGNVSPSKMDET 340  
DB 361 VSKDQGNITVYDVNVGALVNVQNLQNSGNMLDSKAVAGSSGKVIISGNVSPSKMDET 420  
QY 341 VNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPV 400  
DB 421 VNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPV 480  
QY 401 RITNVAQVKEGADVNTVAOLKGVANLNNRIDNVGNAIRAGIAQAIATAGLVQAVLPGRSM 460  
DB 481 RITNVAQVKEGADVNTVAOLKGVANLNNRIDNVGNAIRAGIAQAIATAGLVQAVLPGRSM 540  
QY 461 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 512  
DB 541 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592

RESULT 4  
Q930Y3 PRELIMINARY; PRT; 591 AA.  
AC Q930Y3: 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE nhha outer membrane protein.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
CX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157606; AAK68867.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
DR PIR; P03895; Yada; 1.  
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;  
Query Match 97.6%; Score 2538.5; DB 2; Length 591;  
Best Local Similarity 86.3%; Pred. No. 5.5e-100;  
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;  
QY 1 MNKIRIIMNSALNAWVVSSELTNRHTRKASATVKTAVLATLLEFATVQASANNE----- 54  
DB 1 MNKIRIIMNSALNAWVVSSELTNRHTRKASATVKTAVLATLLEFATVQASANNEQEEDL 60  
QY 55 ----- 54  
DB 61 YLDVPLKRVAVLIVNSDKETGEGEKEVEENSDMAVYFNEKGLTAREITLAKGDNLIK 120  
QY 55 -----TDLTSVTEKLSFSANGKNVITSDPTKGLNFAKETAGTNGDTVHLN 101  
DB 121 NGNTFTYSLKDLTDLTSVTEKLSFSANGKNVITSDPTKGLNFAKETAGTNGDTVHLN 180  
QY 102 GIGSTLDTLLNTGATTNTNDVTDDEKKRAASVKKDVLNAGWNKGVKPGTTASDNVD 161  
DB 181 GIGSTLDTLLNTGATTNTNDVTDDEKKRAASVKKDVLNAGWNKGVKPGTTASDNVD 240  
QY 162 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKERDGLVTKDKGENSS 221  
DB 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKERDGLVTKDKGENSS 300  
QY 222 TDEGEGLVTAKEVIDAVNKAQWRRKTTTANGOTQADKFEFVTSNTVTFASGKTATV 281  
DB 301 TDEGEGLVTAKEVIDAVNKAQWRRKTTTANGOTQADKFEFVTSNTVTFASGKTATV 360  
QY 282 SKDQGNITVYDVNVGALVNVQNLQNSGNMLDSKAVAGSSGKVIISGNVSPSKMDETV 341  
DB 361 SKDQGNITVYDVNVGALVNVQNLQNSGNMLDSKAVAGSSGKVIISGNVSPSKMDETV 420  
QY 342 NINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPV 401  
DB 421 NINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPV 480  
QY 402 ITNVAQVKEGADVNTVAOLKGVANLNNRIDNVGNAIRAGIAQAIATAGLVQAVLPGRSM 461  
DB 481 ITNVAQVKEGADVNTVAOLKGVANLNNRIDNVGNAIRAGIAQAIATAGLVQAVLPGRSM 540  
QY 462 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 512  
DB 541 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 5  
Q9JP6 PRELIMINARY; PRT; 600 AA.  
AC Q9JP6: 01-DEC-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
NCBI\_TaxID=487;  
RX  
RP SEQUENCE FROM N.A.  
RC STRAIN=NE26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scariato V., Masianni V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappunli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
EMBL: AF226371; AAF42520.1; --  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 95.7%; Score 2488; DB 2; Length 600;  
Best Local Similarity 83.7%; Pred. No. 7, 6e-98;  
Matches 502; Conservative 2; Mismatches 8; Indels 88; Gaps 1;

QY 1 MNKIRIINNSALNANVAVVSELTNRNHTKRASATVKTAVLATLLFAVQASANNE----- 54  
DB 1 MNKIRIINNSALNANVAVVSELTNRNHTKRASATVKTAVLATLLFAVQASADN 60  
QY 55 ----- 54  
DB 61 EEEETLEPVYRTAPVLSFSDAEDFGKEVENTNNGIYFDKNGVIAKGTITLAKGDNK 120  
QY 55 ----- 54  
DB 121 IKONTDEBNTNASSFTYSLKKEFLDTLSVGTREKLSFGANGKNVITSDTKGLNFAKETAGT 92  
DB 121 IKONTDEBNTNASSFTYSLKKEFLDTLSVGTREKLSFGANGKNVITSDTKGLNFAKETAGT 180  
QY 93 NGCTVYHLNGISGTLTDTLTNLTGATTNVTNDNTDDEKKRAASVKDVLNAGNINIKGVKPG 152  
DB 181 NGDTVYHLNGISGTLTDTLTNLTGATTNVTNDNTDDEKKRAASVKDVLNAGNINIKGVKPG 240  
QY 153 TTSADNVDFRYRTDYEFELSDADTKTTTVNYESKDNKGKTEVKIGAKTSVYKEDGKLYNG 212  
DB 241 TTSADNVDFRYRTDYEFELSDADTKTTTVNYESKDNKGKTEVKIGAKTSVYKEDGKLYNG 300  
QY 213 KDKGENGSTDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEVTSGSTVNTFA 272  
DB 301 KKGKGENGSTDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEVTSGSTVNTFA 360  
QY 273 SGCGTATYASKDQGNITWYDVNVDALNVLNOLNSGMNLSKAAVAGSSGKATISGVNSP 332  
DB 361 SGCGTATYASKDQGNITWYDVNVDALNVLNOLNSGMNLSKAAVAGSSGKATISGVNSP 420  
QY 333 SKRKMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVGDALNNG 392  
DB 421 SKRKMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVGDALNNG 480  
QY 393 SKRKNRPVRLTNVAPGVKEGSDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLV 452  
DB 481 SKRKNRPVRLTNVAPGVKEGSDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLV 540  
QY 453 QATLPKSKMAIGGGTGRGAGTAIGYSSISDGGNNI IKCTASGNSRGHFGASASVGYQM 512  
DB 541 QATLPKSKMAIGGGTGRGAGTAIGYSSISDGGNNI IKCTASGNSRGHFGASASVGYQM 600

RESULT 6  
Q9JPS3

ID Q9JPS3 PRELIMINARY; PRT; 590 AA.  
AC Q9JPS3;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
NCBI\_TaxID=487;  
RX  
RP SEQUENCE FROM N.A.  
RC STRAIN=NE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scariato V., Masianni V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappunli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
EMBL: AF226378; AAF42527.1; --  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 95.2%; Score 2474; DB 2; Length 590;  
Best Local Similarity 84.7%; Pred. No. 2, 9e-97;  
Matches 500; Conservative 4; Mismatches 8; Indels 78; Gaps 2;

QY 1 MNKIRIINNSALNANVAVVSELTNRNHTKRASATVKTAVLATLLFAVQASANNE----- 54  
DB 1 MNKIRIINNSALNANVAVVSELTNRNHTKRASATVKTAVLATLLFAVQANATDEDEEDL 60  
QY 55 ----- 54  
DB 61 DPQRTVAVLIIVNSDKEGTGEKKEVEENSDMAVYFNKGVLTAGTITTIKAGNLIKONG 120  
QY 55 ----- 54  
DB 121 TNFTYLSKLDLDTLSVGTREKLSFGANGKNVITSDTKGLNFAKETAGTGDVTHLNGI 180  
QY 104 GSTLTDTLTNLTGATTNVTNDNTDDEKKRAASVKDVLNAGNINIKGVKPGTASDNDVFR 163  
DB 181 GSTLTDTLTNLTGATTNVTNDNTDDEKKRAASVKDVLNAGNINIKGVKPGTASDNDVFR 240  
QY 164 TYDTVEFLSADTKTTTVNYESKDNKGKTEVKIGAKTSVYKEDGKLYNGKNGENGSST 223  
DB 241 TYDTVEFLSADTKTTTVNYESKDNKGKTEVKIGAKTSVYKEDGKLYNGKNGENGSST 300  
QY 224 EGGGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEVTSGSTVNTFA 283  
DB 301 EGGGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEVTSGSTVNTFA 360  
QY 284 DDGNTWYDVNVDALNVLNOLNSGMNLSKAAVAGSSGKATISGVNSP 343  
DB 361 DDGNTWYDVNVDALNVLNOLNSGMNLSKAAVAGSSGKATISGVNSP 420  
QY 344 MAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVGD -ALNNGSKDNRPVRL 402  
DB 421 MAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVDEGALNNGSKDNRPVRL 480  
QY 403 TNVAPGVKEGSDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQATLPKSKMA 462  
DB 481 TNVAPGVKEGSDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQATLPKSKMA 540  
QY 463 AIGGGTGRGAGTAIGYSSISDGGNNI IKCTASGNSRGHFGASASVGYQM 512  
DB 541 AIGGGTGRGAGTAIGYSSISDGGNNI IKCTASGNSRGHFGASASVGYQM 590

## RESULT 7

09JPR8 PRELIMINARY; PRT; 599 AA.  
AC 09JPR8;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992 (Nha outer membrane protein).  
GN GNA992 OR NHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH38;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappunli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H38;  
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226383; AAF42532.1; -  
DR EMBL: AF157608; AAK68869.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 94.4%; Score 2453.5; DB 2; Length 599;  
Best Local Similarity 83.0%; Pred. No. 2,2e-96;  
Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

QY 1 MNKIRIINNSALNANWVVELTRNHRKRSATVKTAVLATLLFATVQASANNE----- 54  
DB 1 MNKIRIINNSALNANWVSELTRNHRKRSATVKTAVLATLLFATVQANATDEDEEEL 60  
QY 55 ----- 54  
DB 61 EPVYSALVLOFMIDKEGNGENESTGNGISYIYNHNTLHGATVTLKAGDNLIKONTN 120  
QY 55 -----TDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNG 94  
DB 121 KNTNEMTNDSSFTYSLKLDJLTLVSVEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
QY 95 DTTVHLNGISLTJLTLLNTGATVTNTDNDVDEKKRAASVKDVLNAGNINIKVPGTT 154  
DB 181 DTTVHLNGISLTJLTLLNTGATVTNTDNDVDEKKRAASVKDVLNAGNINIKVPGTT 240  
QY 155 ASNVPFVRTYDVEFLSADTKTTTVNVEESKNGKREVKIGAKTSVIRKEDKLVYKGD 214  
DB 241 ASNVPFVRTYDVEFLSADTKTTTVNVEESKNGKREVKIGAKTSVIRKEDKLVYKGD 300  
QY 215 KGENGSTDEGLVTAKEVIDAVNKAQGRMKTTTANGOTGOADKFEFTVSGTNVTFASG 274  
DB 301 KGENGSTDEGLVTAKEVIDAVNKAQGRMKTTTANGOTGOADKFEFTVSGTNVTFASG 360  
QY 275 KGTATYVSKDDGNTIYMYVNVGDLNVLQNLONGNLDNSKAVAGSGGVISGNVSPSK 334  
DB 361 KGTATYVSKDDGNTIYMYVNVGDLNVLQNLONGNLDNSKAVAGSGGVISGNVSPSK 420

QY 335 GKMEDEVINAGNNIEITRNGKNIDATSMTPDESSVSLGAGADAPTLVSDG-DALNVGS 393  
DB 421 GKMEDEVINAGNNIEITRNGKNIDATSMTPDESSVSLGAGADAPTLVSDGKALNVGS 480  
QY 394 KDNKAPVRIINNVAPGVEGDVTNVAOLKGYAQNLNRRIDNVDGNARAGIAQAIATAGLVQ 453  
DB 481 KDANKPVRITNVAPGVEGDVTNVAOLKGYAQNLNRRIDNVDGNARAGIAQAIATAGLVQ 540  
QY 454 AYLPGKSMALIGGTYRGEAGYALGYSSISDGNWIIKGTASGNSRCHFASASVGYQW 512  
DB 541 AYLPGKSMALIGGTYRGEAGYALGYSSISDGNWIIKGTASGNSRCHFASASVGYQW 599

## RESULT 8

09JPS2 PRELIMINARY; PRT; 594 AA.  
AC 09JPS2;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappunli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;  
Best Local Similarity 83.5%; Pred. No. 3e-96;  
Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

QY 1 MNKIRIINNSALNANWVVELTRNHRKRSATVKTAVLATLLFATVQASANNE----- 54  
DB 1 MNKIRIINNSALNANWVSELTRNHRKRSATVKTAVLATLLFATVQASTDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVQRTAPVLSFHADSEGTGEKEVTEDSNMGVYFDKKKVLTAGTTTLKAGDNLIKONTDE 120  
QY 55 -----TDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVH 99  
DB 121 NTNASSFTYSLKLDJLTLVSVEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDTTVH 180  
QY 100 LINGGSTLTJLTLLNTGATVTNTDNDVDEKKRAASVKDVLNAGNINIKVPGTTASDNV 159  
DB 181 LINGGSTLTJLTLLNTGATVTNTDNDVDEKKRAASVKDVLNAGNINIKVPGTTASDNV 240  
QY 160 DFVRTYDVEFLSADTKTTTVNVEESKNGKREVKIGAKTSVIRKEDKLVYTKGKENG 219  
DB 241 DFVRTYDVEFLSADTKTTTVNVEESKNGKREVKIGAKTSVIRKEDKLVYTKGKENG 300  
QY 220 SSTDEGEGLVTAKEVIDAVNKAQGRMKTTTANGOTGOADKFEFTVSGTNVTFASGKGT 279  
DB 301 SSTDEGEGLVTAKEVIDAVNKAQGRMKTTTANGOTGOADKFEFTVSGTNVTFASGNGT 360

QY 280 TVSKDDQGNITVWYDVNVDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKME 339  
 DB 361 TVSKDDQGNITVWYDVNVDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKME 420  
 QY 340 TVNINAGNNIETTRNGKNIDITATSMTPPOSSVSLGAGADAPLISYDGD-ALVNGSKKDK 398  
 DB 421 TVNINAGNNIETTRNGKNIDITATSMTPPOSSVSLGAGADAPLISYDDEBALVNGSKDK 480  
 QY 399 PVRTINAVPVGKEDVTNVAOLKGYAQNINRNDVNDGNARAGIAOAIATAGLYOAYLP 458  
 DB 481 PVRTINAVPVGKEDVTNVAOLKGYAQNINRNDVNDGNARAGIAOAIATAGLYOAYLP 540  
 QY 459 KSMMAIGGCTYRGEAGYALGYSSISDGNWIIKGTASGNSRCHFGASASVGYOW 512  
 DB 541 KSMMAIGGCTYRGEAGYALGYSSISDGNWIIKGTASGNSRCHFGASASVGYOW 594

RESULT 9

Q930Y4 PRELIMINARY; PRT; 594 AA.  
 AC Q930Y4;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Outer membrane protein.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_Taxid=487;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EG327;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of Neisseria meningitidis.  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBU databases.  
 DR EMBL; AF157605; AAK68866.1;  
 DR InterPro; IPR005594; Yada.  
 DR Pfam; PF03895; Yada; 1.  
 SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 94.2%; Score 2449; DB 2; Length 594;  
 Best Local Similarity 83.3%; Pred. No. 3.3e-96;  
 Matches 495; Conservative 6; Mismatches 11; Indels 82; Gaps 2;

QY 1 MNKRIIINSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASANNE----- 54  
 DB 1 MNKRIIINSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASTDDDDLYLE 60  
 QY 55 ----- 54  
 DB 61 PVQRTAVVLSFRSDKEGTEKEVEDSNMGVYFDKKGVLTAGTITLKAGDNLIKQNTME 120  
 QY 55 ----- 54  
 DB 121 NTNASFFYSLKKKDLTLDSVTEKLSFGANSKNVITSDTKGLNFAKTAETNGDTVH 180  
 QY 100 LMGISTLTDLTLNLTGATTVNDVNTDDEKRAASVKNVLAAGNVIKGVKGTASDNV 159  
 DB 181 LMGISTLTDLTLNLTGATTVNDVNTDDEKRAASVKNVLAAGNVIKGVKGTASDNV 240  
 QY 160 DEVRTYDVEFLSADTKTTTVNVEESKDKNGKTEVRIKAGTSYIKKEDGLVYTKDKGENG 219  
 DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKNGKTEVRIKAGTSYIKKEDGLVYTKDKGENG 300  
 QY 220 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGQGTQADKFEVTVSGTVNTPASGKGT 279  
 DB 301 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGQGTQADKFEVTVSGTVNTPASGKGT 360  
 QY 280 TVSKDDQGNITVWYDVNVDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKME 339

DB 361 TVSKDDQGNITVWYDVNVDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKME 420  
 QY 340 TVNINAGNNIETTRNGKNIDITATSMTPPOSSVSLGAGADAPLISYDGD-ALVNGSKKDK 398  
 DB 421 TVNINAGNNIETTRNGKNIDITATSMTPPOSSVSLGAGADAPLISYDDEBALVNGSKDK 480  
 QY 399 PVRTINAVPVGKEDVTNVAOLKGYAQNINRNDVNDGNARAGIAOAIATAGLYOAYLP 458  
 DB 481 PVRTINAVPVGKEDVTNVAOLKGYAQNINRNDVNDGNARAGIAOAIATAGLYOAYLP 540  
 QY 459 KSMMAIGGCTYRGEAGYALGYSSISDGNWIIKGTASGNSRCHFGASASVGYOW 512  
 DB 541 KSMMAIGGCTYRGEAGYALGYSSISDGNWIIKGTASGNSRCHFGASASVGYOW 594

RESULT 10

Q93PI3 PRELIMINARY; PRT; 594 AA.  
 AC Q93PI3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Outer membrane protein GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_Taxid=487;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NG3/88, and BZ232;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.  
 RL Science 287:1816-1820(2000).  
 DR EMBL; AF226376; AAF42525.1;  
 DR EMBL; AF226369; AAF42518.1;  
 DR InterPro; IPR005594; Yada.  
 DR Pfam; PF03895; Yada; 1.  
 SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9DD04B46 CRC64;

Query Match 94.1%; Score 2446; DB 2; Length 594;  
 Best Local Similarity 83.3%; Pred. No. 4.5e-96;  
 Matches 495; Conservative 3; Mismatches 14; Indels 82; Gaps 2;

QY 1 MNKRIIINSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASANNE----- 54  
 DB 1 MNKRIIINSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASTDDDDLYLE 60  
 QY 55 ----- 54  
 DB 61 PVQRTAVVLSFRSDKEGTEKEVEDSNMGVYFDKKGVLTAGTITLKAGDNLIKQNTME 120  
 QY 55 ----- 54  
 DB 121 NTNASFFYSLKKKDLTLDSVTEKLSFGANSKNVITSDTKGLNFAKTAETNGDTVH 180  
 QY 100 LMGISTLTDLTLNLTGATTVNDVNTDDEKRAASVKNVLAAGNVIKGVKGTASDNV 159  
 DB 181 LMGISTLTDLTLNLTGATTVNDVNTDDEKRAASVKNVLAAGNVIKGVKGTASDNV 240  
 QY 160 DEVRTYDVEFLSADTKTTTVNVEESKDKNGKTEVRIKAGTSYIKKEDGLVYTKDKGENG 219  
 DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKNGKTEVRIKAGTSYIKKEDGLVYTKDKGENG 300  
 QY 220 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGQGTQADKFEVTVSGTVNTPASGKGT 279

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Db 301 SSTEDEGLVTAKEDIYAVNKGWRMKTTTANGOTGADKREFTVSGTKVTFASGNGTTA 360
Oy 280 TVSKDDOGNITVMTDVNNGDALNNQLONSGMNLDKRAVAGSSGKVISGNSPSKGMDE 339
Db 361 TVSKDDOGNITVMTDVNNGDALNNQLONSGMNLDKRAVAGSSGKVISGNSPSKGMDE 420
Oy 340 TVTNAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDCD-ALNVGSKDNK 398
Db 421 TVTNAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDCD-GALNVGSKDNK 480
Oy 399 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 458
Db 481 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 540
Oy 459 KSMMAIGGTYRGEGYAIYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512
Db 541 KSMMAIGGTYRGEGYAIYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594
```

## RESULT 11

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O9JPH7 PRELIMINARY; PRT; 594 AA.
ID O9JPH7 AC O9JPH7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992 (Nhha outer membrane protein).
GN GMA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198; and 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
```

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RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198;
RA Peak I.R., Srikhanta V., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226358; AAF42517.1; -
DR EMBL; AF226358; AAF42507.1; -
DR EMBL; AF157604; AAK6885.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE682635C5C CRC64;
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Query Match 93.9%; Score 2442; DB 2; Length 594;
Best Local Similarity 83.3%; Pred. No. 6.6e-96;
Matches 495; Conservative 4; Mismatches 13; Indels 82; Gaps 2;
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Oy 1 MNKIYRIITWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAASNNNE----- 54
Db 1 MNKIYRIITWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAANATDDDLTXLE 60
Oy 55 ----- 54
Db 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAAVYFDEKRVLLKAGAITLKAGDNLIKONTNE 120
```

```
Oy 55 -----TDLTIVGTEKLSFSANGKNVNTISDTKGINFAKETAGTNGDTTVH 99
Db 121 NTNDSFPTYSLKLDLTIVTEKLSFGANGKNVNTISDTKGINFAKETAGTNGDPTVH 180
Oy 100 LINGIGSTLTDPLLTGATTNTNTNDVTDDEKRAASVADVUNAGNITKGVAPGTTASDNV 159
Db 181 LINGIGSTLTDPLLTGATTNTNTNDVTDDEKRAASVADVUNAGNITKGVAPGTTASDNV 240
Oy 160 DVFRTYDVEFLSADTKTTTNVESKDKGTEKIGAKTSVIREKDGKLTGKDKGEN 219
Db 241 DVFRTYDVEFLSADTKTTTNVESKDKGTEKIGAKTSVIREKDGKLTGKDKGEN 300
Oy 220 SSTEDEGLVTAKEDIYAVNKGWRMKTTTANGOTGADKREFTVSGTNTVTFASGNGTTA 279
Db 301 SSTEDEGLVTAKEDIYAVNKGWRMKTTTANGOTGADKREFTVSGTNTVTFASGNGTTA 360
Oy 280 TVSKDDOGNITVMTDVNNGDALNNQLONSGMNLDKRAVAGSSGKVISGNSPSKGMDE 339
Db 361 TVSKDDOGNITVMTDVNNGDALNNQLONSGMNLDKRAVAGSSGKVISGNSPSKGMDE 420
Oy 340 TVTNAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDCD-ALNVGSKDNK 398
Db 421 TVTNAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDCD-GALNVGSKDNK 480
Oy 399 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 458
Db 481 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 540
Oy 459 KSMMAIGGTYRGEGYAIYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512
Db 541 KSMMAIGGTYRGEGYAIYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594
```

## RESULT 12

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O9JPS9 PRELIMINARY; PRT; 592 AA.
ID O9JPS9 AC O9JPS9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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```
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A347151AFD3C879 CRC64;
```

```
Query Match 93.9%; Score 2441; DB 2; Length 592;
Best Local Similarity 83.6%; Pred. No. 7.2e-96;
Matches 495; Conservative 3; Mismatches 14; Indels 80; Gaps 2;
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```
Oy 1 MNKIYRIITWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAASNNNE----- 54
Db 1 MNKIYRIITWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAANATDDEEBEL 60
```

QY 55 ----- 54  
 Db 61 ESVOASVGSIQASMEGSELETTISLMTNDSKEFVPIVLTAKGADNLKIKONTNENT 120  
 QY 55 -----TDLTSVGTETKLSFANGKNVITSDTGLNFAKTAGTNGDTYHLN 101  
 Db 121 MASSFTYSLKDLTGLINTEKLSFGANGKRVNIIISDTGLNFAKTAGTNGDTYHLN 180  
 QY 102 GISTITDILLNLTGATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKGGTASDVDF 161  
 Db 181 GISTITDILLNLTGATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKGGTASDVDF 240  
 QY 162 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDKLYTGKDGKENGSS 221  
 Db 241 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDKLYTGKDGKENGSS 300  
 QY 222 TDEGELVYTAKEVIDAVNKAQWKKTTTANGOTGOADKFEVTSVSGTNVTFASCKGTTATY 281  
 Db 301 TDEGELVYTAKEVIDAVNKAQWKKTTTANGOTGOADKFEVTSVSGTNVTFASCKGTTATY 360  
 QY 282 SKDDGNITVMDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVIISGNVSPSKGMDYV 341  
 Db 361 SKDDGNITVMDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVIISGNVSPSKGMDYV 420  
 QY 342 NINAGNNIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDG-DALNVSGKDKMPV 400  
 Db 421 NINAGNNIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDG-DALNVSGKDKMPV 480  
 QY 401 RITNVAPGVESGVTVNAOLKGYAQNINNDVNDGARNAGIAQALATAGLYQAYLPKGS 460  
 Db 481 RITNVAPGVESGVTVNAOLKGYAQNINNDVNDGARNAGIAQALATAGLYQAYLPKGS 540  
 QY 461 MMAIGGTYRGEAGVYAGYSSISDGNWIIKGTASGNSRHFAGSASVGYQW 512  
 Db 541 MMAIGGTYRGEAGVYAGYSSISDGNWIIKGTASGNSRHFAGSASVGYQW 592

RESULT 13  
 Q9JPR9 PRELIMINARY; PRT; 598 AA.  
 AC Q9JPR9;  
 DT 01-OCT-2000 (TremBurel. 15, Created)  
 DT 01-OCT-2000 (TremBurel. 22, Last sequence update)  
 DE Outer membrane protein GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NGH36;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappunli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226382; AAF42531.1; -  
 DR InterPro: IPR005594; Yada.  
 DR Pfam: PF03895; Yada; 1.  
 SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 93.8%; Score 2440; DB 2; Length 598;  
 Best Local Similarity 82.8%; Pred. No. 8.1e-96;  
 Matches 495; Conservative 4; Mismatches 13; Indels 86; Gaps 2;

QY 1 MNKRIIINNSALNAVWVSELTNRHTRKASATVKTAVIATLLFATVQASANNE----- 54  
 Db 1 MNKRIIINNSALNAVWVSELTNRHTRKASATVKTAVIATLLFATVQANATDDDDLYLE 60  
 QY 55 ----- 54  
 Db 61 PVQRTAVVLSFRSDKEGTGEGTEGDEDSMNAVPEDEKRVLKAGATITLKAGDNLKIKONTNE 120  
 QY 55 -----TDLTSVGTETKLSFANGKNVITSDTGLNFAKTAGTNGD 95  
 Db 121 NTNENTNDSFTYSLKDLTDLTSVETKLSFGANGKRVNIIISDTGLNFAKTAGTNGD 180  
 QY 96 TTVHLNGISGTLTDLTLNLTGATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKGGTGA 155  
 Db 181 PTVHLNGISGTLTDLTLNLTGATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKGGTGA 240  
 QY 156 SDNVDFVRYDYEFISADTKTTTVNVEESKDKKTEVKIGAKTSYIKEDKLYTGKDK 215  
 Db 241 SDNVDFVRYDYEFISADTKTTTVNVEESKDKKTEVKIGAKTSYIKEDKLYTGKDK 300  
 QY 216 GENGSTDEGELVYTAKEVIDAVNKAQWKKTTTANGOTGOADKFEVTSVSGTNVTFASCK 275  
 Db 301 GENGSTDEGELVYTAKEVIDAVNKAQWKKTTTANGOTGOADKFEVTSVSGTNVTFASCK 360  
 QY 276 GTTATVSKDDGNITVMDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVIISGNVSPSKG 335  
 Db 361 GTTATVSKDDGNITVMDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVIISGNVSPSKG 420  
 QY 336 KMEETVNNAGNNIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDG-DALNVSGK 394  
 Db 421 KMEETVNNAGNNIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDG-DALNVSGK 480  
 QY 395 KDNKPVRTNVAPGVESGVTVNAOLKGYAQNINNDVNDGARNAGIAQALATAGLYQAY 454  
 Db 481 DTKKPVRTNVAPGVESGVTVNAOLKGYAQNINNDVNDGARNAGIAQALATAGLYQAY 540  
 QY 455 YLPKSMMAIGGTYRGEAGVYAGYSSISDGNWIIKGTASGNSRHFAGSASVGYQW 512  
 Db 541 YLPKSMMAIGGTYRGEAGVYAGYSSISDGNWIIKGTASGNSRHFAGSASVGYQW 598

RESULT 14  
 Q9JPS0 PRELIMINARY; PRT; 598 AA.  
 AC Q9JPS0;  
 DT 01-OCT-2000 (TremBurel. 15, Created)  
 DT 01-OCT-2000 (TremBurel. 22, Last sequence update)  
 DE Outer membrane protein GNA992 (Nhla outer membrane protein).  
 GN GNA992 OR NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NH15;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappunli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H15;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer



RT membrane protein of Neisseria meningitidis." ;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF226381; AAF42530.1; -  
 DR EMBL: AF157607; AAK68868.1; -  
 DR InterPro: IPR005594; Yada.  
 DR Pfam: PF03895; Yada; 1.  
 SO SEQUENCE 598 AA; 62763 MW; E6C7AEF0DB8A63CB CRC64;

Query Match 93.3%; Score 2427; DB 2; Length 598;  
 Best Local Similarity 82.3%; Pred. No. 2.9e-95;  
 Matches 492; Conservative 5; Mismatches 15; Indels 86; Gaps 2;

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QY 1 MNKIYRIIWNLSALNAMYVSELTRNHTKRASATVATLALTLFATYQASANNE----- 54
Db 1 MNKIYRIIWNLSALNAMYVSELTRNHTKRASATVATLALTLFATYQANATDDDLXLE 60
QY 55 ----- 54
Db 61 PVQRTAVVLSFRSDKEGTEGEKEDSNMAYVFEDEKRYLKAGAITLKAGDMLKIKONTNE 120
QY 55 -----TDLTSVTEKLSFSANGKNVNTSDTKGINFAKETAGTNGD 95
Db 121 NTNENTDSSFTTSLKADLDLDTLSVTEKLSFGANGKNVNTSDTKGINFAKETAGTNGD 180
QY 96 TTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASYKDYLNAGMNKIGVPGTTA 155
Db 181 PTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASYKDYLNAGMNKIGVPGTTA 240
QY 156 SDNVDFRTYTVFELSDRTKTTVNVESKDNKRTVEKIGAKTSVIREKDGKLVGTGDK 215
Db 241 SDNVDFRTYTVFELSDRTKTTVNVESKDNKRTVEKIGAKTSVIREKDGKLVGTGDK 300
QY 216 GENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTSCTNTYTFASGK 275
Db 301 DENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTSCTNTYTFASGK 360
QY 276 GTTATVSKDDOGNTTVMYDVNVGDALNVNOLONGSMWLDKRAVAGSSGKTVISGNVSPSKG 335
Db 361 GTTATVSKDDOGNTTVMYDVNVGDALNVNOLONGSMWLDKRAVAGSSGKTVISGNVSPSKG 420
QY 336 KMDTVNINAGNNIEITRNGKNIDIAISMTPOFSSVSIGAGADAPTLSVDGD-ALNVGSK 394
Db 421 KMDTVNINAGNNIEITRNGKNIDIAISMTPOFSSVSIGAGADAPTLSVDEGALNVGSK 480
QY 395 KDNKPVRTITNVAPEVKEGDTVNVNQLKGVNQLNNRINDVNGNARAGIAQAIATAGLVQA 454
Db 481 DANKPVRTITNVAPEVKEGDTVNVNQLKGVNQLNNRINDVNGNARAGIAQAIATAGLVQA 540
QY 455 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGMNIIKGTASGNSRGHGASASVGYOW 512
Db 541 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGMNIIKGTASGNSRGHGASASVGYOW 598

```

RESULT 15

Q9JPT0 PRELIMINARY; PRT; 598 AA.

AC Q9JPT0;  
 DT 01-OCT-2000 (Tremblurel. 15, Created)  
 DT 01-OCT-2000 (Tremblurel. 15, Last sequence update)  
 DT 01-OCT-2002 (Tremblurel. 22, Last annotation update)  
 DE Outer membrane protein GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 CC Neisseriaceae; Neisseria.  
 CX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC STRAIN=2996;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scariato V., Malignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
 RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.,  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing." ;  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226359; AAF42508.1; -  
 DR InterPro: IPR005594; Yada.  
 DR Pfam: PF03895; Yada; 1.  
 SO SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 93.3%; Score 2427; DB 2; Length 598;  
 Best Local Similarity 82.1%; Pred. No. 2.9e-95;  
 Matches 491; Conservative 6; Mismatches 15; Indels 86; Gaps 2;

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QY 1 MNKIYRIIWNLSALNAMYVSELTRNHTKRASATVATLALTLFATYQASANNE----- 54
Db 1 MNKIYRIIWNLSALNAMYVSELTRNHTKRASATVATLALTLFATYQANATDDDLXLE 60
QY 55 ----- 54
Db 61 PVQRTAVVLSFRSDKEGTEGEKEDSNMAYVFEDEKRYLKAGAITLKAGDMLKIKONTNE 120
QY 55 -----TDLTSVTEKLSFSANGKNVNTSDTKGINFAKETAGTNGD 95
Db 121 NTNENTDSSFTTSLKADLDLDTLSVTEKLSFGANGKNVNTSDTKGINFAKETAGTNGD 180
QY 96 TTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASYKDYLNAGMNKIGVPGTTA 155
Db 181 PTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASYKDYLNAGMNKIGVPGTTA 240
QY 156 SDNVDFRTYTVFELSDRTKTTVNVESKDNKRTVEKIGAKTSVIREKDGKLVGTGDK 215
Db 241 SDNVDFRTYTVFELSDRTKTTVNVESKDNKRTVEKIGAKTSVIREKDGKLVGTGDK 300
QY 216 GENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTSCTNTYTFASGK 275
Db 301 GENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTSCTNTYTFASGK 360
QY 276 GTTATVSKDDOGNTTVMYDVNVGDALNVNOLONGSMWLDKRAVAGSSGKTVISGNVSPSKG 335
Db 361 GTTATVSKDDOGNTTVMYDVNVGDALNVNOLONGSMWLDKRAVAGSSGKTVISGNVSPSKG 420
QY 336 KMDTVNINAGNNIEITRNGKNIDIAISMTPOFSSVSIGAGADAPTLSVDGD-ALNVGSK 394
Db 421 KMDTVNINAGNNIEITRNGKNIDIAISMTPOFSSVSIGAGADAPTLSVDEGALNVGSK 480
QY 395 KDNKPVRTITNVAPEVKEGDTVNVNQLKGVNQLNNRINDVNGNARAGIAQAIATAGLVQA 454
Db 481 DANKPVRTITNVAPEVKEGDTVNVNQLKGVNQLNNRINDVNGNARAGIAQAIATAGLVQA 540
QY 455 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGMNIIKGTASGNSRGHGASASVGYOW 512
Db 541 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGMNIIKGTASGNSRGHGASASVGYOW 598

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Search completed: October 6, 2003, 09:30:33  
 Job time : 42.6045 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.90659 Seconds  
(without alignments)  
3045.266 Million cell updates/sec

Title: US-09-771-382-23  
Perfect score: 2600  
Sequence: 1 MNKIRILINMSALNMAVYVS.....TASGNSRGHFGASASVGYQW 512

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	245	9.4	1039	1 AG43_ECOLI	P39180 escherichia
2	222	8.5	1286	1 AIDA_ECOLI	Q03155 escherichia
3	214.5	8.2	1325	1 YDEK_ECOLI	P32051 escherichia
4	195.5	7.5	2003	1 YDBA_ECOLI	P33666 escherichia
5	193.5	7.4	2249	1 OMPA_RICRI	P15921 rickettsia
6	178.5	6.9	1577	1 HLVA_PROMI	P16466 proteus mir
7	176.5	6.8	993	1 SLAP_CAME	P35827 campylobact
8	176	6.8	1655	1 OMPB_RICCN	Q9kxk3 r outer mem
9	174.5	6.7	1025	1 SLAP_CAUCR	P35828 caulobacter
10	174.5	6.7	1645	1 OMPB_RICRY	P96989 r outer mem
11	174	6.7	1654	1 OMPB_RICRI	Q53047 r outer mem
12	173.5	6.7	1608	1 HLVA_SPRMA	P15320 serratia ma
13	170.5	6.6	1953	1 BIGA_SALTY	P25927 salmonella
14	169.5	6.5	2660	1 YEEB_ECO57	Q8x8v7 salmonella
15	169	6.5	1567	1 ICEN_XANCT	P18127 xanthomonas
16	166.5	6.4	1861	1 APU_THETU	P38536 t amylopull
17	166	6.4	1569	1 YPUA_ECOLI	P52143 escherichia
18	166	6.4	2021	1 OMPA_RICCN	O52657 rickettsia
19	165	6.3	1300	1 120K_RICRI	P14914 rickettsia
20	164	6.3	3178	1 YS89_CABEL	Q08624 caenorhabd1
21	163.5	6.3	550	1 FLIC_SHIFL	Q08860 shigella fl
22	163.5	6.3	1148	1 ICEN_PSSSX	O30611 pseudomonas
23	163.5	6.3	1656	1 OMPB_RICJA	O06653 r outer mem
24	162.5	6.2	917	1 HXA3_HAEIN	P45385 haemophilus
25	162	6.2	737	1 ALV5_ENTFA	P37710 enterococcu
26	161.5	6.2	1007	1 Y741_CHLMU	O9pj16 chlamydia m
27	160.5	6.2	1036	1 HP12_DEIRA	P13126 deinococcus
28	159.5	6.1	507	1 FLIC_SALON	O06974 salmonella
29	159.5	6.1	537	1 TEE6_STRPY	P18481 streptococc
30	158.5	6.1	487	1 FLIC_ECOLI	P04949 escherichia
31	157.5	6.1	507	1 FLIC_SALBE	O06968 salmonella
32	157.5	6.1	1643	1 OMPB_RICPR	O53020 r outer mem
33	156.5	6.0	928	1 PM10_CHLPP	O9rb65 chlamydia p

34	156	6.0	642	1 FLID_CAME	Q9phw6 campylobact
35	156	6.0	508	1 YMB_CABEL	P34487 caenorhabd1
36	155	6.0	914	1 FLIC_SALNA	O52959 salmonella
37	155	6.0	504	1 FLIC_SALRO	O06982 salmonella
38	155	6.0	575	1 FLA2_CAME	P22251 campylobact
39	155	6.0	1153	1 PVDB_PLAKN	P50493 plasmodiun
40	154	5.9	1196	1 ICEN_PSSSX	O33479 pseudomonas
41	153.5	5.9	1637	1 MRSP_STRAU	P80544 staphylococ
42	153.5	5.9	2358	1 YEEJ_ECOLI	P76347 escherichia
43	153	5.9	504	1 FLIC_SALBU	O06969 salmonella
44	153	5.9	504	1 FLIC_SALDU	O06971 salmonella
45	153	5.9	1200	1 ICEN_PSSSX	P06620 pseudomonas

## ALIGNMENTS

RESULT 1  
ID AG43\_ECOLI STANDARD: PRT: 1039 AA.  
AC P39180: P75614: P76360: P97241: Q46771:  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (AG43) (Flufluff protein).  
GN FLU OR B2000.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia..  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "the complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Isano K.,  
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,  
RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,  
RA Yamamoto Y., Horinouchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML 308-225;  
RA Henderson I.R., Owen P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP PRELIMINARY SEQUENCE OF 53-78.  
RC STRAIN=ML 308-225;  
RX MEDLINE=89291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN [5]  
RP SEQUENCE OF 53-63.  
RC STRAIN=K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded

Query Match	Best Local Similarity	9.4%;	Score 245;	DB 1;	Length 1039;
Matches 135;	Conservative 76;	Mismatches 185;	Indels 170;	Gaps 33;	
1 MNKTYRITMNSALNAAWVVSLETRNNHTRKASATVKTAVLTLLEFATYQAS----- 50					

DB	5	INTCYRLVWMMNTGAFVVASFLARARGRGVAAALSLAAATSLPLAADLVPHRGVEYN	64
OY	51	---ANNETDLTSGTEKLSFANGKNVITSDTKLNFPAKET-----AGTNGD	95
Db	65	GGTLANHEDNQIVFGTNGMTIST-----GLEYGPDNBAANTGGQWODGGTANK	112
OY	96	TTVHLNGI-----GSTLIDTLNLTGATTN-----TNNVDDEK-----KRAASYVDLYN-A	142
Db	113	TTVTSGGELQRNPGGSVDIVISAGGOSLOGRAVNTTLINGEOMMEGALATGTVIDK	172
OY	143	GWNTKGVKPGTASDNDVEFVT-----YDVEFLSADTKTTTVNVESKDNGKTE	192
Db	173	GMQV--VKPGTVAIDTV--VNTGAEGGPDALENGDTGQVRGDVAFTTIN--KNGRIY	224
OY	193	VKIG-AKTSVKEKDGKLYTSKDKGENSSIDE-----GEGLY-----TAKEYIDAVNKAQW	243
Db	225	RAEGTANTTV-----YAGDDTVHGHADTLTLNGYQYVHANGASADIV--VNSDGW	275
OY	244	RM-----KTTYANGOTQADKEFEVYSGTNVFPASG-----KGTPTVSKDDQG-NITY	291
Db	276	QIVANGVAGATTYN-QKGRL-QYDAGGTATNVTLKQGALVYSTAFTV-----GINRLG	329
OY	292	MYDVNVGDALVNOLONGMNLDSKRAVAGSSGKVIISGVNSPFSKKMDETVINANGNIET	351
Db	330	AFSVVEGKADIV--VLENG--RLD-----VLTGHTATN-----TFVDDGGTLDV	370
OY	352	TRNGKNIDIASMTPOFSSVSLGAGADAPLTLSYGDALNVSKKKDNKPVRTITNAPGVKE	411
Db	371	RNG-----GTAIT-----VSMNGG--VLLADSGAAVSSTBRDG-----AFSTGG	409
OY	412	GDVTNVAOLKVAONLNRIDNVDGNARAGIAQAIATAGVQAYVLPKSMIAIGGTYRG	471
Db	410	QADALMLEKSSFTLN-----ACDTATDTT-----VNGGLEFTA	443
OY	472	EAGYAIIGYSISDGGNMIIKGTASGN	497
Db	444	RGTLAGTTTLNNGAILTLGSKTYNN	469

RESULT 2

AIDA\_ECOLI

ID	AIDA_ECOLI	STANDARD:	PRT:	1286 AA.
AC	Q03155:			
DT	01-JUN-1994	(Rel. 29, Created)		
DT	01-JUN-1994	(Rel. 29, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Adhesin aidA-1 precursor.			
GN	AIDA-1.			
OS	Escherichia coli.			
OG	Plasmid pIB6.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.			
RC	STRAIN=0126:H27 / 2787;			
RC	MEDLINE=9232638; PubMed=1625582;			
RA	Benz I', Schmidt M.A.;			
RT	"AIDA-1, the adhesin involved in diffuse adherence of the			
RT	diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is			
RT	synthesized via a precursor molecule.";			
RL	Mol. Microbiol. 6:1539-1546(1992).			
CC	-I- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE			
CC	ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI			
CC	TO EPITHELIAL CELLS.			
CC	-I- SUBCELLULAR LOCATION: Outer membrane.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X65022; CAA46156.1; -

DR PIR: S28634; S28634.

DR InterPro: IPR006315; Autotransport.

DR InterPro: IPR005546; Autotransporter.

DR InterPro: IPR004899; Pertactin.

DR Pfam: PF03797; Autotransporter; 1.

DR Pfam: PF03212; Pertactin; 1.

DR TIGRfams: TIGR01414; autotrans\_bar1; 2.

DR Cell adhesion; Signal; Outer membrane; Plasmid.

FW SIGNAL 1 49

FT CHAIN 50 ? ADHESIN AIDA-1.

FT PROPEP 1286

SO SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 8.5%; Score 222; DB 1; Length 1286;  
Best Local Similarity 21.6%; Pred. No. 0.00038;  
Matches 142; Conservative 88; Mismatches 229; Indels 198; Gaps 31;

QY 1 MNKRIIRIINMIALAMVYVSLTRNH--TKRASIVTAVLATL--LEATVQASANNETD 56  
DB 1 MNKRVSIIMSHSRQAWIVASELARGHFLAKNTLLAVAVSTIGMAFAVNIISGVSSGC 60

QY 57 LTVGTEKLSEFANGNKVNITSPTKGL--NFAKETAGT-NGDPTVHLNGISLTLDTL 111  
DB 61 TVSSGEGQIYVSSGNGS-NATVNSGQIYVNSGKTRATYVNSGSGNQVSGATIS-TI 118

QY 112 LNTGATNTVNDVNTDDEKRAASVKDLNAGNMIKVGPGTASDVNVEVRYTVEFL 171  
DB 119 VNSGQIYVSSGNGV--ASATNISGGAQNIYV--GHAISNTYIFEGSGNQTIF-S 166

QY 172 SADRTTIVN-----VESKNGKTEYKIGAKTSVIEKDKGKLVTKDKEN-----GS 220  
DB 167 GGTIDSTNIISSGGOORVSSGVASNTIINSSGAONILSE-EGALSTHIISSGNGYISAGA 225

QY 221 STDEGELVYAKEDVAVNKAQWBMKT-----TFANGQF-----GOADKFEVTVST 267  
DB 226 NATE-----TIVNSGQFQVNSGAVATGTVLSGQTONVSSGSAISTSVNSGV 274

QY 268 NVTASGKGTAVYSKD-----DOGNITVMYVNV-----GDALNVN-----QLONS 309  
DB 275 QTVFAGAVTDTFTVNSGNGONISSGQIVSETTVSGTONIYSSGSAISANIKSQIYVS 334

QY 310 -GNWLDKAKAVAG-----SSGXYI--SGNVSPEKGDDEVNINAGNIEITRNG- 355  
DB 335 EGTAINTLVSDGYQHIRNGIAGTIVNOSGVYNISSGVAESTTILNSGGTLRVLSDGY 394

QY 356 -----KNID-----IATSMTFQFSSVSLGAGADA 379  
DB 395 ARGITLNNSGRENVSGVSNAMINTGNGNOYIYSDGEMTAIYNTSGFQKIN--SGGTA 452

QY 380 P-----TLS-----VDGDALNVGSKK-----DNKPVRTINVAQVEGDVTN 416  
DB 453 PVQNSVYVTRTVSSAAKPFDAEYVSSGKQFYVLMRGIMYSNFLAVVSMFPGTASGANVN 512

QY 417 VA-OLKGAQNLNRRINQSN-----ARGIA 443  
DB 513 LSGFLNAPAGNVGTTINQEGROYVSGATATSTVGNNGREYVLSGGITDGTVLNSGGL 572

QY 444 QAITAGLVQAYL--PGKSMAIG-----GGTYRGAGVAYGYSISDGCN 487  
DB 573 QAVSSGKASATVINEGGAQFYVDGGQVYTGNTINKGTIRVDSASALNTALSSGCN 629

RESULT 3  
YDEK\_ECOLI  
ID YDEK\_ECOLI STANDARD: PRT; 1325 AA.  
AC P33051; P76140; P77168;  
DT 01-OCT-1993 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical lipoprotein ydek precursor (ORF1).

GN YDEK OR ORF1 OR B1510.

OS Escherichia coli.

CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

CC Enterobacteriaceae; Escherichia.

OX NCBI\_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97251357; PubMed=9097039;

RA Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Ison K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Samped G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";

RT DNA Res. 3:363-377(1996).

RL [3]

RN [3]

RP SEQUENCE OF 595-1325 FROM N.A.

RX MEDLINE=94100243; PubMed=8274505;

RA Cartwright P.J., Tims M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.; "An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and MOM38.";

RT Biochim. Biophys. Acta 1153:345-347(1993).

RL -1 SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (potential).

CC -1 SIMILARITY: TO E. COLI YFAL.

CC -1 SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS ISP42 AND MOM38.

CC -1 CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653.

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CC -----

CC EMBL: AE000248; AAC74583.1; -

DR EMBL: D90793; BA15190.1; ALT\_INIT.

DR EMBL: D90794; BA15197.1; ALT\_INIT.

DR EMBL: X73295; CA51730.1; ALT\_FRAME.

DR PIR: A64905; A64905.

DR Ecogene; E611780; ydek.

DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.

DR Hypothetical protein; Membrane; Lipoprotein; Signal;

KW Complete proteome.

FT SIGNAL 1 18

FT CHAIN 19 1325

FT LIPID 19 19

FT CONFLICT 884 884

FT CONFLICT 1317 1317

FT SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 8.2%; Score 214.5; DB 1; Length 1325;  
Best Local Similarity 24.5%; Pred. No. 0.00093;  
Matches 146; Conservative 62; Mismatches 250; Indels 137; Gaps 28;



QY 429 NRIDNV-DGNARAGIAQAIATAGLV-----QAYLPKSKMAIGGTYRGEGAG 474  
 Db 721 SRQNLFDGSAE-----KTSGLVIGDGTVMNNGSLIGKKNLADDSQYTSLATG 773  
 QY 475 YAI-----GYSSIDGGNMIKG 492  
 Db 774 YSYTSVIWVGSSSVYINGDTTISG 798

RESULT 5  
 OMPA\_RICRI STANDARD; PRT: 2249 AA.  
 ID OMPA\_RICRI  
 AC P15921;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmpA).  
 GN OMPA.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 CC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-R;  
 RA MEDLINE=90354033; PubMed=2117568;  
 RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
 RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";  
 RL Infect. Immun. 58:2760-2769(1990).  
 CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC -1- SLAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- Ptm: GLYCOSYLATED (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M31227; AAA26380.1; -;  
 DR PIR: A41477; A41477.  
 DR InterPro: IPR006315; Autotransport.  
 DR InterPro: IPR005946; Autotransporter.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR TIGRfams: TIGR01414; autotrans\_bar1; 3.  
 KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.  
 FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.  
 FT REPEAT 212 286 A (TYPE I).  
 FT REPEAT 287 358 B (TYPE II).  
 FT REPEAT 359 430 C (TYPE II).  
 FT REPEAT 431 505 D (TYPE II).  
 FT REPEAT 506 577 E (TYPE II).  
 FT REPEAT 578 652 F (TYPE I).  
 FT REPEAT 653 724 G (TYPE II).  
 FT REPEAT 725 799 H (TYPE I).  
 FT REPEAT 800 874 I (TYPE I).  
 FT REPEAT 875 949 J (TYPE I).  
 FT REPEAT 950 1021 K (TYPE II).  
 FT REPEAT 1022 1093 L (TYPE II).  
 FT REPEAT 1094 1165 M (TYPE II).  
 FT REPEAT 1166 1180 TYPE I (INCOMPLETE).  
 SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Matches 152; Conservative 52; Mismatches 211; Indels 187; Gaps 32;  
 QY 30 ASATPKT-AVLTATLFAVQASANNEDLTISGTEKLSFSAANGKVNITSDTKGNFKE 88  
 Db 730 ALATVNVAGGTRATGAVIKATTTKLTNAASVLT-----LTNAANV-----LTGAID 776  
 QY 89 TAGTNGDT--TVHLNGIGSTLTDLTNT-----GATTNVTNDVNTDDEK 130  
 Db 777 NT-TGGDNVGVNLNLGALSQYTGDTGNNTSLATISVAGTATLGAATKATTTKLTN--- 832  
 QY 131 KRAASVXDVLNAGMNKGVKPGTTASNDVDFRYDVEFLSADTKTTTVNESKDNKK 190  
 Db 833 --AASVLTLTNNAVLGAVDNTTGGDNVGVNLNLGALSQYTDIGNT-----NSLA 882  
 QY 191 TEVKIGAT-----SVIEKRGKL----- 209  
 Db 883 T-ISVAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAIDNTTGGDNVGVNLNG 941  
 QY 210 ----VTGKDKENGSSST-DEGEGLVT-----AKEVIDAVNRKMGKTTTANNGTGQADK 259  
 Db 942 ALSQVTDIGTGNNTSLATISVAGTATLGAATKATTTLTDAASAVKFTTNPVYTGALDN 1001  
 QY 260 FEYVTSGTNVTFASGKGTATVSKDDGNITVMDVNVGALNVNQLNSGWNLDKAVA 319  
 Db 1002 TGNANNGI-VTFGTGNTVTVGNV-----GNTNALATVNVAGL--LVGGGVKANTINLT 1053  
 QY 320 GSSGKVISGNVSPSKGRKDEVTNINAG-----NNIEITRNKNIDIAISMPQSSVSLG 374  
 Db 1054 DNASAVFTNPVVYTGALDNTGNANNGIVTFGTGNTVTVGNV-----TNALATVNVG 1106  
 QY 375 AGADAPLTSDVDGL--NVGSKKDN-KVRLTNNAPVKEGQVTVNAQLKVAQVNLNRI 431  
 Db 1107 AG-----LVGGGVKANTINLTNDASAVTNTN--PVYVTAIDNTG-----NANNGI 1153  
 QY 432 DNVGDNARA-----GTAQAIAT-----AGL-VQAYLPKSKMA-----TGG 466  
 Db 1154 VTFGTGNTVTDIGTGNNTSLATVNVAGGTTLGA-----GSLAANNIDFGARSTLEFNGPIDG 1210  
 QY 467 GTYRGEAGYAIQY---SSISDGGNMIK-----GTASGNSRGH---FGASAS 507  
 Db 1211 G-----GKAIPYFKGAIANGNNAIENVMTKLLTASHLITGVAEINIGAGNLTPTDAS 1264  
 QY 508 VG 509  
 Db 1265 VG 1266

RESULT 6  
 HLYA\_PROMI STANDARD; PRT: 1577 AA.  
 ID HLYA\_PROMI  
 AC P16466;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Hemolysin precursor.  
 GN HPMa.  
 OS Proteus mirabilis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Proteus.  
 OX NCBI\_TaxID=584;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.  
 RC STRAIN-Isolate 477-12;  
 MEDLINE=90170827; PubMed=2407716;  
 RA Uphoff T.S., Welch R.A.;  
 RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";  
 RL J. Bacteriol. 172:1206-1216(1990).  
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
 CC DEFINED.  
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM

Query Match 7.4%; Score 193.5; DB 1; Length 2249;  
 Best local similarity 25.2%; Pred. No. 0.02;

CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA  
CC REQUIRES HPMB FUNCTION.  
CC -1- SUBCELLULAR LOCATION: Outer membrane.  
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA  
CC MAY BE RESPONSIBLE FOR PORE FORMATION.  
CC -1- SIMILARITY: TO S.MARCSSENS HEMOLYSIN (SHLA).  
CC  
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CC  
DR EMBL; M30186; AAA25657.1; -  
DR PIR; A35140; A35140.  
KW Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL  
FT CHAIN 1 29  
FT SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;  
  
Query Match 6.9%; Score 178.5; DB 1; Length 1577;  
Best Local Similarity 21.4%; Pred. No. 0.076;  
Matches 129; Conservative 82; Mismatches 188; Indels 203; Gaps 33;  
  
QY 23 TRNRTRKASATVTAVALATLTFATVOASANNETDLTSVTEKLSFANGKVNITSPDK 82  
DB 710 TSTETEDQANISG-----ANVDLQANK--DYFAGSDLTATG--ASTGTGNAVA 756  
QY 83 LNAKETAGT--NDDTYVH-----LNGTGS-----TLTDTLLTGTATNTND 123  
DB 757 FVSTENKQDNTDPTISGFSYTGVDKYSKADFOYDQKHQTEVTKNRGSETEVAGD 816  
QY 124 -----NVTDEKRRASVKNVLAGNMI----- 146  
DB 817 LTTANKDLHEGASHHVEGRYSEGENIOHLAVNDEISKTPDSLVNGLDVGVALDYSGV 876  
QY 147 -----KGVKPG-----TTASDNVDF--VRYDVEFLS--ADTKTTFVNV----- 183  
DB 877 TKPVKKAIEDGVMTTRKGNNTDLKKYTAARDALANLANSLNLETPNVGVEVGIKGGSSQ 936  
QY 184 SKNGKTEVKIGAKTSVIEKDKLVTKDKGBNGSSDTEGEGLVTAKEVIDA-VNKAG 242  
DB 937 SQTDGQAVSTSIAGKIDI-DSNNKL--HDGTHYOSTOEGISLTANTHTSEATLDKHQ 992  
QY 243 WRKKTTPANGFOADKFETVTSNTVFA--SGKGTA-----TVSKDQGNITVYDY 295  
DB 993 TTTHETKGGQIGVSTK-----TGSDDITVAIKGBGQTTDNALMETTKAGSQSFTSGDISI 1047  
QY 296 NVGDALNVNQLQNSGNMLDSKAVAGSSGKVIYSGNVSPSKGMDVTAIAGNNIETLR-- 353  
DB 1048 NVGE-----NAHYEAGQFDAQ-----KKG---TV--INAGGDLTLAQA 1081  
QY 354 -----NGK--RTDIATSKTPQFSSVSLGAGADAPL--SYGDALNVGSKDKPKV 400  
DB 1082 DFHSEGSNVNGSANKLVGT--TPE--SKDYGGGFNAGTTHHSKEQTAVAGVITGSGGI 1137  
QY 401 RITNVAPGVEGVTVAQLKGVAONLNRIID-----NDGNAARAGIAQ--- 444  
DB 1138 ELNAGHNLITLG--THLSSEQDIALNTKRVLDQSASSETEKGNNSGGVQAGFGKMT 1195  
QY 445 --AIAATAGVQAOLPCKSMAIG-----GGTYRGEAGYAIGSSISDGNWIKG 492  
DB 1196 DDASSVNGL-----GSAQFAIKQDEKSVSREGT-----INSGNLTING 1236  
QY 493 TA 494  
DB 1237 NS 1238

ID SLAP\_CAMFE STANDARD; PRT; 933 AA.  
AC P35827;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE S-layer protein (surface array protein) (SAP).  
GN SAPA.  
OS Campylobacter fetus.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_Taxid:196;  
RN  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
RC STRAIN=84-32 / 23D;  
RX MEDLINE=90354448; PubMed=2387868;  
RA Blaser M.J., Gotschlich E.C.;  
RT "Surface array protein of Campylobacter fetus. Cloning and gene  
RT structure."  
RL J. Biol. Chem. 265:14529-14535(1990).  
RN  
RP ERRATUM.  
RX MEDLINE=91035477; PubMed=2229082;  
RA Blaser M.J., Gotschlich E.C.;  
RL J. Biol. Chem. 265:19372-19372(1990).  
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
CC CRITICAL FOR VIRULENCE.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC  
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CC  
DR EMBL; J05577; AAA23032.1; -  
KW Cell wall; S-layer.  
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;  
  
Query Match 6.8%; Score 176.5; DB 1; Length 933;  
Best Local Similarity 21.9%; Pred. No. 0.052;  
Matches 136; Conservative 74; Mismatches 236; Indels 175; Gaps 30;  
  
QY 1 MNKIYRINMSAL--NAAVYSELTRNHRKRSATVYKAVLATLTFATVOASANNETDL 57  
DB 246 LNAIFTRAIALLTDQAEILIT-----TKRRTVENINIIISDL-----ETSGDF 289  
QY 58 TSVGTEKLSFSANGKNVNITS-D--TKGLNFAKETAGT----- 92  
DB 290 VFNQGEYKGVNVLGDIYSFATDASKSVN--ETGTITATPAGTGKVDVYVACKISALTA 347  
QY 93 NGDTYHNLNGIGSTLDTLTNTGATTVYNDVNTD-----DEKKRA----- 134  
DB 348 DSRSTVNLRTNTDITITLISANAATSYNLKORAKADATITSAMOOKYNNRRRIATITSAT 407  
QY 135 -----SKVDLNLGWNKNGKVGPGTTASDNVDVRYDVEFLSADPTFTTVN--VESKNG 188  
DB 408 AVENTLVKHTATNALNGMDKLATVTLDNALTAIDI-----KSATLNLINSSVNG 460  
QY 189 -----KTEVAKIGAKTSVIEK-----DGRLVYTKDKGNGSSSTDEG 225  
DB 461 PKHLYSKRRYCKFKRAAAKVKLNTTAATQGYTLKANATDNLSEPD SATAKTTSTYASG 520  
QY 226 EG--LVTAKEVIDAANKACRMKTTTAN-----GQTGQADKFTVTSQTVNTPASGK 275  
DB 521 SGKTLVYKGAETVELVN-----IDTFAFNALQSVSFGKGTGGKGF--SVKGTGDDDKIEFV 574  
QY 276 GTTATYSK--DDGNITVYMDVAVGDALANVNOQNSGNMLDSKAVAG--SSGKVIISGV 330  
DB 575 GTTLTEGVSIDAGNDITAMKSAALTSANFTMIKNLENVAISDAVYATADLSSAFKNSVI 634

RESULT 7  
SLAP\_CAMFE





RESULT 9  
SLAP CAUCH STANDARD: PRT: 1025 AA.  
AC P35828; 046015; 099F12;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE S-layer protein (paracrystalline surface layer protein).  
GN R5AA OR C01007.  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_Taxid=155892;  
RN  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.  
RC STRAIN-ATCC 19089 / CB15;  
RX MEDLINE=93007489; PubMed=1393820;  
RA Gilchrist A., Fisher J.A., Smit J.K.;  
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter  
RL crescentus paracrystalline surface layer protein.";  
RL Can. J. Microbiol. 38:193-202(1992).  
RN  
RP REVISIONS TO 376; 636 AND 842-843.  
RA  
RA Awram P.;  
RL Submitted (OC1-1999) to the EMBL/GenBank/DBJ databases.  
RN  
RN SEQUENCE FROM N.A.  
RC STRAIN-JS3001;  
RA Bingle W.H., Awram P.A., Nommellini J.F., Smit J.K.;  
RT "The secretion signal of C. crescentus S-layer protein is located in  
RL the C-terminal 82 amino acids of the molecule.";  
RL Submitted (OC1-1999) to the EMBL/GenBank/DBJ databases.  
RN  
RN SEQUENCE FROM N.A.  
RC STRAIN-ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonyak J.E., Smit J., Craven M.B., Khouri H., Shetty K.,  
RA Salzberg S.L., Venter J.C., Vamathevan J., Ermolaeva M., White O.,  
RA "Complete genome sequence of Caulobacter crescentus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
RN  
RN SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.  
RP STRAIN-ATCC 19089 / CB15;  
RX MEDLINE=89008089; PubMed=3049545;  
RA Fisher J.A., Smit J.K., Agabian N.;  
RT "Transcriptional analysis of the major surface array gene of  
RL Caulobacter crescentus.";  
RL J. Bacteriol. 170:4706-4713(1988).  
RN  
RN CHARACTERIZATION.  
RP STRAIN-ATCC 19089 / CB15;  
RX MEDLINE=98292737; PubMed=9620954;  
RA  
RA Awram P., Smit J.K.;  
RT "The Caulobacter crescentus paracrystalline S-layer protein is  
RL secreted by an ABC transporter (type 1) secretion apparatus.";  
RL J. Bacteriol. 180:3062-3069(1998).  
RN  
RN -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A  
CC PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER  
CC (TYPE 1) SECRETION APPARATUS.  
CC -1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE  
CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A  
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.  
CC -----

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CC -----  
DR EMBL: AF062345; AAC38665.2; -  
DR EMBL: AF193063; AAF19365.1; -  
DR EMBL: AE005779; AAK22991.1; ALT\_INIT.  
DR PIR: A48995; A48995.  
DR HSSP: P22629; ISWC.  
DR TIGR: CC1007; -  
DR InterPro: IPR001343; Hemlysn\_Ca\_bind.  
DR Pfam: PF00353; hemolysincbind; 3.  
DR PRINTS: PRO0313; CABNDNGRPT.  
KW Cell wall; S-layer; Calcium-binding; Complete proteome.  
FT INIT\_MET 0  
FT SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;  
SQ  
Query Match 6.7%; Score 174.5; DB 1; Length 1025;  
Best Local Similarity 22.8%; Pred. No. 0.073;  
Matches 136; Conservative 65; Mismatches 223; Indels 173; Gaps 28;  
QY 34 VKTAVLATLL-----FATVQASANNETDLSVGTETKL-----SFSANGNK 73  
DB 191 VKAALIGTILNATVATGIGYATATFAMINDSLDGLSTDMAGVNLFTAYSSGVSGST 250  
QY 74 VNITSDTKGLN-----FAKETAG-----TNGDITVHLANGISTITLD-----TLNMT 114  
DB 251 LSLTITGDTPLTGATANDTFVAGVAGAAATLVGDTL--SGGAGTDLVLMVQAAVYALPT 308  
QY 115 GAT-TNVTNDVNTDDEKRAASVQDLVNLGMNKGKPGTASDNDVFRTYDVFELSA 173  
DB 309 GVTISGIEIMNVTS-----GAAL--TLNSSGVYTGTLALNTNSGAQVYTAGAGCNLTA 361  
QY 174 DRTTTTVNESKNGKRTVEKIGAKTSVIREKDKGLVTKDKGENG-----SSTDE 224  
DB 362 TTAQAQANNAVADGAGNVTV--ASTGV--TSGTTVGANSMAAGTSVANSSTTTT 415  
QY 225 GEGVYAKVEIDAVNKAQRMTT-----TANG-----QFGQADKEFTVYSGTN 268  
DB 416 GAIYAVGTAATVAGTAGANVNTLLQADVTVYVGNSSSTAATVYVYTAATAFAGVAGRVN 475  
QY 269 --VTF-----ASGKGTATVSKDQGNITV---MYDVNYGD----- 299  
DB 476 GAVTITDSAAASFTTAGKIAITVTLGSGFCAATTDSALTYVNLSTGTSLSIGRGALTATP 535  
QY 300 -----ALNVNOLNDSGNLDSKRAVAGS-----SGKVISGNVSPSKGMDETVINAGN 347  
DB 536 TANTLTPLNVNGTLTTGATIDSEAAADGFTTINIASTASTIASLVAADATLTNISGDA 595  
QY 348 NIETIRN-----GKNT--DIATSMTPPFSSVSGAGADAPPLSYVDGALNV 391  
DB 596 RVYITSTAAALGTVTNSVGAITLGAELATGLV--FTG---GAGADSTILATYTKAIY 650  
QY 392 GSKKDKKPVRTINVARP--VKEGDYVNVQALGVANLNNRIDNV-----GN 437  
DB 651 GAGDDTVYVSSATLGAAGSYNGGDTDY-----LVANVNGSSRSADPAEGEPTLVYAA 705  
QY 438 ARAG-----IAQAIATAGLVQ---AYLPKSKMAIIGGTYRGEAGYAIIGYSI 482  
DB 706 AAGGSHNANGFTALQIGATAGATTFNVAVNVGLTVLAAPTGTVTVLNAGTSDV 762  
RESULT 10  
OMP\_RICTY STANDARD: PRT: 1645 AA.  
AC P96989;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DT -----

DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOMP B)  
 DE (Comp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB OR SLIP.  
 OS Rickettsia typhi.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=785;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Williamington;  
 RX MEDLINE=94040787; PubMed=8224886;  
 RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;  
 RT "Cloning and sequence analysis of the gene encoding the crystalline  
 RT surface layer protein of Rickettsia typhi.";  
 RL Gene 133:129-133(1993).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC STRAIN=Williamington;  
 RX MEDLINE=92114896; PubMed=1370573;  
 RA Ching W.M., Carl M., Dasch G.A.;  
 RT "Mapping of monoclonal antibody binding sites on CNBr fragments of  
 RT the S-layer protein antigens of Rickettsia typhi and Rickettsia  
 RT prowazekii.";  
 RL Mol. Immunol. 29:95-105(1992).  
 RN [3]  
 RP IDENTIFICATION OF CLEAVAGE SITE.  
 RC MEDLINE=92104668; PubMed=1729180;  
 RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;  
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer  
 RT membrane protein of rickettsiae: Identification of an avirulent  
 RT mutant deficient in processing.";  
 RL Infect. Immun. 60:159-165(1992).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPB/OMP FAMILY.  
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 CC -----  
 DR EMBL: L04661; AAB48987.1; -;  
 DR PIR: JN0896; JN0896;  
 DR InterPro: IPR005315; Autotransport.  
 DR InterPro: IPR005346; Autotransporter.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR TIGRFAMS: TIGR01414; autotrans\_bar1; 1.  
 KW Antigen; S-layer; Transmembrane; Cell wall.  
 FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.  
 FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
 FT CONFLICT 657 657 H -> N (IN REF. 2).  
 FT CONFLICT 842 842 V -> I (IN REF. 2).  
 FT CONFLICT 1071 1071 G -> A (IN REF. 2).  
 FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
 SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB155EE CRC64;

Query Match 6.7%; Score 174.5; DB 1; Length 1645;  
 Best Local Similarity 21.2%; Pred. No. 0.13;  
 Matches 120; Conservative 81; Mismatches 208; Indels 157; Gaps 26;

OY 27 TKRSATVYKAVTLATLFAIVQASANNETDLTSTGTEKLSANGNKVNTISDPKGLNFA 86  
 DB 141 TAOQAATTKSA--ONVYSKVNAIAINDLDSGVSIDFTAPSPVLEFNLINPT-----T 193

OY 87 KETAGTNGDTVHLNGIGSTLTLDLNTGATTNVTNDVTDDEKKRAASVKNAGNMI 146  
 DB 194 QEAPLTLGDNAKIYNGANGIL-----NITNGV-----KVSDFTFAG--I 231  
 OY 147 KGVPCTTASDNVDVFVRTYDVEFLSADTKTTTVNVESSD-----NGKTEVRI- 195  
 DB 232 KTIINGD--NGLMFNTPPDAAANLNLGGGNTINFNRODGTGLVLSKNGMATEFVVT 289  
 OY 196 ---GAKTSVIREKD-----GKL-----VTGKDKGENS-----STDEG-----EGL 228  
 DB 290 GSLGKLVKGYIEFTTAAAGKLIANGANAVIGTDNAGAPAGFIYSVDGNMATTISGQ 349  
 OY 229 VTAKVIDAVNAKAMPMKTTTANOT-----GGADKFEVYTSGTNTVPASGKGT 278  
 DB 350 VYAKDIY-----IOSANAGQVTFEHLVDVGLGKTFFKTAADSVIITENASFGST 400  
 OY 279 ATVSKDDGNTVYVDVN-----VGDALNVNOLNSGMNLSKRAVAGSSGKVVISGN 329  
 DB 401 -----DEGNLAQIVAPNNKILNGNFIGDA-----KNGC--NAGVITFANAGTLVSGN 447  
 OY 330 VSPS-----GKMDERYNT-----NAGNNIETTRNGKIIDATSKTPQFS 369  
 DB 448 TDPNIVVTNKAIEVEGAGIVQLSGIHGAELELRLNAGSIFKLA--DGFVINGPVQNPLVN 506  
 OY 370 SVSLGAGADAPTLASVDGAL---NVGSKKDKPVRITVAVPAGVEGDVTNVAOLKGVAN 426  
 DB 507 NNALAG-----STLDGSAITTDIGNCAVNAALODITLA-----NDASKLITLSGA--- 554  
 OY 427 LNNRIDVYGNARAGIAQATAGLVQAYLPKSKMAIGGTYRGEAGYAIGSISDPG 486  
 DB 555 -----NIGANAGAGAHIFQANGGTIQLTSTQNNILVDFDVTDTDQGVVDASLSLTNQ 608  
 OY 487 NWITKGT-----ASGNSRKHFGASAS 507  
 DB 609 TLTINGSIGTIGANTKTLGRNVGSS 634

RESULT 11  
 OMPB\_RICRI  
 ID OMPB\_RICRI STANDARD; PRT; 1654 AA.  
 AC Q53047;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOMP B)  
 DE (Comp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=92167802; PubMed=1724278;  
 RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;  
 RT "The 120 kilodalton outer membrane protein (rOMP B) of Rickettsia  
 RT rickettsii is encoded by an unusually long open reading frame:  
 RT evidence for protein processing from a large precursor.";  
 RL Mol. Microbiol. 5:2361-2370(1991).  
 RN [2]  
 RP SEQUENCE OF 279-1654 FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=90136087; PubMed=2515418;  
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the  
 RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
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-----  
DR EMBL; X16353; CAA34403.1; -  
DR PIR; S18227; S18227.  
DR InterPro; IPR006315; Autotransport.  
DR InterPro; IPR005546; Autotransporter.  
DR Pfam; PF03797; Autotransporter; 1.  
DR TIGRfams; TIGR01414; autotrans\_bar1; 2.  
KW Antigen; S-layer; Cell wall.  
FT CHAIN 1 1333 120 kDa SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1334 1654 32 kDa BETA PEPTIDE.  
FT DOMAIN 1181 1188 POLY-PHR.  
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;  
-----  
Query Match 6.7%; Score 174; DB 1; Length 1654;  
Best Local Similarity 21.9%; Pred. No. 0.13;  
Matches 149; Conservative 76; Mismatches 236; Indels 220; Gaps 32;  
-----  
QY 9 WNSALNAAVYVSELTNRHTRKASATYKTVAVLATLRLATVOASANNEDLTSG----- 61  
DB 123 FNLTLNAGKTLITGGGVNNAQAATKNAQNVVVFNGAIDNN-DLKGVRIDEGAP 180  
QY 62 -----TEKL-----SEFANG--NKVNIT-----SDTK 81  
DB 181 ASLVENRIANPTOKAPLIGDNAVJANGVNGTILNTNGTIOYSNKSFAVKAINTADGQ 240  
QY 82 GLNFAKETAGT-----GDTVHLNGISLTLDLTNTGATNTVNDVNTDEKKRAAS 135  
DB 241 GILFNDANNANFLNLQAGSTTINFCTDGTGRVLISKHA--ATNFNTITG----- 290  
QY 136 VKVYLAAGNIKVKRETTASDNDVPRITDYEFLSADPKRTTVN-----VESKD 187  
DB 291 -----SLGGLNKGVIEFNTVA-----VDGQLTANAGANAVIGTNNAGRAAGFVSV 340  
QY 188 GKTEV--KIGAKTSYIKEDGKLYTK-----DKGEGS----- 220  
DB 341 GKATIDGQYVADMTYQSAN--ATGQVFRHIVDGADGTTAFKTAASKVITTDQSNF 397  
QY 221 -STDESEGLVTAKEVIDAV-----NKAGWRMKTITANG--OTGOADKFEV 263  
DB 398 GNTDFG-NLAAQIKVFNALITLGNFTGDASNPGNTAG--VITPDANGTLESASADNAVAV 454  
QY 264 TSGTNTVTFASGKT-----TATVSKDQDGNITTVADVANGALN--VOQLONGNLD 314  
DB 455 TNNITALEASGAVVOLSGTHAEELRLGNAGSIFKLAD--GTVINGKVAQTLVGGALA 511  
QY 315 SKVASSSGKVISGNSPSKGM-----DEYNINA-GN 347  
DB 512 AGTITLDGSAITTGIDGNAGGAALQRIITLANDAKTLITLGANIIGAGGCTIDLOANG 571  
QY 348 NIEITRNGKNI-----DIATSMTPQFSSVSLGAGADAPTLSDV-----DALNY 391  
DB 572 TIKLTSTQNNIIVDFDLAIA-TDQGVYDASSLTLNQTLITNKGIGTIGANNKTLQGFNI 630  
QY 392 GSKK---DNKPVITVAPGVKEGDV-----TNVAQLKVAQNLNLRINDVDGNAR 439  
DB 631 GSKSTYLSNGNVAINELVIG-NDGAVOFAHDTYLIPTTNAAGCGKIIFNPVYNNGTTLA 689  
QY 440 AGIAQAIAATAGLVOAVLPK-----SMALIGGFTYREAGYA-----IGYSSISDG 485  
DB 690 AGNIGASATNPPLAEINFGSKGVAVDTVLNVEGVNL---YATNITTTDANVGSFVNAG 745

QY 486 GNNIIGKTASGNSRGHFGASA 506  
DB 746 GTNIVSGTVGQGGQGNKFNTVA 766  
-----  
RESULT 12  
ID HLYA\_SERMA STANDARD; PRT; 1608 AA.  
AC P15320;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Hemolysin precursor.  
GN SHLA.  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
RP STRAIN-SM8;  
RX MEDLINE=88257037; PubMed=3290200;  
RA Poole K., Schiebel E., Braun V.;  
RT "Molecular characterization of the hemolysin determinant of Serratia  
RT marcescens";  
RL J. Bacteriol. 170:3177-3188(1988).  
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
CC DEFINED.  
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
CC REQUIRES SHLB FUNCTION.  
CC -1- SUBCELLULAR LOCATION: Outer membrane.  
CC -1- SIMILARITY: TO P. MIRABILIS HEMOLYSIN (HPMA).  
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DR EMBL; M22618; AAA50323.1; -  
DR PIR; A28182; A28182.  
KW Hemolysis; Toxin; Outer membrane; Signal.  
FT STGNAL 1 30  
FT CHAIN 31 1608 HEMOLYSIN.  
SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;  
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Query Match 6.7%; Score 173.5; DB 1; Length 1608;  
Best Local Similarity 21.9%; Pred. No. 0.14;  
Matches 113; Conservative 72; Mismatches 207; Indels 125; Gaps 22;  
-----  
QY 28 KRASATYKAVLATLLEPAVQASANNEDLTSGTEKLSFSGANKKNVITS----- 78  
DB 933 KRSSSS--QAVVSSVOAGSIDINAKGE--VRDQGTQ---YQASKGAVNLTADSHREAA 985  
QY 79 -----DKGILNFAKETAGTNGDPTVHLNGISLTLDLTDLTGATNTV 121  
DB 986 NRDEGSRDTRGSAGVAVYTTGSDLTVDKAGGEGTORS--NSSASQAVTGSIDANGI 1042  
QY 122 NDNVTDDEKKRASV-----KDVINA-----GNNIKGVKPGTTASDN 158  
DB 1043 NVNVKKDAITOGALNGRKRTAVNMGDRLDOASDKQSESGSFVAKSAGGFTADS 1102  
QY 159 VDFKTYDVEFLSADTKTTTVVESKDNKKTVEKIGAK-----TSVIREKDKLVTG- 212  
DB 1103 KNFGAGGCGGTH-NGESSSTAGVGNISGQGVELAKGRDLTLOGTDVKSQGDVSLSAGN 1161  
QY 213 -----KDKGEGSSTDEGELVTAKEVIDAVNKAAGRMKTITANSGTGADKF 260  
DB 1162 KVALQAESTQTREKESKLSGIDLAGGSSDSKE-----KTGGLN---SGAGAFDIKAVN 1212

OY 261 ETVTSGTNTVFEAS-GKGTATATVSKD-----OGNITVMDVNVGDALN--VNOLO 307  
 DB 1213 ESATEROGATIASOGKVTLSANGKDDALHOGAKVSGSAALEAKNGGILLESKAKNOH 1272  
 OY 308 NSGNWLDKSAVAGSS--GKVISGNVSPSKGMDETVINAGNNIETRNKKNIDATSM 364  
 DB 1273 KDNWSLGIKANAKGQGFENKDGAGKVDNPNTGK--DTHRLGAGLKVGVQDQKTHANNGI 1330  
 OY 365 TPQSSSVSLGAGAPLTL--VDDGA-----LWNSKDKNKEVRTTNAPGVKEDV 414  
 DB 1331 TA--GDVTLNSGKDTRLAGARVADDSVQKVGDLHVESRD-----VENGVKVDVD 1380  
 OY 415 TNVAOLKGAONLNNRIDNVGNARAGIAQIATAGL 451  
 DB 1381 AGLSHNDPSSSITSKLSKVGTPTXAGKVKEXLEAGV 1417  
 RESULT 13  
 BIGA\_SALTY STANDARD: PRT: 1953 AA.  
 AC P25927: P25928: O9XCQ3:  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative surface-exposed virulence protein biga precursor.  
 GN BIGA OR STM3478.  
 OS Salmoneilla typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmoneilla.  
 OX NCBI\_taxid=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14028;  
 RA Stojiljkovic I., Valentine P., Heffron F.;  
 RT "Salmoneilla typhimurium rhs homolog."  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RA MEDLINE=21534948; Pubmed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Portwolk S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmoneilla enterica serovar Typhimurium  
 LT2."  
 RL Nature 413:852-856(2001).  
 RN [3]  
 RP SEQUENCE OF 1-765 FROM N.A.  
 RC STRAIN=LT2;  
 RA MEDLINE=91100301; Pubmed=1987123;  
 RA Wu J.Y., Siegel L.W., Kredich N.M.;  
 RT "High-level expression of Escherichia coli NADPH-sulfite reductase:  
 RT requirement for a cloned cysG plasmid to overcome limiting streheme  
 cofactor."  
 RL J. Bacteriol. 173:325-333(1991).  
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
 CC in positions 414 and 732.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: AF133696; AAD39458.1; -  
 DR EMBL: AE008859; AAL22340.1; -  
 DR EMBL: M64606; AAA27042.1; ALT\_FRAME.  
 DR EMBL: M64606; AAA27043.1; ALT\_FRAME.

DR StyGene: SG10437; biga.  
 KM Virulence: Repeat; Signal; Complete proteome.  
 FT SIGNAL 1 27  
 FT CHAIN 28 1953  
 FT  
 FT DOMAIN 101 252  
 FT REPEAT 101 103  
 FT REPEAT 104 113  
 FT REPEAT 114 122  
 FT REPEAT 123 133  
 FT REPEAT 134 144  
 FT REPEAT 145 155  
 FT REPEAT 167 177  
 FT REPEAT 178 188  
 FT REPEAT 189 199  
 FT REPEAT 200 210  
 FT REPEAT 211 221  
 FT REPEAT 222 232  
 FT REPEAT 233 243  
 FT REPEAT 244 252  
 FT CONFLICT 207 207  
 FT CONFLICT 514 514  
 FT CONFLICT 1698 1698  
 FT CONFLICT 1795 1798  
 FT CONFLICT 1836 1837  
 SQ SEQUENCE 1953 AA; 200150 MW; 61B3F1C954D91AE CRC64;  
 Query Match 6.6%; Score 170.5; DB 1; Length 1953;  
 Best Local Similarity 23.1%; Pred. No. 0.25;  
 Matches 124; Conservative 60; Mismatches 199; Indels 154; Gaps 28;  
 OY 68 SANGKRVITSDTKLNRAKETAGT-----NGDT-----YVHLNGISITL----- 108  
 DB 422 SGNGTTTTPAGD-----IAVSGGTAIIIDGNATIKNTGTSIDAGSTGTVDGNAR 476  
 OY 109 -----DTLNTGATTNTVNDVNT--DDEKRRASVYK-----VLNAG--WNKIG 148  
 DB 477 VNNDGDMITTDGCTGHTGDNVVIDNAGSTTVSGADATALYIEGDNALVINEGNOTISG 536  
 OY 149 VKPGTASDNVDFRTYDVEFLSADRTTTVNVESKDNKTEVKGAKTSVIREKDGK 208  
 DB 537 GAVGTRIDG-----DAHTTNGDIAVDGAGSAVYI----- 568  
 OY 209 LVTKGDKKENGSSPDEGEIVT--AKEYI--DAVKAAGRMKTTTANQOTGADKFEYTV 264  
 DB 569 -----NGDNGSLVQAGDLVTDGAMGITTYGTGNEA-----KNTGNATVRDADSVGFVY 617  
 OY 265 SGTNTVF-----ASGKGTATVSKDOGNITVYDVNVGDALNVNOLONGMWLDKSA 317  
 DB 618 AGEKTFRNKKGIDIVSLNGTALVS--GMSQVTLTLDGDLNV--VSQDSSEGVFSATGVS 673  
 OY 318 VAGSSGKV-IGSNVSPS-----KKMDETVINAGNNIETRNK--NI--DIATS 363  
 DB 674 VSGDSNAVDITGNVVISADYGDDDLAAGAPLTVGVVGGNGTIVLNGALNIDDDLSAT 733  
 OY 364 MTPQSSSVSLGAGAPLTLVDGDALNVGSKKDKNPVITTNAPGVKEDVNVNQLKGV 423  
 DB 734 GGQYLDVVGSLVTDGDNDEIDG--GINITHSD--PLDGT-----ADITGISVSGNS 783  
 OY 424 AONLNNRIDNVGNARAG-----IAQIATAGLV-----QAYLP-----GKSMA 463.  
 DB 784 TVTLNGH--STIDTNTVVGGHVLAIVNNGGSLILDDSDVDVNVSYITPTGYTTVALLMA 842  
 OY 464 IGGTYRGEAG-----YAI-----GYSIDSGWMITKGTASGSKRHFPGASASVG 509  
 DB 843 DGEQTSIENKGDITSHGVYSVIRADNGSEVNSCDILVYATSSNSEDRAATRASG 899  
 RESULT 14  
 YEED\_ECO57 STANDARD: PRT: 2660 AA.  
 AC Q8X8V7; Q8X2B9; Q8X2C0;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Hypothetical protein yeeJ.  
 GN 23135 OR ECS2775/ECS2776.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomous K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch K.A., Blattner F.R.;  
 RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:529-533(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=0157:H7 / RMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,  
 RA Iida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,  
 RA Kohara S., Shiba T., Hatori M., Shnagawa H.;  
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12";  
 RL DNA Res. 8:11-22(2001).  
 CC -1- SIMILARITY: BELONGS TO THE INTIMIN/INVASIN FAMILY.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a  
 CC frameshift in position 1315.  
 CC  
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 CC  
 CC -----  
 CC EMBL: AE005423; AAG57041.1; -  
 CC EMBL: AP002559; BAB36198.1; ALT\_FRAME.  
 CC EMBL: AP002559; BAB36199.1; ALT\_FRAME.  
 CC InterPro: IPR003344; Big\_1.  
 CC InterPro: IPR003353; IntImIn.  
 CC InterPro: IPR000601; PKD\_domain.  
 CC Pfam: PF02369; Big\_1; 16.  
 CC PRINTS: PRO1369; INTIMIN.  
 CC SMART: SM00634; BID\_1; 16.  
 CC SMART: SM00089; PKD; 8.  
 KW Hypothetical protein; Repeat; Complete proteome.  
 FT DOMAIN 738 834  
 FT DOMAIN 840 929  
 FT DOMAIN 931 1033  
 FT DOMAIN 1042 1132  
 FT DOMAIN 1134 1236  
 FT DOMAIN 1245 1335  
 FT DOMAIN 1337 1439  
 FT DOMAIN 1438 1539  
 FT DOMAIN 1448 1652  
 FT DOMAIN 1454 1750  
 FT DOMAIN 1653 1750  
 FT DOMAIN 1751 1855  
 FT DOMAIN 1856 1957  
 FT DOMAIN 1963 2056  
 FT DOMAIN 2065 2156  
 FT DOMAIN 2157 2252  
 FT DOMAIN 2254 2355  
 SQ SEQUENCE 2660 AA; 280062 MW; 01EB92A08F5C09D2 CRC64;

Query Match 6.5%; Score 169.5; DB 1; Length 2660;  
 Best Local Similarity 23.8%; Pred. No. 0.4;  
 Matches 135; Conservative 56; Mismatches 258; Indels 119; Gaps 26;  
 QY 18 VSEELRNHTRKRSATV-----KTAVALTLFAVAQASANNMETLTSVGTCKLSFSAANGK 73  
 DB 1424 VTATLSNNNTSDSPQVPEVADKTSALVLQISKEITGNVDASATLATVAKDQFDEEVN 1483  
 QY 74 VNITSDP--KGLNFAKETAGTN--GDTTVLNGIG--STVPTDLLNMGATVTVNDNVT 126  
 DB 1484 LPVFTSTASSGLLTLLTEGESNTNNGIAQATLAQVAFGEQTVTASLANNGASDNKKTTHFIC 1543  
 QY 127 DDEKR--AAVKDYLMAG--WNKGVKGTASNDVDEVRTYVEFLSADTKTTVN 181  
 DB 1544 DTAARKIELTPPDSTIIAGTPQSSGVITATVVDNNGPPVGVNFTSNATFAMFN 1603  
 QY 182 ---VESKDNCKTEVKIGATSVYKEKDGKLVTKDKGENGST-----DEEGLY 229  
 DB 1604 GGGAVTNEQKATVYTYNTRSI--ESGAPDVEASLENGSSSTLSTISVNADASTAHL 1661  
 QY 230 TAKEVIDAVNKAQ-----WRMKT TANQGTGQ-----ADKFETVSGTN----- 268  
 DB 1662 TLLQALPDTYSADDTNLTLEVNDNGVPOQDEVLTSVSPSEGVTPSNNAITTHNDGN 1721  
 QY 269 --VFASGKG---TATVSKDDQGNITVYDVNVDALNVQNLQNSGMNLSKAVAGSS 322  
 DB 1722 FVASFTATKAGVYQVATLENGDSMQQTVYVNVANA-----EISLAASK 1767  
 QY 323 GKVISGN-----VSPSKGKMDENVNNAQNNIEITNGKNIDATSMTPQFSSVL 373  
 DB 1768 DPVIANNNDITLTATVADTEG-----NAINSEVFTLPE-DVRAFT-----L 1811  
 QY 374 GAGADAPTLTSDGDA--LNVGSKKDNKPVRTYNAPGVKEGDYTN-VAQLKGVAQNINRI 421  
 DB 1812 GDGGKVT--DTEKAKVTLTKGAKHTVYASAGKSEDLVYVNFADTLTAQVNLNVTPE 1870  
 QY 432 DN-VDCNARAGIAQAIATAG-----LYQATLPKGSMAIGGTYRGEAGYAIQYSS 482  
 DB 1871 DNFIANVGMTRTQATVYTDGNGNPLANEAVFTFLPAD---VASFTLGGGSAI--TDI 1924  
 QY 483 SDGGMNITKTAGSN-----SRGHFGAS 505  
 DB 1925 NGRAEVTLSGTSKSTYPTVSVNNYVS 1952  
 RESULT 15  
 ICEN\_XANCT STANDARD; PRT; 1567 AA.  
 AC P18127;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Ice nucleation protein.  
 OS Xanthomonas campestris (pv. translucens).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_TaxID=343;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=X56S;  
 RX MEDLINE=91080859; PubMed=2259339;  
 RA Zhao J., Orser C.S.;  
 RT "Conserved repetition in the ice nucleation gene *inx* from  
 RT *Xanthomonas campestris* pv. *translucens*.";  
 RL Mol. Gen. Genet. 223:163-166(1990).  
 CC -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE  
 CC CRYSTALLIZATION IN SUPERCOOLED WATER.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane (by similarity).  
 CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS  
 CC OCTAPEPTIDE A-G-Y-G-S-T-L-T. FURTHER ON A 16-RESIDUE AND A  
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

```
CC -!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52970; CAA37140.1; -.
DR HSSP; P06620; 11NA.
DR InterPro; IPR000258; Ice_nucleatn.
DR Pfam; PF00818; ICE_nucleation; 81.
DR PRINTS; PR00327; ICENUCLEATN.
DR PROSITE; PS00314; ICE_NUCLEATION; 57.
KM Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

Query Match 6.58; Score 169; DB 1; Length 1567;
Best Local Similarity 20.3%; Pred. No. 0.23;
Matches 112; Conservative 81; Mismatches 243; Indels 116; Gaps 22;

QY 20 SELTRNHTKRASATVKTAVLA-----TLLEFATVQASANNETDLT---SVG 61
DB 760 SDVTAGSTGTGTAGADSTLTAGYGSTQTSGSDSSLTAGYGSTQ-TARKGSDITAGYGSTG 818
QY 62 TEKL-----SFSANGKNVITSDPKGLNFAKE-----TAGTNGDPTVHLNGI 103
DB 819 TAGADSTLTAGYGSTQTSGSDSSLTAGYGSTGTAREGSDVTAGYGSTGTAGADSTLISGY 878
QY 104 GSTLT--DPLLTGATNTVNDNVTDDEKKRAASVADVNLACGNINIKVKGPTTASDNVD 160
DB 879 GSTGTAGSDSSLTAGYGSTGTARKGSD-----VTAGYGSTG---TAGADST 921
QY 161 FVRTYDVEFLSADTFTTVNVESKDKGKTEVKIGAKTSVIEKDGKLVTKDKGENGS 220
DB 922 LINGYGSTQTSGSDSSLTAGYGSTGTARKGSDMTAGYGSTGTAGADSTLTAG-----YGS 976
QY 221 STDEGEGLVTAKEVIDAVNKAQMRKMTTANQOTGQADKPEVYTSCTNVTFASGKTTAT 280
DB 977 TQTSQS-----DSLTAGYGSTGTAREGSDVTAGYGSTGTAGADSTLTAGYGSTGT 1027
QY 281 VSKDDGNTVTMDVNVGDLNVNQLONSGMNLDSKAVAGSSGKVISGNVSPSKKMDET 340
DB 1028 AGSD--SSLTGY----GSTGTARQGSQDVYAGYGSTGTAGADSTLTLAGYGSTGTAGSDSS 1081
QY 341 VNINAGNNIEITRNGKNIDTATMTPOFSSVSLGAGADAPTLISVDGDLNVGSKKDKPV 400
DB 1082 LITAGYGST-OTARQGSIT-----TAGYGSTGT-AGADSSLTLAGYGSTGTAGYD----- 1127
QY 401 RITNVAPGV-----KEGDTVNVQOLKGYAQNLMNRIDVNGNARAGIAQAIATA-GLV 452
DB 1128 --SNLTAGYGSTGTAREGSDSLTLAGYGSTGTAGHDSLTLAGYGSTGTAGYNSILTGYGST 1185
QY 453 QATLPKGSMAATGGGTYRGEAGY---AIGYSSISDGG--NWITIKTAGSNSRGH----- 501
DB 1186 QTAQESSSLTLAGYGST--STAGYDSTLTLAGYGSTGTAGYKSTLTLAGYGSNSTAGHESLI 1243
QY 502 --FGASASVGYO 511
DB 1244 AGIGSTQIAGYE 1255
```

Search completed: October 6, 2003, 09:23:55  
Job time: 11.9066 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 : Search time 14.6561 Seconds  
(without alignments)  
3359.577 Million cell updates/sec

Title: US-09-771-382-23

Perfect score: 2600

Sequence: 1 MNKIYRIINMSALNMAVYVS.....TASGNSRGHFASASVGYQW 512

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2550.5	98.1	591	2 G81133	adhesin NMB0992 [i
2	2269	88.0	592	2 A81888	adhesin surface f
3	536.5	20.6	298	2 I64138	adhesin homolog HI
4	378	14.5	2059	2 D82671	surface protein XF
5	372.5	14.3	1190	2 A82615	surface protein XF
6	371.5	14.3	1107	2 AC0976	probable adhesin
7	370.5	14.2	1588	2 A66036	probable adhesin
8	370.5	14.2	1588	2 H91188	probable adhesin
9	338	13.0	658	2 AH0110	probable adhesin
10	245	9.4	1091	2 G64964	hypothetical prote
11	234	9.0	1004	2 C82672	surface-exposed ou
12	222	8.5	1286	2 S28634	adhesin AIDA-I pre
13	214.5	8.2	1325	2 A64905	Adhesin - Esc
14	214	8.2	949	2 D90803	Adhesin -lik
15	214	8.2	1005	2 H85611	probable adhesin
16	208	8.0	4919	2 T31105	hypothetical prote
17	207	8.0	1536	2 A43855	high-molecular-we
18	204	7.8	1018	2 H83135	probable adhesin
19	201.5	7.8	1910	2 AF0394	probable adhesin
20	198	7.6	936	2 I40711	sapB protein - Cam
21	197.5	7.6	585	2 F90961	flagellin [impor
22	197.5	7.6	385	2 F85809	hypothetical prote
23	197	7.6	3705	2 AD0123	hypothetical prote
24	196.5	7.6	1343	2 E90893	hypothetical prote
25	196.5	7.6	1477	2 B43855	high-molecular-we
26	195.5	7.5	2020	2 C48399	ABC-type transport
27	194	7.5	2468	2 A83412	hypothetical prote
28	194	7.5	3029	2 S76109	hypothetical prote
29	193.5	7.4	2249	2 A41477	190K surface anti

30	193.5	7.4	5188	2 B85547	probable RTX fam1
31	191.5	7.4	1343	2 D85724	hypothetical prote
32	191.5	7.4	5291	2 F90696	hypothetical prote
33	190.5	7.3	2232	2 T34434	hypothetical prote
34	190	7.3	1109	2 A56143	surface-array prot
35	188	7.2	3013	2 AB0480	probable invasin
36	185	7.1	365	2 AB3486	cell surface prote
37	184	7.1	1428	2 AC2224	hypothetical prote
38	184	7.1	1461	2 E90696	hypothetical prote
39	183	7.0	584	2 C48658	flagellin - Esc
40	183	7.0	1335	2 T17508	glycoprotein VP260
41	183	7.0	1651	2 JC1340	outer membrane pro
42	182	7.0	2551	2 B98047	hypothetical prote
43	181.5	7.0	980	2 H90681	probable flagellin
44	181.5	7.0	980	2 D85332	probable structura
45	181	7.0	364	2 A81019	adhesin/invasin, p

## ALIGNMENTS

## RESULT 1

G81133 adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Accession: G81133

R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masigiani, V.; Pizze, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <RET>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:ANF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match	Score	2550.5	DB 2	Length	591
Best Local Similarity	86.6%				
Matches	512	Conservative	0	Mismatches	0
				Indels	79
				Gaps	1
QY	1	MNKIYRIINMSALNMAVYVSELTNRNHTKRASATVKTAVLTLLFATVQASANNE-----	54		
DB	1	MNKIYRIINMSALNMAVYVSELTNRNHTKRASATVKTAVLTLLFATVQASANNEDEQEDL	60		
QY	55	-----	54		
DB	61	YLDPVORTAVAVLVNSDEKGTGKEKEVENSMAVYFNEKGVLTAREITLKAGDNLIKQ	120		
QY	55	-----	101		
DB	121	NGNFTYSLKKDLTDLTLSVTEKLSPSANKNKNIITSDTGLNFAKTAAGTNGDTYHLN	180		
QY	102	GIGSTLTDLTLNLTGATTVTNDVNTDDEKRRASVYKDVLAAGNNIKGVKGTASDVNF	161		
DB	181	GIGSTLTDLTLNLTGATTVTNDVNTDDEKRRASVYKDVLAAGNNIKGVKGTASDVNF	240		
QY	162	VRTYDVVEELASDPTKTTTVAVESKDKNKTEVTKGATSVYKEDKLVYKDKGKENGSS	221		
DB	241	VRTYDVVEELASDPTKTTTVAVESKDKNKTEVTKGATSVYKEDKLVYKDKGKENGSS	300		
QY	222	TDEGEGLVTAKEVIDAVNKRAGMKTTTAGCGTADKFEFTVSGTWTVPASGKTATV	281		
DB	301	TDEGEGLVTAKEVIDAVNKRAGMKTTTAGCGTADKFEFTVSGTWTVPASGKTATV	360		
QY	282	SKDDGNTVYVDVNVGDLNVLNOLNSGNLDSKAVAGSSGVISGNVSPSKGMDTV	341		

Db 361 SKDDGNTITVWYDVNVGDALNVNOLQNSGMNLSKRAVAGSSGKVISGNVSPSKMKDETV 420

QY 342 NNNAGNNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPPR 401

Db 421 NNNAGNNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPPR 480

QY 402 ITNVA PGVEGDTVVAOQLKGYAQNLRNDRVNDGNARAGIAQAATATAGLVOAYLPKSKM 461

Db 481 ITNVA PGVEGDTVVAOQLKGYAQNLRNDRVNDGNARAGIAQAATATAGLVOAYLPKSKM 540

QY 462 MAIGGCTTREGAGYALIGSSISDGGNWIITKGTASGNSRGHFGASASVGTOW 512

Db 541 MAIGGCTTREGAGYALIGSSISDGGNWIITKGTASGNSRGHFGASASVGTOW 591

RESULT 2

A:1888

probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis (strain 2249

C:Species: Neisseria meningitidis

C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001

C:Accession: A81888

R:Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jørgensen, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.

A:Reference number: A81775; MUID:20222596; PMID:10761919

A:Accession: A81888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-References: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989

A:Experimental source: serogroup A, strain 22491

C:Genetics:

A:Gene: NMA1200

Query Match 88.0%; Score 2289; DB 2; Length 592;

Best Local Similarity 79.1%; Pred. No. 1,6e-111;

Matches 470; Conservative 12; Mismatches 28; Indels 84; Gaps 4;

QY 1 MKKIRIINNSALNMAVYSELTRNHTKRASATVKTAVLATLLEFATVOASANNE----- 54

Db 1 MKKIRIINNSALNMAVYSELTRNHTKRASATVKTAVLATLLEFATVOANADEDEEEL 60

QY 55 ----- 54

Db 61 ESORSVGSIOASMEGSELEFISLMTNDSKEFDPYIVYTLKAGDNLKIKONTNEMT 120

QY 55 -----TDLTSTGTEKLSFSAANGKVNITSDPKGLNFAKETGCTGDTTVHLN 101

Db 121 NASSFTYSLKDLTGTLINETERKLSFGANGKVNIIISDTKGLNFAKETAGTNGDTPVHLN 180

QY 102 GIGSTLTDLTFLNMGATNTVNDNVDDEKRAASVYKDVNAGNKGVRGTTA--SDNV 159

Db 181 GIGSTLTDLTFLNMGATNTVNDNVDDEKRAASVYKDVNAGNKGVRGTTA--SDNV 238

QY 160 DEVRITDYVEPLSADTKTTTVNESKDNKKTVEKIGATSVYKEKDKGLVYKDKGENG 219

Db 239 DEVRITDYVEPLSADTKTTTVNESKDNKKTVEKIGATSVYKEKDKGLVYKDKGENG 298

QY 220 SSTDEEGELVTAKEVDAVNAKAGMRKTTTANGQTQADKFEFVTSIGVNTVTRASGKTGA 279

Db 299 SSTDEEGELVTAKEVDAVNAKAGMRKTTTANGQTQADKFEFVTSIGVNTVTRASGKTGA 358

QY 280 TVSKDDGNTITVWYDVNVGDALNVNOLQNSGMNLSKRAVAGSSGKVISGNVSPSKMKDE 339

Db 359 TVSKDDGNTITVWYDVNVGDALNVNOLQNSGMNLSKRAVAGSSGKVISGNVSPSKMKDE 418

QY 340 TVNINAGNNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNK 398

Db 419 TVNINAGNNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNK 478

QY 399 PVRTITNVA PGVEGDTVVAOQLKGYAQNLRNDRVNDGNARAGIAQAATATAGLVOAYLP 458

Db 479 PVRTITNVA PGVEGDTVVAOQLKGYAQNLRNDRVNDGNARAGIAQAATATAGLVOAYLP 538

QY 459 KSMMAIGGCTTREGAGYALIGSSISDGGNWIITKGTASGNSRGHFGASASVGTOW 512

Db 539 KSMMAIGGCTTREGAGYALIGSSISDGGNWIITKGTASGNSRGHFGASASVGTOW 592

RESULT 3

A:16138

adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997

C:Accession: I64138

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirnness, E.F.; Kervavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: I64138

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <TIGR>

A:Cross-References: GB:U32846; GB:U42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.6%; Score 536.5; DB 2; Length 298;

Best Local Similarity 44.7%; Pred. No. 4,6e-21;

Matches 132; Conservative 28; Mismatches 62; Indels 73; Gaps 8;

QY 1 MKKIRIINNSALNMAVYSELTRNHTKRASATVKTAVLATLLEFATVOA----- 49

Db 1 MKKIRIINNSALNMAVYSELTRNHTKRASATVKTAVLATLLEFATVOA----- 60

QY 50 -----SANNETD-----LT-----SVGPRK 64

Db 61 STEDIEDSAATKDKNKNQALKAGDTLTLKAGKNLAKIKIDGCKSVTEPALAKDLDVTKAK 120

QY 65 LS--FSANGN-----KVNITSPTKGLNFAKETAGTNGDTPVHLNIGSTLNDTLN 113

Db 121 VSDTLIGNTPTAAGATPKVSIITSTADLKLAK---GNGDPTVHLNLAISTLDVPTN 177

QY 114 TGAATNTVNDNTDDEKRAASVYKDVNAGNKGVRGTTA--SDNVDPYRTDYVEFLA 173

Db 178 TGAATNTVNDNTDDEKRAASVYKDVNAGNKGVRGTTA--SDNVDPYRTDYVEFLA 236

QY 174 DTKTTTVNESKDNKKTVEKIGATSVYKEKDKGLVYKDK--KQENGSTPEGE 226

Db 237 DTKTTTVNESKDNKKTVEKIGATSVYKEKDKGLVYKDK--KQENGSTPEGE 291

#### RESULT 4

A:162671

surface protein Xf1529 [Imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: D82671

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82671

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2059 <SIK>

A:Cross-References: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simmons, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Deiry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak  
A.; Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak  
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: Xf1529

Query Match 14.58; Score 378; DB 2; Length 2059;  
Best Local Similarity 25.48; Pred. No. 8.2e-12;

Matches 158; Conservative 77; Mismatches 184; Indels 202; Gaps 27;

QY 47 VQASAN-----NETDLTS-VGTEKLSFSAN---NKVNITSPTKGLNFAKETAGTNGDT 96  
DB 1486 VKVSSNVLLDSNELVITSHSSTSVKTLANGESVNVNRTVNGD-----GVNID 1534  
QY 97 TVHLNGI-----GSTLDFLNTGA--TNNVT-----NDNVTDDEKKRAASYKDYLNAG 143  
DB 1535 VVVVNDIGLSTVGASLITSGINAGSHKITTNTAGTEDDVAVPSQLK---SVSEAVDKG 1591  
QY 144 WNI-----KGVKPGTASDNVD-----FVRTYDVEFLSADTK-----TTVN 181  
DB 1592 WTLTASGANGSKYVSGTVDLKNITDGLAISKSGSDNDVFNLSKPEKVDVETAGTNNVN 1651  
QY 182 VESKDNKTEVYIGAKTSYIKEDGKLYTGKDKGEN-----GSSTDEGEGLVTAKEV 234  
DB 1652 TDDVKG--SDVSLGAMGLEIANGPSVTASGFNAGCKVISHVAVGADTDVAVNSQLKQA 1709  
QY 235 IDVNVKAGMVKTTT-----ANGOTG--ADKFEYVSGTNV-----TTPASG 275  
DB 1710 VQSYTKATRYTSTNOGCTGGNVDGATGSKALIAVGCTQASGEGAAVSGAASGK 1769  
QY 276 GTTA-----TVS-----KDOGN 288  
DB 1770 GSTAIGRNATASADGVALDGAKDGRGAESTYKSGYQNNVTGTVSGDAKGETRS 1829  
QY 289 ITMYNVYVNG--DALNNOL-----QNSGMNDS----- 315  
DB 1830 ISVNAAKEMADVNLRQIDAIVAOKSNLQTDKRHEINNIEDYFKITKGDSSASYKMGV 1889  
QY 316 KAVAGSSGKYISGNVSPSKGMDFTVINAGNNIETIRNGKNIDIATSMTPPSSVSLGA 375  
DB 1890 NMAAIGTNAVSGTESVALCK---NTNVSADNAVAI--GNC-----STADRANSVSGS 1938  
QY 376 GADAPTLVDGALNVGSKKDKNPKVRIITNVAPGVKEGDTNVAQLKGVACNLNRRIDNVD 435  
DB 1939 G-----GSEK-----QVTNVAAGTADTDVAVNSQLNGCLITAKOYTDCMV 1978  
QY 436 GNR-----AGIAQATATAGLVQAYLPKSKMAITGGTYRGEAGYAIGTSSISDGMNITK 491  
DB 1979 GNRRETSGGVAALITANLPQAYVYRGMTSVGSSYOGOSAIANGVSAVSGHWFVK 2038  
QY 492 GTASGNRCHFGFASASVGYOW 512  
DB 2039 FSGSANTRSHVGVAGVGYOW 2059

## RESULT 5

A82615  
surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 11190 <SIM>

A:Cross-references: GB:AE004017; GB:AE003849; MID:99107083; PIDN:AAF84783.1; GSPDB:GN  
A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincaul, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
chado, M.A.; Madeira, A.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava  
A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:  
A:Gene: Xf1981

Query Match 14.38; Score 372.5; DB 2; Length 1190;

Best Local Similarity 24.88; Pred. No. 8.1e-12;

Matches 143; Conservative 77; Mismatches 209; Indels 147; Gaps 21;

QY 17 VVSELRNTRKASATVKAVALATLFAVQASANNEDTLTSGTEKLSFSAN----- 70  
DB 682 VTSSGISAGNQKTTNAAAGTADPDVAVNSQLQAVNST--AARGMNLASGNSSVAP 737  
QY 71 GNRVNITSDDKGLNFAKETAG-----TNGDTTVHLNGISTLTDLLNT 114  
DB 738 GESVDLKNITDGNIVISKESSNDVFNFLSSSLKLDKLTVEGDTYWTNGV-----TVGS 790  
QY 115 GATTNTNDVTDDEKKRAASVVDVNLG--WNIGKVPQTASD----- 157  
DB 791 GVTLSGMLVITDGPSTVSGI-----NAGSQKITTNAAGTADPDVAVNLSQLNTAMAGSGA 846  
QY 158 -NVDFVETVTEFLSADTGTTVTVNVESSKNGKTEVIGAKTSYIKEDGKLYTGKDKG 216  
DB 847 KSVHYISTYD-----GTOGNGNKGDAITGTSIAGVGTTLASA---EGATAVSGAA 896  
QY 217 ENG--STDEGEGLVTAKEVIDAVNKAQRKKTJTTANGQDQADKFEFTVSTNTVFAASK 275  
DB 897 ASGGSFALIRNVAASDGSVALGD--GAKGANGAESEYTGKYSGLQNNVTGTVSGDASK 955  
QY 276 GTTATVSKDQGNITVYDVNVGDALNVOL-----QNSGMNLSKAVAGSSGKYISGNVS 331  
DB 956 GETRTVS---NVADAKEAT--DAVNLRLDRAVADANRYVNNKTESLSEQTF----- 1003  
QY 332 PSKGMDEFYNINAGNNIETIRNGKNIDIATSMTPPSSVSLGAGADAPTLV-----DG 386  
DB 1004 -----KVNSLNN-----SATP-----IAGVDATVIGCATRSGA 1034  
QY 387 DALNVGSK---KDNKEV-----RTNVAPGVKEGDTNVAQL 420  
DB 1035 DSIAMGNKASASADNNAVALNHSVADRANTVSGASGEQGVNVNVAAGTADTDVAVNSQL 1094  
QY 421 KQVAQNLNRRIDNVGNAR---AGIAQATATAGLVQAYLPKSKMAITGGTYRGEAGYA 476  
DB 1095 NOGLITAKOYTDDGVGSLRRDTPDGVAALATFANLPQAYIPGRKMTSVGSSYRGOSAI 1154  
QY 477 IGYSTSDDGNMIIKGTASGNSRCHFGFASASVGYOW 512  
DB 1155 VGVSVSSESGRWVFKFSGSANTRSQVIGAGVGYOW 1190

## RESULT 6

AC0976  
probable autotransporter sabp [imported] - Salmonella enterica subsp. enterica serova  
C:Species: Salmonella enterica subsp. enterica serovar Typh  
A:Note: this species has also been called Salmonella typh  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002













Db	495	GHRESTLTLAAGSLSGRTQLSKGASMYLNGDVSTGDIYNAGEI-----RPDN-QT	544
QY	437	NARAGIAQATATAG-----LYOAYLPK-----SMAIGGTYRGEA	473
Db	545	TPNALSRVAVKSNSPVTFHKLTTTNLTGGGTINMRVRLDGSNASDQLVYINGGOATGKT	604
QY	474	GVA---IGYSSI	482
Db	605	WLFTNVGNSNL	616

Search completed: October 6, 2003, 09:33:13  
 Job time : 19.6561 secs

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PT meningitidis infections  
 XX  
 PS Claim 1: Page 118-120; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of *Neisseria*  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 XX Sequence 592 AA:  
 SQ  
 Query Match 100.0%; Score 2735; DB 20; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-150;  
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TDEDEEEELSVORSVSGSIQASMEGSELEETISLMTNDSKEFVDPYIVTLKAGDMLK 60  
 DB 52 TDEDEEEELSVORSVSGSIQASMEGSELEETISLMTNDSKEFVDPYIVTLKAGDMLK 111  
 QY 61 IKONTNENTNASSFTYSLKADLTGLINTEKLSFGANGKKVNIISDTKGLNFAKETAGT 120  
 DB 112 IKONTNENTNASSFTYSLKADLTGLINTEKLSFGANGKKVNIISDTKGLNFAKETAGT 171  
 QY 121 NGDFTVHNGTGSTLTDLMLNTGATNTYNDVTDDEKKRAASVDVNLNAGNIGVAPG 180  
 DB 172 NGDFTVHNGTGSTLTDLMLNTGATNTYNDVTDDEKKRAASVDVNLNAGNIGVAPG 231  
 QY 181 TTASDNVDFVRTYDVEELASADTKTTYNVESKDKGKTEVKIGAKTSYIKEDKGLVTG 240  
 DB 222 TTASDNVDFVRTYDVEELASADTKTTYNVESKDKGKTEVKIGAKTSYIKEDKGLVTG 291  
 QY 241 KKGKNGSSTDEBGLVTAKEVIDAVNKAGRMKTTTANGOTGADKEFTVTSGRKVTFA 300  
 DB 292 KKGKNGSSTDEBGLVTAKEVIDAVNKAGRMKTTTANGOTGADKEFTVTSGRKVTFA 351  
 QY 301 SGNGTATVSKDQGNITVKKYDVNVGDALNVNQLNSGMNLDKRAVAGSSGKVIISGNTSP 360  
 DB 352 SGNGTATVSKDQGNITVKKYDVNVGDALNVNQLNSGMNLDKRAVAGSSGKVIISGNTSP 411  
 QY 361 SKGKDETVNINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPTLVSVDDEGALNV 420  
 DB 412 SKGKDETVNINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPTLVSVDDEGALNV 471  
 QY 421 GSKDANKRVRTTNVAPGVKEGDTVVAQLKGYAQLNNRINDVNGNARAGIAQAIATAGL 480  
 DB 472 GSKDANKRVRTTNVAPGVKEGDTVVAQLKGYAQLNNRINDVNGNARAGIAQAIATAGL 531  
 QY 481 VQAYIPGKSMMAIGGGTYLGEAGVAGYSSISAGSNWIIKGTASNSRGHFGASASVGYO 540  
 DB 532 VQAYIPGKSMMAIGGGTYLGEAGVAGYSSISAGSNWIIKGTASNSRGHFGASASVGYO 591  
 QY 541 W 541  
 DB 592 W 592

OS *Neisseria meningitidis* strain H41.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..51  
 FT Peptide /label= Signal\_peptide  
 FT 1..50  
 FT Region /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..102  
 FT Region /label= V1  
 FT /note= "Variable region 1"  
 FT 52..592  
 FT Protein /label= Mature\_Nhha  
 FT /note= "Predicted mature protein, specifically  
 FT claimed in claim 12"  
 FT 103..114  
 FT Region /label= C2  
 FT /note= "Conserved region 2"  
 FT 115..124  
 FT Region /label= V2  
 FT /note= "Variable region 2"  
 FT 125..188  
 FT Region /label= C3  
 FT /note= "Conserved region 3"  
 FT 189..210  
 FT Region /label= V3  
 FT /note= "Variable region 3"  
 FT 211..229  
 FT Region /label= C4  
 FT /note= "Conserved region 4"  
 FT 230..236  
 FT Region /label= V4  
 FT /note= "Variable region 4"  
 FT 237..592  
 FT Region /label= C5  
 FT /note= "Conserved region 5"  
 FT  
 FT W020015182-A1.  
 FT  
 FT 02-AUG-2001.  
 FT  
 FT 25-JAN-2001; 2001WO-AU000069.  
 FT  
 FT 25-JAN-2000; 2000US-0177917.  
 FT  
 FT (UYOU ) UNIV QUEENSLAND.  
 FT  
 FT Peak IRA, Jennings MP;  
 FT  
 FT WPI; 2001-488774/53.  
 FT  
 FT N-PSDB; AAS09162.  
 FT  
 FT New Nhha surface antigen polypeptides and polynucleotides from  
 FT *Neisseria meningitidis*, useful in producing vaccines for treating or  
 FT preventing broad spectrum of *Neisseria meningitidis* -  
 FT  
 FT Claim 9; Fig 1; 91pp; English.  
 PS  
 XX  
 CC The present invention relates to the isolation of novel *Neisseria*  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain H41 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 CC  
 XX

[illegible]

```

FT      /note= "Variable region 2"  

FT      125...188  

FT      Region  

FT      /label= C3  

FT      /note= "Conserved region 3"  

FT      189...208  

FT      Region  

FT      /label= V3  

FT      /note= "Variable region 3"  

FT      209...227  

FT      Region  

FT      /label= C4  

FT      /note= "Conserved region 4"  

FT      228...236  

FT      Region  

FT      /label= V4  

FT      /note= "Variable region 4"  

FT      237...592  

FT      Region  

FT      /label= C5  

FT      /note= "Conserved region 5"  

FT      .  

FN      WO200155182-A1.  

PD      02-AUG-2001.  

PF      25-JAN-2001; 2001WO-AU00069.  

PR      25-JAN-2000; 2000US-O177917.  

PA      (UYQU ) UNIV QUEENSLAND.  

PI      Peak IRA, Jennings MP;  

PX      WPI: 2001-486774/53.  

DR      N-PSDB; AAS09170.  

XX      New Nhha surface antigen polypeptides and polynucleotides from  

XX      Neisseria meningitidis, useful in producing vaccines for treating or  

XX      preventing broad spectrum of Neisseria meningitidis -  

XX      Claim 9; Fig 1; 91pp; English.  

XX      The present invention relates to the isolation of novel Neisseria  

XX      meningitidis mutant polypeptides of the surface antigen Nhha  

XX      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  

XX      characterised by deletions of non-conserved amino acids, particularly  

XX      the deletion of variable regions. The deletion mutants are useful in  

XX      diagnostics, therapeutic and prophylactic vaccines against a broader  

XX      spectrum of N. meningitidis, and in designing and/or screening of  

XX      medicaments. The mutant proteins when used as a vaccine can effectively  

XX      immunise against a broader spectrum of N. meningitidis strains than  

XX      would be expected from a corresponding wild-type surface antigen.  

XX      The present sequence representing the wild type surface antigen Nhha  

XX      from N. meningitidis strain 23491 is 1 of 10 Nhha polypeptide sequences  

XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  

XX      the present invention.  

SQ      Sequence    592 AA:  

Query Match          92.4%; Score 2527; DB 22; Length 592;  

Best Local Similarity 93.4%; Pred. No. 1.3e-138;  

Matches 507; Conservative 9; Mismatches 23; Indels 4; Gaps 2  

QY      1 TDEDEEELESYORSVGSIOASMGSVELETSISMINDSEKFPDPTIYTTLAKGDNLK 60  

Db       ||||||| | : : : |||||  

        52 TDEDEEEELSESORSVGSIQSMGSGELETSISMINDSKFDPDYITVTLLKAGDNLK 111  

        ||||||| | : : : |||||  

QY      IKONTNNTWNASFFYSILKKDITGLINETEKLSGANGKKVNIIISDRKLNFAKETAGT 120  

Db       ||||||| | : : : |||||  

        112 IKONTNNTNASSFFYSILKKDITGLINETERKLSGANGKKVNIIISDRKLNFAKETAGT 171  

        ||||||| | : : : |||||  

QY      NGDTTVHLNGIGSTLIDMLMTLGATTVNTNDNVTDERRKAASVDVYNAGNNIGVPGC 180  

Db       ||||||| | : : : |||||  

        172 NGDTTVHNLNGIGSTLTDFDLGSSASHVDAGNST--HYTRRAISKDVNLAGNNIGKVTC 229  

        ||||||| | : : : |||||  

QY      181 TTA--SDNVDFRITYDIVELSADTKTTTVNVESKDNGKRTVEKTIQAGTSVIKEKGDKLV 238  

        : : : ||||||| | : : : |||||

```

```

Db      230 STTGQSENVDFVRYTDVFEFLSADTKTTTVNVESKDNKRTKTEYKIGAKTSVYKEKDGKLV 289
QY      239 TGRKGGENGSTDEGEGLVTAKEVIDAVNKAQGRMKTTTANGOTGQADKFETVTSQTKYT 298
        |||||
Db      290 TGRKGGENGSTDEGEGLVTAKEVIDAVNKAQGRMKTTTANGOTGQADKFETVTSQTKYT 349
QY      299 FASGNGTTATVSKDDOGNITTVKYDVNVGDALNVNOLQNSGWNLDKRAVAGSSGKVI SGNV 358
        |||||
Db      350 FASGKTATVSKDDOGNITTVKYDVNVGDALNVNOLQNSGWNLDKRAVAGSSGKVI SGNV 409
QY      359 SPSKGMDETVINMAGNNIEITRNGKNIDIAISMTPQFSSVSLGACADAPTLSDVEDEGL 418
        |||||
Db      410 SPSKGMDETVINMAGNNIEITRNGKNIDIAISMTPQFSSVSLGACADAPTLSDVEDEGL 469
QY      419 NVGSKDANKPVRITTVNAPGVKEGDVTVNVAOLKGVANLNNRIDNVGNARAGIAQAIAATA 478
        |||||
Db      470 NVGSKDANKPVRITTVNAPGVKEGDVTVNVAOLKGVANLNNRIDNVGNARAGIAQAIAATA 529
QY      479 GLVQAVLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIKGTASGNSRGHFGASASV 538
        |||||
Db      530 GLVQAVLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIKGTASGNSRGHFGASASV 589
QY      539 YQM 541
        |||
Db      590 YQM 592

RESULT 4
AA27203
ID      AA27203 standard; protein; 592 AA.
XX
AC      AA27203;
XX
DT      24-SEP-1999 (first entry)
XX
DE      Amino acid sequence of N. meningitidis protein ORF40a.
XX
KM      Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW      bacterial infection; treatment.
XX
OS      Neisseria meningitidis.
XX
PN      WO936544-A2.
XX
PD      22-JUL-1999.
XX
PF      14-JAN-1999; 99WO-IB00103.
XX
PR      09-OCT-1998; 98GB-0022143.
PR      14-JAN-1998; 98GB-0000760.
PR      01-SEP-1998; 98GB-0019015.
XX
PA      (CHIR-) CHIRON SPA.
XX
PI      Grandi G, Masignani V, Pizze M, Rappuoli R, Scarlato V;
DR      WPI; 1999-444400/37.
DR      N-PSDB; AA299125.
XX
PT      New protein and its nucleotide sequence, useful in vaccines or
PT      diagnostic compositions for treating and/or preventing Neisseria
PT      meningitidis infections
XX
PS      Claim 1; Page 63; 123pp; English.
XX
XX      The invention provides proteins (AA27201-245) from Neisseria
CC      meningitidis (strains A and B) and nucleic acid sequences (AA299123-167)
CC      encoding the proteins. Compositions comprising the protein, nucleic acid
CC      or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC      vaccine composition or a diagnostic composition. The composition is also
CC      useful for treating or preventing an infection due to Neisseria
CC      bacteria, especially Neisseria meningitidis.
XX

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SQ      Sequence      592 AA:
Query Match      91.6%; Score 2504; DB 20; Length 592;
Best Local Similarity 92.4%; Pred. No. 2,9e-137;
Matches 502; Conservative 10; Mismatches 27; Indels 4; Gaps 2;

QY      1 TDEDEEEELSVQRSVYGSIQASMEGSVELETISLSTMTNDSKEFDPPIVTVTLKAGDNK 60
        |||||
Db      52 TDEDEEEELSVQRSVYGSIQASMEGSVELETISLSTMTNDSKEFDPPIVTVTLKAGDNK 111
QY      61 IKONTNENTNASSFTYSLKKDLJGLINVEETKLSGANKKYNII SDTGLNPAKETAGT 120
        |||||
Db      112 IKONTNENTNASSFTYSLKKDLJGLINVEETKLSGANKKYNII SDTGLNPAKETAGT 171
QY      121 NGDTTVHLNGISSTLLDMLNTGATTVTVNDVVTDEDEKRAASVXVDVLNAGNNIKGVKPG 180
        |||||
Db      172 NGDTTVHLNGISSTLLDMLNTGATTVTVNDVVTDEDEKRAASVXVDVLNAGNNIKGVKPG 229
QY      181 TTA--SDNVDVRYRTDVFELSLADTKTTTVNVESKDNKRTKTEYKIGAKTSVYKEKDGKLV 238
        |||||
Db      230 STTGQSENVDFVRYTDVFEFLSADTKTTTVNVESKDNKRTKTEYKIGAKTSVYKEKDGKLV 289
QY      239 TGRKGGENGSTDEGEGLVTAKEVIDAVNKAQGRMKTTTANGOTGQADKFETVTSQTKYT 298
        |||||
Db      290 TGRKGGENGSTDEGEGLVTAKEVIDAVNKAQGRMKTTTANGOTGQADKFETVTSQTKYT 349
QY      299 FASGNGTTATVSKDDOGNITTVKYDVNVGDALNVNOLQNSGWNLDKRAVAGSSGKVI SGNV 358
        |||||
Db      350 FASGKTATVSKDDOGNITTVKYDVNVGDALNVNOLQNSGWNLDKRAVAGSSGKVI SGNV 409
QY      359 SPSKGMDETVINMAGNNIEITRNGKNIDIAISMTPQFSSVSLGACADAPTLSDVEDEGL 418
        |||||
Db      410 SPSKGMDETVINMAGNNIEITRNGKNIDIAISMTPQFSSVSLGACADAPTLSDVEDEGL 469
QY      419 NVGSKDANKPVRITTVNAPGVKEGDVTVNVAOLKGVANLNNRIDNVGNARAGIAQAIAATA 478
        |||||
Db      470 NVGSKDANKPVRITTVNAPGVKEGDVTVNVAOLKGVANLNNRIDNVGNARAGIAQAIAATA 529
QY      479 GLVQAVLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIKGTASGNSRGHFGASASV 538
        |||||
Db      530 GLVQAVLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIKGTASGNSRGHFGASASV 589
QY      539 YQM 541
        |||
Db      590 YQM 592

RESULT 5
AA23743
ID      AA23743 standard; protein; 599 AA.
XX
AC      AA23743;
XX
DT      08-SEP-1999 (first entry)
XX
DE      A surface protein of Neisseria meningitidis.
XX
KM      Surface protein; surface glycoprotein; infection; vaccine;
KW      immunoreactive peptide.
XX
OS      Neisseria meningitidis.
XX
PN      WO9311132-A1.
PD      24-JUN-1999.
XX
PF      14-DEC-1998; 98WO-AU01031.
PR      12-DEC-1997; 97GB-0026398.
XX
PA      (ISTS-) ISTS INNOVATION LTD.
PA      (UYOU ) UNIV QUEENSLAND.
XX

```

PI Jennings MP, Moxon ER, Peak IRA;  
 XX WPI: 1999-418754/35.  
 DR N-PSDB: AAX85795.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 114-115; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 SQ Sequence 599 AA;  
 Query Match 89.5%; Score 2447.5; DB 20; Length 599;  
 Best Local Similarity 90.3%; Pred. No. 5.5e-134;  
 Matches 496; Conservative 11; Mismatches 33; Indels 9; Gaps 4;  
 QY 1 TDEDEPELEPVORS-VGSIQASMEGSELEET---TSLMTNDSKFEVDPIYVTKAG 56  
 DB 52 TDEDEPELEPVRSALVLOFMIDKNGENESIGNISYDNNHTLHG-ATVTLKAG 110  
 QY 57 DNLKIQ---NTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKNVNIISDTKGLN 112  
 DB 111 DNLKIQNTNKNNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKKNVNIISDTKGLN 170  
 QY 113 FAKETAGTNDTTHVHLNGISITLDMNLNTGATTNVTNDVTDDEKRAASVDVYNAGW 172  
 DB 171 FAKETAGTNDTTHVHLNGISITLDMNLNTGATTNVTNDVTDDEKRAASVDVYNAGW 230  
 QY 173 NIKGVKRGTTASNVNDEVRTDYVEFLSADTKTTTVESKDNKKEVIGAKTSVIKE 232  
 DB 231 NIKGVKRGTTASNDVDFVHTYDVEFLSADTKTTTVESKDNKKEVIGAKTSVIKE 290  
 QY 233 KDKRLVTKGKGENSGSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEPTV 292  
 DB 291 KDKRLVTKGKGENSGSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEPTV 350  
 QY 293 SGTKVTFASGNGTTATVSKDDGNITVYKVVNVDALNVQLONGSNLDSKAVAGSSGK 352  
 DB 351 SGTKVTFASGNGTTATVSKDDGNITVYKVVNVDALNVQLONGSNLDSKAVAGSSGK 410  
 QY 353 VIGSNVSPSKGKDEETNINAGNNIETTRGKNIDATSMTPQSSVSLGADAPPLSV 412  
 DB 411 VIGSNVSPSKGKDEETNINAGNNIETTRGKNIDATSMTPQSSVSLGADAPPLSV 470  
 QY 413 DDEGALNVGSKDANKPVRTITNVAAGVEGDTNVAQKGAQNLNRIIDVNGNARAGIA 472  
 DB 471 DDEGALNVGSKDANKPVRTITNVAAGVEGDTNVAQKGAQNLNRIIDVNGNARAGIA 530  
 QY 473 QATATAGLVQATYLPKGSMAIGGTYLGEAGVAGYSSISAGGNIITKTAGSGNSRHF 532  
 DB 531 QATATAGLVQATYLPKGSMAIGGTYLGEAGVAGYSSISAGGNIITKTAGSGNSRHF 590  
 QY 533 ASASVGYQW 541  
 DB 591 ASASVGYQW 599

DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis H38 surface antigen Nhma polypeptide sequence.  
 XX  
 KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain H38.  
 XX  
 FH Key  
 FT Region  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT /label= V2  
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 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 XX  
 PN W020015182-A1.  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI: 2001-488774/53.  
 DR N-PSDB: AAS09166.  
 XX  
 PT New Nhma surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 9; Fig 1; 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhma  
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhma  
 CC from N. meningitidis strain H38 is 1 of 10 Nhma polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX

Seq	Sequence	599 AA:	89.5%:	Score 2447.5:	DB 22:	Length 599:					
Query Match	Best Local Similarity	90.3%:	Pred. No. 5.3e-134:								
Matches 496:	Conservative 11:	Mismatches 33:	Indels 9:	Gaps 4:							
QY	1	TDEDEEEELSEVOSS-VYGSIOASMEGSVELET---ISLSMTNDSEKEFDPYIVYTLKAG	56								
DB	52	TDEDEEEELSEVPVRNALVLOFMIDKEGGENESSTNICMSIYYDHNLHG-AIYTLKAG	110								
QY	57	DNLIKQ---NTNENTNASSFTYSLKADLTGLINVEFEKLSFGANGKVNITSDTKGIN	112								
DB	111	DNLIKQTKNTNNTNENTNDSSFTYSLKADLTGLISVEFEKLSFGANGKVNITSDTKGIN	170								
QY	113	FAKETAGNNGPTVYHLNGIGSTLMDMLNTGATVTNDNTVNDNDDEKKAASVYKDYLNAGM	172								
DB	171	FAKETAGNNGPTVYHLNGIGSTLMDMLNTGATVTNDNTVNDNDDEKKAASVYKDYLNAGM	230								
QY	173	NIKGVKPGTPTASDNVDVFRITYDYVEFLSADTKTTTVNVESSKDKNGKTEVYKIGAKTSVIKE	232								
DB	231	NIKGVKPGTPTASDNVDVFRITYDYVEFLSADTKTTTVNVESSKDKNGKTEVYKIGAKTSVIKE	290								
QY	233	KDGLIYNGCKGGENSSSTDEEGELVTAKEVIDAVKAKGRMKTITTAANGOTGADKFEIYT	292								
DB	291	KDGLIYNGCKGGENSSSTDEEGELVTAKEVIDAVKAKGRMKTITTAANGOTGADKFEIYT	350								
QY	293	SGTKVTFASNGGTTATVSKDOGNITTVYDVVNGDALVNOLONSGWNLDKRAVAGSSGK	352								
DB	351	SGTNTVTFASNGGTTATVSKDOGNITTVYDVVNGDALVNOLONSGWNLDKRAVAGSSGK	410								
QY	353	VISGNVSPSSKGMDETIVINAGNNITETRNKNDIDATSMTPQESSVSLGAGADAPTLISV	412								
DB	411	VISGNVSPSSKGMDETIVINAGNNITETRNKNDIDATSMTPQESSVSLGAGADAPTLISV	470								
QY	413	DDEGALNAGSKDANKPVRITTVNAPGVKRGDVTYNAQLKGAVQNLNRRIDVNGNARAGIA	472								
DB	471	DDKALNAGSKDANKPVRITTVNAPGVKRGDVTYNAQLKGAVQNLNRRIDVNGNARAGIA	530								
QY	473	QAIATAGLVQAYLPEKSMMAIGGGTYLCEBAGYAIGYSISAGANNIITKGTASGNSRGHG	532								
DB	531	QAIATAGLVQAYLPEKSMMAIGGGTYLCEBAGYAIGYSISAGANNIITKGTASGNSRGHG	590								
QY	533	ASASVGYQW 541									
DB	591	ASASVGYQW 599									
RESULT 7											
ID	AAAY23738										
AC	AAAY23738	standard; Protein; 598 AA.									
DT	08-SEP-1999	(first entry)									
DE	A surface protein of Neisseria meningitidis.										
KM	Surface protein; surface glycoprotein; infection; vaccine;										
OS	Neisseria meningitidis.										
PN	W09931132-A1.										
PD	24-JUN-1999.										
PE	14-DEC-1998;	98WO-AU01031.									
PR	12-DEC-1997;	97GB-0026398.									
RA	(ISIS-) ISIS INNOVATION LTD.										
RA	(UTOU ) DNIT QUEENSLAND.										

Query Match	Best Local Similarity	88.7%	Score 2426.5	DB 20	Length 598	
Matches	Conservative	12	Mismatches	28	Indels 21	Gaps 5
3	EDEEELESVOR-SVYGSIOAESGSEVELETETSLMTNKSKEFVDYI-----VVT	52				
53	DDDLVLEPYQRTAVLVSPRSDEKTEGEK-----TEDSMNAV--YFDEKRVLRKAGALT	105				
53	LKAGDNLKIKONTNENTNA---SSFTYSLLKADLGLINVEFEKLSFGANGKKVNIISPT	108				
106	LKAGNLKIKONTNENTNENTNDSPFYSLLKDLDTLSVEFEKLSFGANGKNNVTSDT	165				
109	KGINPAKETAGNGDTVTYHLNGISLTFTDMLNTGATVNTNDVTDDEKKRAASYKDV	168				
166	KGINPAKETAGNGDPTVYHLNGISLTFTDMLNTGATVNTNDVTDDEKKRAASYKDV	225				
169	NAGNNIKGVKPGCTASDNVDVRYTDVFEFLSADTKTTTVNVEBSKDNKGKTEYKIGAKTS	228				
226	NAGNNIKGVKPGCTASDNVDVRYTDVFEFLSADTKTTTVNVEBSKDNKGKTEYKIGAKTS	285				
229	VTKKEDGLVNGKKGGENSSSTDEGGLVTAKEVIDAVNKAQGRMKTTTANGOTGQADKF	288				
286	VTKKEDGLVNGKKGGENSSSTDEGGLVTAKEVIDAVNKAQGRMKTTTANGOTGQADKF	345				
289	ETVTSIGRTVFAASGNGTTATVSKDDOGNTTVKYDVNVGDALNVNQLNSGWNLDKSAVAG	348				
346	ETVTSIGRTVFAASGNGTTATVSKDDOGNTTVKYDVNVGDALNVNQLNSGWNLDKSAVAG	405				
349	SSGKVIISGNVSSSKGMDETVININAGNNIETIRNGKNIDIAISMTPTQFSSVSLGAADAP	408				
406	SSGKVIISGNVSSSKGMDETVININAGNNIETIRNGKNIDIAISMTPTQFSSVSLGAADAP	465				
409	TLVSUDEGALNVSQDANKPVRITVNPAPVCEKGDVTVNQLKGVAONLNRRIDNVNGNAR	468				
466	TLVSUDEGALNVSQDANKPVRITVNPAPVCEKGDVTVNQLKGVAONLNRRIDNVNGNAR	525				
469	AGIAQALITAGLVQAVLPCKSMMAIGCGTGYLDEBAGYAIGSSISAGCNMIKGTASGNSR	528				
526	AGIAQALITAGLVQAVLPCKSMMAIGCGTGYLDEBAGYAIGSSISIDGNNVIKGTASGNSR	585				
529	GHEGASASVGYOW 541					
586	GHEGTSASVGYOW 598					



DT 08-SEP-1999 (first entry)  
 XX A surface protein of Neisseria meningitidis.  
 DE  
 XX  
 KW Surface protein; surface glycoprotein; infection; vaccine;  
 KW Immunoreactive peptide.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN MO9931132-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-AU01031.  
 XX  
 PR 12-DEC-1997; 97GB-0026398.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA;  
 XX  
 DR WPI: 1999-418754/35.  
 DR N-PSDB: AAX85794.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 108-110; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 XX  
 XX Sequence 598 AA;  
 Query Match 88.7%; Score 2426.5; DB 20; Length 598;  
 Best Local Similarity 89.2%; Pred. No. 9.1e-133;  
 Matches 493; Conservative 11; Mismatches 28; Indels 21; Gaps 5;

QY 409 TLSDDEGALNVGSKDANKPVRIITNVA PGVEGDTNVAOLKGYAONLNNRIDNVNGNAR 468  
 |||||||  
 DB 466 TLSVDDEGALNVGSKDANKPVRIITNVA PGVEGDTNVAOLKGYAONLNNRIDNVNGNAR 525  
 QY 469 AGIAQAIAATAGLVAOYLPGKSMMAIGGTYLGEGYAI GYSSISAGNMWIIKGTASGNSR 528  
 |||||||  
 DB 526 AGIAQAIAATAGLVAOYLPGKSMMAIGGTYLGEGYAI GYSSISAGNMWIIKGTASGNSR 585  
 QY 529 GHFGASASVGYOW 541  
 |||||||  
 DB 586 GHFGASASVGYOW 598  
 RESULT 9  
 AAU06177  
 ID AAU06177 standard; Protein: 598 AA.  
 XX  
 AC AAU06177;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DT  
 XX N. meningitidis H15 surface antigen Nhha polypeptide sequence.  
 DE  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 KW  
 XX Neisseria meningitidis strain H15.  
 OS  
 XX  
 FH Key  
 FT Region  
 FT Location/Qualifiers  
 FT 1..50  
 FT /label=C1  
 FT /note="Conserved region 1"  
 FT 51..104  
 FT /label=V1  
 FT /note="Variable region 1"  
 FT 105..116  
 FT /label=C2  
 FT /note="Conserved region 2"  
 FT 117..130  
 FT /label=V2  
 FT /note="Variable region 2"  
 FT 131..194  
 FT /label=C3  
 FT /note="Conserved region 3"  
 FT 195..216  
 FT /label=V3  
 FT /note="Variable region 3"  
 FT 217..235  
 FT /label=C4  
 FT /note="Conserved region 4"  
 FT 236..242  
 FT /label=V4  
 FT /note="Variable region 4"  
 FT 243..598  
 FT /label=C5  
 FT /note="Conserved region 5"  
 PN WO20015182-A1.  
 XX  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI: 2001-488774/53.  
 DR N-PSDB: AAS09167.  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from



Query Match	88.7%	Score 2426.5	DB 22	Length 598
Best Local Similarity	89.0%	Pred. No. 9.1e-133		
Matches 492	Conservative 12	Mismatches 28	Indels 21	Gaps 5
QY	3	EDEEEELLSVQR-SVYSGISIQAMSESVLEETISLSMTDSKEFVPPYI-----VYT	52	
DB	53	DDDDLYLEPVPQRTAVVLSPRSDKEGTGEKGEK-----TEDSNMAV--YFDEKRVLKAGAIT	105	
QY	53	LKAGNLEIKONTNENTNA-----SSFTYSLKKDLTLGLINVEPEKISFGANKKKVNIISDT	108	
DB	106	LKAGNLEIKONTNENTNENTNDSEFTYSLKKDLTLGLISVETKLSFGANKKKVNIISDT	165	
QY	109	KLNFPAKETAGTNGDTTVHLNGISGTLTDLMLNTGATNVATINDNTDDEKKRAASVQVYL	168	
DB	166	KLGNPAKTAETAGTNGDPTVHLNGISGTLTDLTLNTGATNVATINDNTDDEKKRAASVQVYL	225	
QY	169	NAGNNIKGVKPGTTASDNVDFVRYDYVEFLSADTKTTTVNVESSKDNKKTEVKIGARTS	228	
DB	226	NAGNNIKGVKPGTTASDNVDFVRYDYVEFLSADTKTTTVNVESSKDNKKTEVKIGARTS	285	
QY	229	VIRKEDKGLVYKGGKGGENGSSSTDEEGVLTAKVEDAVANNAKGRMKRTTANGQOTQADKF	288	
DB	286	VIRKEDKGLVYKGGKGGENGSSSTDEEGVLTAKVEDAVANNAKGRMKRTTANGQOTQADKF	345	
QY	289	ETVTSIGTVPFASGNGTATATVSKDOGNITVYKDYVNVGDALNVNOLQNSGNNLDSKAVAG	348	
DB	346	ETVTSIGTVPFASGNGTATATVSKDOGNITVYKDYVNVGDALNVNOLQNSGNNLDSKAVAG	405	
QY	349	SSGKIVSGNVSPSKGKMDETVINAGNNEIETTRNKNIDIAISMTPOESSVSLGAGADAP	408	
DB	406	SSGKIVSGNVSPSKGKMDETVINAGNNEIETTRNKNIDIAISMTPOESSVSLGAGADAP	465	
QY	409	TLSDVDEBALVWGSNDANKPVRITNVAPGVKEGDTVNAQLKGVAQNLNRRIDVYNGAR	468	
DB	466	TLSDVDEBALVWGSNDANKPVRITNVAPGVKEGDTVNAQLKGVAQNLNRRIDVYNGAR	525	
QY	469	AGIQALITAGLVQAYLPGKSMMAIGGTYLGEAGYAGYSSISAGNMIIKGTASGNSR	528	
DB	526	AGIQALITAGLVQAYLPGKSMMAIGGTYLGEAGYAGYSSISDTGMVILKGTASGNSR	585	
QY	529	GHFGASASVGYQW 541		
DB	586	GHFGTSASVGYQW 598		
RESULT 11				
AAAY23739				
ID	AAAY23739	standard; Protein: 594 AA.		
AC	AAAY23739;			
XX	08-SEP-1999	(first entry)		
XX	A	surface protein of Neisseria meningitidis.		
DE	Surface protein: surface glycoprotein; infection; vaccine;			
KM	immunoreactive peptide.			
XX	Neisseria meningitidis.			
OS	MO9931132-A1.			
PN	24-JUN-1999.			
XX	14-DEC-1998;	98WO-AU01031.		
PF	12-DEC-1997;	97GB-0026398.		
PR	(ISIS-) ISIS INNOVATION LTD.			
XX	(UYOU ) UNIT QUEENSLAND.			
PA				
XX				

PI	Jennings MP, Moxon ER, Peak IRA:
xx	
DR	WPI: 1999-418754/35.
DR	N-PSDB: AAX85791.
xx	
PT	Neisseria meningitidis surface proteins useful for treating N.
PT	meningitidis infections
PS	
xx	
CC	Claim 1; Page 95-97; 132pp; English.
CC	
CC	The present sequence represents a surface protein of Neisseria
CC	meningitidis which is approximately 62 kDa. The N. meningitidis
CC	surface glycoproteins, nucleic acids, the primers and optionally
CC	a thermostable polymerase, or antibodies are useful in a kit for
CC	the detection or diagnosis of N. meningitidis infection in humans.
CC	The N. meningitidis surface glycoproteins can also be used to
CC	prevent or treat N. meningitidis infection in humans, especially
CC	in the form of vaccines. The proteins and antibodies can also
CC	be used to identify immunoreactive peptides.
xx	
SQ	Sequence 594 AA:
Query Match	88.6%; Score 2423.5; DB: 20; Length 594;
Best Local Similarity	89.4%; Pred. No. 1.3e-132;
Matches 491; Conservative 10; Mismatches 31; Indels 17; Gaps 4.	
QY	3 EDEEELSYVOR-SVVGSIQAMSESVLEETISLMTNDSKEFVDPYI-----VVT 52
DB	53 DDDDLIYLPVQRTAVVLSFRSKETGEKEG-----TEDSKMAV--YDEKRVLKAGAIT 105
QY	53 LKAGDLNLIKONTNENTNASSFTYSLLKDLTGLINVETEKLSFGANGKRVNIISDTKGLN 112
DB	106 LKAGDLNLIKONTNENTNDSPTYSLLKDLTDLTVSETEKLSFGANGKRVNITSDTKGLN 165
QY	113 FAKETAGTNGDTHVNLNGISGTLTDLMLNTGATTNVTNDNTYDDEKKRAASYKDYLANAGW 172
DB	166 FAKETAGTNGDPTVHLNIGISTLTDLTNTGATTNVTNDNTYDDEKKRAASYKDYLANAGW 225
QY	173 NIKGKPCPTTASDNDVFRVTDYVEFLSADPTTQTVNVEESKONGKTEVIGAKTSVYKE 232
DB	226 NIKGKPCPTTASDNDVFRVTDYVEFLSADPTTQTVNVEESKONGKTEVIGAKTSVYKE 285
QY	223 KDGLVYTKGKGENGSTDEBEGVLTAKAEVIDAVNKAQMRKTTTANGOTGADKFEFVY 292
DB	286 KDGLVYTKGKGENDENSTDEBEGVLTAKAEVIDAVNKAQMRKTTTANGOTGADKFEFVY 345
QY	293 SGTKVTFASGNGTTATVSKDDOGNITVKKYDVNVGDLNVNQLQNSGMILDSKAVAGSSGK 352
DB	346 SGTNVTFFASGKGTATVSKDDOGNITVKKYDVNVGDLNVNQLQNSGMILDSKAVAGSSGK 405
QY	353 VISGVNVSQSKKMDTETVINMGNNTEITRNCKNIDIASMTPOFSSVSLGAGADAPTLTSLV 412
DB	406 VISGVNVSQSKGMDTETVINMGNNTEITRNCKNIDIASMTPOFSSVSLGAGADAPTLTSLV 465
QY	413 DDEGALNYSKDKANKPVRITNVAPGVKGGEDVTNVNQLGVAQNLRNIDNVNAGNARAGIA 472
DB	466 DDEGALNYSKDKANKPVRITNVAPGVKGGEDVTNVNQLGVAQNLRNIDNVNAGNARAGIA 525
QY	473 QAIATAGLVQAVYLPKSKMAIGGTYGIEAGYAIIGSSISAGGNMI IKGTASGNSRGHFG 532
DB	526 QAIATAGLVQAVYLPKSKMAIGGTYGIEAGYAIIGSSISAGGNMI IKGTASGNSRGHFG 585
QY	533 ASASYGYOW 541
DB	586 ASASYGYOW 594
RESULT 12	
ID	AAU06179
AC	AAU06179 standard; Protein; 594 AA.
xx	AAU06179;
xx	

DT	24-OCT-2001	(first entry)
XX		
DE	N. meningitidis BZ198 surface antigen NhhA polypeptide sequence.	
XX		
KW	Surface antigen NhhA; meningococcal disease; meningitis vaccine.	
XX		
OS	Neisseria meningitidis strain BZ198.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..50
F7		/label= C1
FT		/note= "Conserved region 1"
FT	Region	51..104
F7		/label= V1
FT		/note= "Variable region 1"
FT	Region	105..116
F7		/label= C2
FT		/note= "Conserved region 2"
FT	Region	117..126
F7		/label= V2
FT		/note= "Variable region 2"
FT	Region	127..190
F7		/label= C3
FT		/note= "Conserved region 3"
FT	Region	191..212
F7		/label= V3
FT		/note= "Variable region 3"
FT	Region	213..231
F7		/label= C4
FT		/note= "Conserved region 4"
FT	Region	232..238
F7		/label= V4
FT		/note= "Variable region 4"
FT	Region	239..594
F7		/label= C5
FT		/note= "Conserved region 5"
XX		
PN	WO200155182-A1.	
XX		
PD	02-AUG-2001.	
XX		
PE	25-JAN-2001; 2001WO-AU00069.	
XX		
PR	25-JAN-2000; 2000US-0177917.	
XX		
PA	(UYQU ) UNIV QUEENSLAND.	
XX		
PI	Peak IRA, Jennings MP;	
XX		
DR	WPI; 2001-488774/53.	
DR	N-PSDB; AAS09169.	
XX		
PT	New NhhA surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
FT	preventing broad spectrum of Neisseria meningitidis .	
XX		
PS	Claim 9; Fig 1; 91pp; English.	
XX		
CC	The present invention relates to the isolation of novel Neisseria	
CC	meningitidis mutant polypeptides of the surface antigen NhhA	
CC	(AAU06182-AAU06186). The modified or mutant NhhA polypeptides are	
CC	characterised by deletions of non-conserved amino acids, particularly	
CC	the deletion of variable regions. The deletion mutants are useful in	
CC	diagnosis, therapeutic and prophylactic vaccines against a broader	
CC	spectrum of N. meningitidis, and in designing and/or screening of	
CC	medicaments. The mutant proteins when used as a vaccine can effectively	
CC	immunise against a broader spectrum of N. meningitidis strains than	
CC	would be expected from a corresponding wild-type surface antigen.	
CC	The present sequence representing the wild type surface antigen NhhA	
CC	from N. meningitidis strain BZ198 is 1 of 10 NhhA polypeptide sequences	
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in	
CC	the present invention.	
XX		

Seq	Sequence	594 AA:	88.6%;	Score 2423.5;	DB 22;	Length 594;
QY	Query Match		88.6%;	Score 2423.5;	DB 22;	Length 594;
Db	Best Local Similarity	89.4%;	Pred. No. 1.3e-133;			
	Matches 491; Conservative 10; Mismatches 31; Indels 17; Gaps 4					
QY	3 EDEEELSESVQV-SVVGSTIOASMEGSVELEFETISLMTNDSKEFEPDPI-----VVT 52	.....:				
Db	53 DDDDLYLEPVQRTAAVLSFRSDKEGTGEK-----TEDSMVA--YFDEKRLKAGAIT 105	.....:				
QY	53 LKAGDMLKTKOMTNTNASSPTYSLAKDLTGLINVEETKLSFANCKRYNISDPTKGLN 112					
Db	106 LKAGDMLKTKOMTNTNASSPTYSLAKDLTGLINVEETKLSFANCKRYNISDPTKGLN 165					
QY	113 FAKETAGINDPTVHLNGISTLIDMLNGATTNVTNDVTDDEKRAASVKDVLNAGW 172					
Db	166 FAKETAGINDPTVHLNGISTLIDPTLNTGATTNVTNDVTDDEKRAASVKDVLNAGW 225					
QY	173 NIKGVAPGTASDNDVFPRTYDTVVEFLSADTKTTTVNESKDNCKTEVAKIGAKTSYKE 232					
Db	226 NIKGVAPGTASDNDVFPRTYDTVVEFLSADTKTTTVNESKDNCKTEVAKIGAKTSYKE 285					
QY	233 KDKCLVTGKGEKENGSSDEEGELVTAKEVIDAVNKKAGMRKTTTANGQGTGADKPEYTV 292					
Db	286 KDKCLVTGKGEKENGSSDEEGELVTAKEVIDAVNKKAGMRKTTTANGQGTGADKPEYTV 345					
QY	293 SGTKVTFAASGNGTTATVSKDDGNTTVKYDVNVGDALNVNOLONGMNLDSKAVAGSSGK 352					
Db	346 SGTNVTFAASGNGTTATVSKDDGNTTVKYDVNVGDALNVNOLONGMNLDSKAVAGSSGK 405					
QY	353 VISGNVSPKGMDEIVNINAGNNEITRNKNIDIASMTPTQSSVSLGAGADAPLSV 412					
Db	406 VISGNVSPKGMDEIVNINAGNNEITRNKNIDIASMAPOSSVSLGAGADAPLSV 465					
QY	413 DDEGALNVSSKANKPVRTITNAPGVEKGGDTNVAOLKGVAQNLNNTEDVNGNARAGIA 472					
Db	466 DDEGALNVSSKANKPVRTITNAPGVEKGGDTNVAOLKGVAQNLNNTEDVNGNARAGIA 525					
QY	473 QAIATAGLQVALPFGKSMALGGGTYLGEAGYAIGYSISAGNMIIKGTASGNSRGHFG 532					
Db	526 QAIATAGLQVALPFGKSMALGGGTYLGEAGYAIGYSISAGNMIIKGTASGNSRGHFG 585					
QY	533 ASASVGYQW 541					
Db	586 ASASVGYQW 594					
RESULT 13						
AAAY23740						
ID	AAAY23740 standard; Protein; 594 AA.					
XX	AAAY23740;					
AC						
XX						
DT	08-SEP-1999 (first entry)					
XX						
DE	A surface protein of Neisseria meningitidis.					
XX						
KW	Surface protein; surface glycoprotein; infection; vaccine;					
XX	Immunoreactive peptide.					
OS	Neisseria meningitidis.					
XX						
PN	MO9931133-AL.					
XX						
PD	24-JUN-1999.					
XX						
PF	14-DEC-1998; 98WO-AU01031.					
XX						
PR	12-DEC-1997; 97GB-0026398.					
XX						
PA	(ISIS-) ISIS INNOVATION LTD.					
XX	(UYOU) UNIV QUEENSLAND.					
XX						



```
Db      |||||||
226 NIKGVKPGTTASDNDVFRITDYVEFLSADTKTTTVNESKNGKRTVEKIGAKTSVKE 285
QY      233 KDGLVTVGKKGKENGSTDEGEGLVTAKEVIDAVNKAQRMTTANQOTGQADFEFYT 292
Db      266 KDGLVTVGKKGKENGSTDEGEGLVTAKEVIDAVNKAQRMTTANQOTGQADFEFYT 345
QY      293 SGTAVTFASGNGTTATVSKDDQGNITVYKDVNVGDALNVNOLNSGWNLDKRAVAGSSGK 352
Db      346 SGTAVTFASGNGTTATVSKDDQGNITVYKDVNVGDALNVNOLNSGWNLDKRAVAGSSGK 405
QY      353 VTSGNVSPSKGKMDTAVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 412
Db      406 VTSGNVSPSKGKMDTAVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 465
QY      413 DDEGALNVGSKDANKPVRITNVAPGVKEDGVTNVAOLKGVANLNRRIDNVNGNARAGIA 472
Db      466 DDEGALNVGSKDANKPVRITNVAPGVKEDGVTNVAOLKGVANLNRRIDNVNGNARAGIA 525
QY      473 QAIATAGLVQAVLYLPKSKMMAIGGTYLGEAGYAIYSSISAGNMWIKGTASGNSRGHFG 532
Db      526 QAIATAGLVQAVLYLPKSKMMAIGGTYRGGAGYAIYSSISDGNMWIKGTASGNSRGHFG 585
QY      533 ASASVGYOW 541
Db      586 ASASVGYOW 594

RESULT 15
AAU06174
ID      AAU06174 standard; Protein; 594 AA.
AC      AAU06174;
XX      XX
DT      24-OCT-2001 (first entry)
XX      XX
DE      N. meningitidis EG327 surface antigen Noha polypeptide sequence.
XX      XX
KM      Surface antigen Noha; meningococcal disease; meningitis vaccine.
XX      XX
OS      Neisseria meningitidis strain EG327.
XX      XX
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      239..594
      /label= C5
      /note= "Conserved region 5"
XX      XX
PN      WO20015182-A1.
XX      XX
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PD      02-AUG-2001.
XX      XX
XX      25-JAN-2001; 2001WO-AU00069.
PF      XX
XX      25-JAN-2000; 2000US-0177917.
PR      XX
XX      (UYOU ) UNIV QUEENSLAND.
XX      PA
XX      Peak IRA, Jennings MP;
XX      PI
XX      WPI: 2001-488774/53.
DR      N-PSDB: AAS09164.
XX      XX
PT      New Noha surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis -
XX      XX
PS      Claim 9; Fig 1; 91pp: English.
XX      XX
CC      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen Noha
CC      (AAU06182-AAU06186). The modified or mutant Noha polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence representing the wild type surface antigen Noha
CC      from N. meningitidis strain EG327 is 1 of 10 Noha polypeptide sequences
CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC      the present invention.
XX      XX
SQ      Sequence 594 AA:
      Query Match 87.9%; Score 2404.5; DB 22; Length 594;
      Best Local Similarity 88.7%; Pred. No. 1.7e-131;
      Matches 487; Conservative 15; Mismatches 34; Indels 13; Gaps 3;
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QY      53 LKAGDNLKIKONTNENTNASSFTYSLKKDLGLINVEYEKLSFGANGKKNVNIISPTKGLN 112
Db      106 LKAGDNLKIKONTNENTNASSFTYSLKKDLGLDLSVGEKLSFSANSKVNITSPTKGLN 165
QY      113 FAKETAGNGDTVYHLNGISLTLDMLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGW 172
Db      166 FAKTAETNGDTVYHLNGISLTLDMLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGW 225
QY      173 NIKGVKPGTTASDNDVFRITDYVEFLSADTKTTTVNESKNGKRTVEKIGAKTSVKE 232
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QY      353 VTSGNVSPSKGKMDTAVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 412
Db      406 VTSGNVSPSKGKMDTAVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 465
QY      413 DDEGALNVGSKDANKPVRITNVAPGVKEDGVTNVAOLKGVANLNRRIDNVNGNARAGIA 472
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Mon Oct 6 '12:38:39 2003

us-09-771-382-34.rag

Page 13

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 14.4674 Seconds  
(without alignments)  
1582.188 Million cell updates/sec

Title: US-09-771-382-34

Perfect score: 2735

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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SUMMARIES

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2	2735	100.0	592	US-09-669-974-17	Sequence 17, Appl
3	2447.5	89.5	599	US-09-377-155-15	Sequence 15, Appl
4	2447.5	89.5	599	US-09-669-974-15	Sequence 15, Appl
5	2426.5	88.7	598	US-09-377-155-5	Sequence 5, Appl
6	2426.5	88.7	598	US-09-377-155-13	Sequence 13, Appl
7	2426.5	88.7	598	US-09-669-974-5	Sequence 5, Appl
8	2426.5	88.7	598	US-09-669-974-13	Sequence 13, Appl
9	2423.5	88.6	594	US-09-377-155-7	Sequence 7, Appl
10	2423.5	88.6	594	US-09-669-974-7	Sequence 7, Appl
11	2404.5	87.9	594	US-09-377-155-9	Sequence 9, Appl
12	2404.5	87.9	594	US-09-669-974-9	Sequence 9, Appl
13	2330.5	85.2	591	US-09-377-155-21	Sequence 21, Appl
14	2330.5	85.2	591	US-09-669-974-21	Sequence 21, Appl
15	2333.5	85.0	591	US-09-377-155-11	Sequence 11, Appl
16	2333.5	85.0	591	US-09-669-974-11	Sequence 11, Appl
17	2315.5	84.7	592	US-09-377-155-2	Sequence 2, Appl
18	2315.5	84.7	592	US-09-669-974-2	Sequence 2, Appl
19	2256.5	82.5	589	US-09-377-155-19	Sequence 19, Appl
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21	946	34.6	2353	US-09-377-155-33	Sequence 33, Appl
22	946	34.6	2353	US-08-913-942-4	Sequence 4, Appl
23	946	34.6	2353	US-09-669-974-33	Sequence 33, Appl
24	945	34.6	2354	US-09-268-347-47	Sequence 47, Appl
25	930.5	34.0	2411	US-09-268-347-36	Sequence 36, Appl
26	925	33.8	607	US-08-409-995-6	Sequence 6, Appl
27	925	33.8	607	US-08-685-467-6	Sequence 6, Appl

28	925	33.8	607	US-08-913-942-6	Sequence 6, Appl
29	925	33.8	1912	US-08-409-995-4	Sequence 4, Appl
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39	866.5	31.7	658	US-08-685-467-5	Sequence 5, Appl
40	866.5	31.7	658	US-08-913-942-5	Sequence 5, Appl
41	766.5	28.0	679	US-08-913-942-15	Sequence 15, Appl
42	766.5	28.0	679	US-09-268-347-26	Sequence 26, Appl
43	585	21.4	1002	US-09-268-347-24	Sequence 24, Appl
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ALIGNMENTS

RESULT 1					
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; Sequence 17, Application US/09377155					
; Patent No. 6197312					
; GENERAL INFORMATION:					
; APPLICANT: PEAK, Ian Richard Anselm					
; APPLICANT: JENNINGS, Michael Paul					
; APPLICANT: MOXON, E. Richard					
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN					
; FILE REFERENCE: 065064/0128					
; CURRENT APPLICATION NUMBER: US/09/377,155					
; CURRENT FILING DATE: 1999-08-19					
; PRIOR APPLICATION NUMBER: PCT/AU98/01031					
; PRIOR FILING DATE: 1998-12-14					
; PRIOR APPLICATION NUMBER: GB 9726398.2					
; PRIOR FILING DATE: 1997-12-12					
; NUMBER OF SEQ ID NOS: 33					
; SOFTWARE: Patentin Ver. 2.0					
; SEQ ID NO 17					
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; TYPE: PRT					
; ORGANISM: Neisseria meningitidis					
US-09-377-155-17					
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Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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; Sequence 17, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-17

Query Match 100.0%; Score 2735; DB 4; Length 592;  
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Db 172 NGDITVHLNGISSTLDMLTGATTNVNDVTDDEKKRAASVADVNLAGNNINGVYKFG 231  
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Db 232 TTASDNVDFVRTYDVEFLSADTKTTTVNVESEKDKNGKTEVKIGAKTSVIREKDEKLVYG 291  
Qy 241 KKGKNGSSSTDEGBGLVTAKEVIDAVNKAGRMKRTTTANGOTGQADKEFTVTSGTKVYFA 300  
Db 292 KKGKNGSSSTDEGBGLVTAKEVIDAVNKAGRMKRTTTANGOTGQADKEFTVTSGTKVYFA 351  
Qy 301 SGNNGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVGISGNVSP 360  
Db 352 SGNNGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVGISGNVSP 411

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Qy 541 W 541  
Db 592 W 592

RESULT 3  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 89.5%; Score 2447.5; DB 3; Length 599;  
Best Local Similarity 90.3%; Pred. No. 3.1e-185;  
Matches 496; Conservative 11; Mismatches 33; Indels 9; Gaps 4;  
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QY 413 DDEGALNVGSKDANKPVRTITNVA PGVEGDTVVAQLKGYAQNLRNIDVNGNARAGIA 472
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Db 471 DDGALNVGSKDANKPVRTITNVA PGVEGDTVVAQLKGYAQNLRNIDVNGNARAGIA 530
QY 473 QAIATAGLVYAATLPKGSMAIIGGTYLGEAGYAI GYSSISAGGMMIITKTASGNSRCHF 532
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Db 531 QAIATAGLVYAATLPKGSMAIIGGTYLGEAGYAI GYSSISDGGMMIITKTASGNSRCHF 590
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Db 591 ASASVGYOW 599

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RESULT 4
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; Sequence 15, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

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Query Match 89.5%; Score 2447.5; DB 4; Length 599;
Best Local Similarity 90.3%; Pred. No. 3.1e-185;
Matches 496; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

QY 1 TDEDEEELESVORS-VVGSISQASMEGSVELET---ISLSMTNDSKEFVDPIYVTLKAG 56
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Db 52 TDEDEEELEPPYRSALVLOFMIDKSGNGENESGNISYTDNHTLHG-AVTLKAG 110
QY 57 DNLKIQO---NTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDTKGLN 112
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|:|||||
Db 171 FAKETAGTNGDITVHLNGISSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVLNAGW 230
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Db 231 NIGVKGRTTASDNVDVPTDYTFVEFLSADTKTTTVVESKDKGKREYVIGAKTSYIKE 290
QY 233 KDKRLVYTGKKGNGSSTDEGEGLVTAKEVIDAVNKA GPMKTTTANGOTGOADKEFTVT 292
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Db 411 VIGSNVSPSKGKMDDEFYNINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPLTV 470
QY 413 DDEGALNVGSKDANKPVRTITNVA PGVEGDTVVAQLKGYAQNLRNIDVNGNARAGIA 472
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RESULT 5
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

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Query Match 88.7%; Score 2426.5; DB 3; Length 598;
Best Local Similarity 89.0%; Pred. No. 1.4e-183;
Matches 492; Conservative 12; Mismatches 28; Indels 21; Gaps 5;

QY 3 EDEEELESVOR-SVGSISQASMEGSVELETISLSMTNDSKEFVDPIY-----VVT 52
|:|||||
Db 53 DDDDLLEPPORTAVLSPFRSDKEGTGEKEG-----TEDSNMAV--YFDEKRYLAKAGIT 105
QY 53 LKAGDNLKIQONTNENTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDT 108
|:|||||
Db 106 LKAGDNLKIQONTNENTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDT 165
QY 109 KGLNFAKETAGTNGDITVHLNGISSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVL 168
|:|||||
Db 166 KGLNFAKETAGTNGDITVHLNGISSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVL 225
QY 169 NAGMNIKGVRPGTTASDNVDVPTDYTFVEFLSADTKTTTVVESKDKGKREYVIGAKTS 228
|:|||||
Db 226 NAGMNIKGVRPGTTASDNVDVPTDYTFVEFLSADTKTTTVVESKDKGKREYVIGAKTS 285
QY 229 VIREKDGKLVYTGKKGNGSSTDEGEGLVTAKEVIDAVNKA GPMKTTTANGOTGOADKE 288
|:|||||
Db 286 VIREKDGKLVYTGKKGNGSSTDEGEGLVTAKEVIDAVNKA GPMKTTTANGOTGOADKE 345
QY 289 ETVYSGKVTYFASGNGTTATVSKDDGNTVYKYVNVGDALNVQLONSGMNLD SKAVAG 348
|:|||||
Db 346 ETVYSGKVTYFASGNGTTATVSKDDGNTVYKYVNVGDALNVQLONSGMNLD SKAVAG 405
QY 349 SSGKVTYFASGNGTTATVSKDDGNTVYKYVNVGDALNVQLONSGMNLD SKAVAG 408
|:|||||
Db 406 SSGKVTYFASGNGTTATVSKDDGNTVYKYVNVGDALNVQLONSGMNLD SKAVAG 465
QY 409 TLSVDEGALNVGSKDANKPVRTITNVA PGVEGDTVVAQLKGYAQNLRNIDVNGNAR 468
|:|||||
Db 466 TLSVDEGALNVGSKDANKPVRTITNVA PGVEGDTVVAQLKGYAQNLRNIDVNGNAR 525
QY 469 AGIAQAIATAGLVYAATLPKGSMAIIGGTYLGEAGYAI GYSSISAGGMMIITKTASGNSR 528
|:|||||

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Db	526	AGTAAGAAATAGAGAAATLPKSMMAIGCGTYKGEAGYALGYSSIDTGNWYIKGTASNSR	505
QY	529	GHEGASASVGYQM	541
Db	586	GHEGTSASVGYQM	598

RESULT 6  
 US-09-377-155-13  
 Sequence 13, Application US/09377155  
 Patent No. 6197312  
 GENERAL INFORMATION:  
 APPLICANT: PEAK, Ian Richard Anselm  
 APPLICANT: JENNINGS, Michael Paul  
 APPLICANT: MOMON, E. Richard  
 TITLE OF INVENTION: NOVEL SURFACE ANTIGENE  
 FILE REFERENCE: 065064/0128  
 CURRENT APPLICATION NUMBER: US/09/377,155  
 CURRENT FILING DATE: 1999-08-19  
 PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 PRIOR FILING DATE: 1998-12-14  
 PRIOR APPLICATION NUMBER: GB 9726398.2  
 PRIOR FILING DATE: 1997-12-12  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 13  
 LENGTH: 598  
 TYPE: PRN  
 ORGANISM: Neisseria meningitidis  
 US-09-377-155-13

Query Match	88.7%	Score 2426.5	-DB 3	Length 598
Best Local Similarity	89.28%	Pred. No. 1.4e-183		
Matches 493	Conservative 11	Mismatches 28	Indels 21	Gaps 5

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QY 3 EDEBEELLESYOR-SYVGSIOASMGBSVLEIITLSMTYDSKFEVPIYI-----VYT 52
Db 53 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 105
QY 53 LKADNLKIKONTMENTNA-----SSFTYSLKDLGLINVEERKLSFGANGKVMINSDF 108
Db 106 LKADNLKIKONTMENTMENTNDSSFTYSLKDLTDLISVETEKLSFGANGKVMITSDF 165
QY 109 KGLNFAKETAGNGDTVHLNGISGTLMDMLNTGATNTVNTDNTYDDEKKAASVKDL 168
Db 166 KGLNFAKETAGNGDPYVHLNGISGTLDTLLNTGATNTVNTDNTYDDEKKAASVKDL 225
QY 169 NAGNNIKGVKPGTTASDNVDFRYDYVEFLSADTKTTTVNESKDNCKTEVKGAKTS 228
Db 226 NAGNNIKGVKPGTTASDNVDFRYDYVEFLSADTKTTTVNESKDNCKTEVKGAKTS 285
QY 229 VIKKDKGLVYGRKGGENSGSTDSGELVYTAKEVIDAVNKKAGMRKKTITTAHQTOADKF 288
Db 286 VIKKDKGLVYGRKGGENSGSTDSGELVYTAKEVIDAVNKKAGMRKKTITTAHQTOADKF 345
QY 289 ETVYSGTKVYFPASGNGTATVPSKDOQGITAKYDVNVGDALNVNLOLNSGMLDSKAAVG 348
Db 346 ETVYSGTKVYFPASGNGTATVPSKDOQGITAKYDVNVGDALNVNLOLNSGMLDSKAAVG 405
QY 349 SSGKVIISGNVSPSGKMDETVINIAGNNIETLRNCKNIDIASTMPPOFSSVSLGADAP 408
Db 406 SSGKVIISGNVSPSGKMDETVINIAGNNIETLRNCKNIDIASTMPPOFSSVSLGADAP 465
QY 409 TLSVDEGALNVGSKDANKPVIRITNVAPGVKEGDTVNAQLKGVAQNLNRRIDYNGNAR 468
Db 466 TLSVDEGALNVGSKDANKPVIRITNVAPGVKEGDTVNAQLKGVAQNLNRRIDYNGNAR 525
QY 469 AGIAQAIATAGLVQAYLPEKSMMAIGGGTYLGEAGVAGYSSISAGNWIITKGTASGNSR 528
Db 526 AGIAQAIATAGLVQAYLPEKSMMAIGGGTYLGEAGVAGYSSISDTGMWVITKGTASGNSR 585
QY 529 GHFGASASVGYOW 541
|||||

```

Db 586 GHFGASASVGYQW 598

1 APPLICANT: PEAR, Ian Richard Anselm  
 2 APPLICANT: JENNINGS, Michael Paul  
 3 APPLICANT: MOXON, E. Richard  
 4 TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 5 FILE REFERENCE: 065064/0128  
 6 CURRENT APPLICATION NUMBER: US/09/6669, 974  
 7 CURRENT FILING DATE: 2000-09-26  
 8 PRIOR APPLICATION NUMBER: US 09/577,155  
 9 PRIOR FILING DATE: 1999-08-19  
 10 PRIOR APPLICATION NUMBER: PCT/A098/01031  
 11 PRIOR FILING DATE: 1998-12-14  
 12 PRIOR APPLICATION NUMBER: GB 9726398.2  
 13 PRIOR FILING DATE: 1997-12-12  
 14 NUMBER OF SEQ ID NOS: 33  
 15 SOFTWARE: PatentIn Ver. 2.0  
 16 SEQ ID NO 5  
 17 LENGTH: 598  
 18 TYPE: PRN  
 19 ORGANISM: Neisseria meningitidis  
 20 US-09-669,974-5

Query Match	88.7%	Score 2426.5	DB 4	length 598;
Best Local Similarity	89.0%	Pred. No. 14e-183		
Matches 492;	Conservative 12;	Mismatches 28;	Indels 21;	Gaps 5;

QY	3	DEEEELLESVOR--SVGSIQASMGSEVLEETLSLMTNDSEFPDYI-----VYT	52
Dd	53	DDDDLTIEPQORTAVVLFKSDKRGITGEK-----TDSWAAV--YFDEKRVLKACAIT	105
QY	53	LKAGDNLIKONTNEMENTNA-----SSFTYSLKKDLTGLINVBETELKSFSGANGKVIISDT	108
QY	106	LKAGDNLIKONTNEMENTNENTNDSSFTYSLKKDLTDLTSLVETELKSFSGANGKVIISDT	165
QY	109	KGLNFAKETAGTNGDITVHLNGISLSTLDMLLNTGATTNVNDVTDDEKRAASVQVL	168
Dd	166	KGLNFAKETAGTNDPPVHLNGISLSTLDTLLNTGATTNVNDVTDDEKRAASVQVL	225
QY	169	NAGNNIKGVKGTATASNDVDFRTYDVEFLSADTKTTTVVESKDNKKTREVKIGAKTS	228
Dd	226	NAGNNIKGVKGTATASNDVDFRTYDVEFLSADTKTTTVVESKDNKKTREVKIGAKTS	285
QY	229	VIKERDKLVTGKKGKGENGSTDEGELVTAKEVIDAVNKAQMRKTTTANGQTQADKF	288
Dd	286	VIKERDKLVTGKKGKGENGSTDEGELVTAKEVIDAVNKAQMRKTTTANGQTQADKF	345
QY	289	ETVYISGTRKVPFASNGTTATYSKDDGHTYKIVYVNGDALNVQLONSGNNLDSKAVAG	348
Dd	346	ETVYISGTRKVPFASNGTTATYSKDDGHTYKIVYVNGDALNVQLONSGNNLDSKAVAG	405
QY	349	SSGCVIGSNVSPSKGMDETVINAGNNIETTRNGKNIDITSMTPQFSSVSLGADAP	408
Dd	406	SSGCVIGSNVSPSKGMDETVINAGNNIETTRNGKNIDITSMTPQFSSVSLGADAP	465
QY	409	TLVSVDDEGALNVGSKDANKPVRIITNVAPEGVEGDTVNVQOLKGYAQNLRNIDVNGNAR	468
Dd	466	TLVSVDDEGALNVGSKDANKPVRIITNVAPEGVEGDTVNVQOLKGYAQNLRNIDVNGNAR	525
QY	469	AGIAQAIATAGLVOAYLPGKSMAAIGGCTVYGEAGYAIYSSISAGCMMITKTASGNSR	528
Dd	526	AGIAQAIATAGLVOAYLPGKSMAAIGGCTVYGEAGYAIYSSISAGCMMITKTASGNSR	585
QY	529	GHEGASASVGYOW	541
Dd	586	GHEGTSASVGYOW	598

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RESULT 8
US-09-669-974-13
; Sequence 13, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-13
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Query Match      88.7%; Score 2426.5; DB 4; Length 598;
Best Local Similarity 89.2%; Pred. No. 1,4e-183;
Matches 493; Conservative 11; Mismatches 28; Indels 21; Gaps 5;
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QY 3 EDEEELESVOR-SVSGSIQSMGSEVLEETISLMTNDSKEFDPYI-----VVT 52
D 53 DDDDLYLEPQRTAVVLSFRSDKEGTGKEG-----TEDSNMAY--YFDEKRVLKAGAIT 105
QY 53 LKAGDNLIKONTNENTNNA-----SFTYSLKKDLTGLINVEFERKLSFGANGKVVNIISDT 108
D 106 LKAGDNLIKONTNENTNENTNDSFTYSLKKDLTGLINVEFERKLSFGANGKVVNIISDT 165
QY 109 KGLNFAKETAGTNDTVHLNGISGTLTDLMLNTGATTNVTNDVTDDEKRAASVVDVL 168
D 166 KGLNFAKETAGTNDTVHLNGISGTLTDLMLNTGATTNVTNDVTDDEKRAASVVDVL 225
QY 169 NAGNINIGVAPGTASNDVDFVRYDYVEFLSADTKTTTVNVESEKDKGKTEVKIGAKTS 228
D 226 NAGNINIGVAPGTASNDVDFVRYDYVEFLSADTKTTTVNVESEKDKGKTEVKIGAKTS 285
QY 229 VIKEDGKLVYTGKKGNGSSSTDEGEGLVTAKEVIDAVNKGAMRKTTTANGQTGAQDKF 288
D 286 VIKEDGKLVYTGKKGNGSSSTDEGEGLVTAKEVIDAVNKGAMRKTTTANGQTGAQDKF 345
QY 289 ETVYSGRTVPFASNGTATVYSKDDGNIIVKYDVNVGDALNVNOLQNSGWNLDKAVAG 348
D 346 ETVYSGRTVPFASNGTATVYSKDDGNIIVKYDVNVGDALNVNOLQNSGWNLDKAVAG 405
QY 349 SSGKVISGNVSPSKGKDETVNINAGNNIETTRGNKIDIAISMTPOFSSVSLGADAP 408
D 406 SSGKVISGNVSPSKGKDETVNINAGNNIETTRGNKIDIAISMTPOFSSVSLGADAP 465
QY 409 TLSVDEGALNVGSKDANKPVRTNVAPGVKESGDTVNAQLKGVAQNINRINDVNGNAR 468
D 466 TLSVDEGALNVGSKDANKPVRTNVAPGVKESGDTVNAQLKGVAQNINRINDVNGNAR 525
QY 469 AGTATATAGTAVYLPKSKMAIGGGTYLGEAGYAIIGYSSISAGGNNIIGTASGNSR 528
D 526 AGTATATAGTAVYLPKSKMAIGGGTYLGEAGYAIIGYSSISAGGNNIIGTASGNSR 585
QY 529 GHFGASASVGYOW 541
D 586 GHFGASASVGYOW 598
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RESULT 9

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US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7
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Query Match      88.6%; Score 2423.5; DB 3; Length 594;
Best Local Similarity 89.4%; Pred. No. 2,4e-183;
Matches 491; Conservative 10; Mismatches 31; Indels 17; Gaps 4;
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QY 3 EDEEELESVOR-SVSGSIQSMGSEVLEETISLMTNDSKEFDPYI-----VVT 52
D 53 DDDDLYLEPQRTAVVLSFRSDKEGTGKEG-----TEDSNMAY--YFDEKRVLKAGAIT 105
QY 53 LKAGDNLIKONTNENTNASSFTYSLKKDLTGLINVEFERKLSFGANGKVVNIISDTGLN 112
D 106 LKAGDNLIKONTNENTNDSFTYSLKKDLTGLINVEFERKLSFGANGKVVNIISDTGLN 165
QY 113 FAKETAGTNDTVHLNGISGTLTDLMLNTGATTNVTNDVTDDEKRAASVVDVLNAGW 172
D 166 FAKETAGTNDTVHLNGISGTLTDLMLNTGATTNVTNDVTDDEKRAASVVDVLNAGW 225
QY 173 NIKGVKGTASNDVDFVRYDYVEFLSADTKTTTVNVESEKDKGKTEVKIGAKTSVKE 232
D 226 NIKGVKGTASNDVDFVRYDYVEFLSADTKTTTVNVESEKDKGKTEVKIGAKTSVKE 285
QY 233 KDGLVYTGKKGNGSSSTDEGEGLVTAKEVIDAVNKGAMRKTTTANGQTGAQDKFETV 292
D 286 KDGLVYTGKKGNGSSSTDEGEGLVTAKEVIDAVNKGAMRKTTTANGQTGAQDKFETV 345
QY 293 SGTVPFASNGTATVYSKDDGNIIVKYDVNVGDALNVNOLQNSGWNLDKAVAGSSGK 352
D 346 SGTVPFASNGTATVYSKDDGNIIVKYDVNVGDALNVNOLQNSGWNLDKAVAGSSGK 405
QY 353 VISGNVSPSKGKDETVNINAGNNIETTRGNKIDIAISMTPOFSSVSLGADAP 412
D 406 VISGNVSPSKGKDETVNINAGNNIETTRGNKIDIAISMTPOFSSVSLGADAP 465
QY 413 DDEGALNVGSKDANKPVRTNVAPGVKESGDTVNAQLKGVAQNINRINDVNGNARAGIA 472
D 466 DDEGALNVGSKDANKPVRTNVAPGVKESGDTVNAQLKGVAQNINRINDVNGNARAGIA 525
QY 473 QAITATAGTAVYLPKSKMAIGGGTYLGEAGYAIIGYSSISAGGNNIIGTASGNSR 532
D 526 QAITATAGTAVYLPKSKMAIGGGTYLGEAGYAIIGYSSISAGGNNIIGTASGNSR 585
QY 533 ASASVGYOW 541
D 586 ASASVGYOW 594
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```
RESULT 10
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
```

APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 7  
LENGTH: 594  
TYPE: PR  
ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 88.6%; Score 2423.5; DB 4; Length 594;  
Best Local Similarity 89.4%; Pred. No. 2.4e-183;  
Matches 491; Conservative 10; Mismatches 31; Indels 17; Gaps 4;

QY 3 EDEEELESVOR-SVVGSIQASMEGSVELETISLSMTNDSKEFVDPI-----VVT 52  
DB 53 DDDDDLYLEPVQRTAVVLSFRSDKEGTEKE-----TEDSNNAV--YFDEKRVLKAGAIT 105  
QY 53 LKAGNLKIKONTNENTNASSFTYSLKDLTGLINVEFEKLSFGANGKRVNIISPTKGLN 112  
DB 106 LKAGNLKIKONTNENTNASSFTYSLKDLTGLTDLTSVGEFEKLSFGANGKRVNIISPTKGLN 165  
QY 113 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDNVTDDEKRAASVADVLNMG 172  
DB 166 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDNVTDDEKRAASVADVLNMG 225  
QY 173 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKTEVYKIGAKTSVKE 232  
DB 226 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKTEVYKIGAKTSVKE 285  
QY 233 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAARMKTTTANGOTGADKFEYVT 292  
DB 286 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAARMKTTTANGOTGADKFEYVT 345  
QY 293 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 352  
DB 346 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 405  
QY 353 VTSGNVSPSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSV 412  
DB 406 VTSGNVSPSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSV 465  
QY 413 DDEGALNNGSKDANKPVRTITNVAPEVKEDVTNVQOLKVAONLNRRIDNVGNARAGIA 472  
DB 466 DDEGALNNGSKDANKPVRTITNVAPEVKEDVTNVQOLKVAONLNRRIDNVGNARAGIA 525  
QY 473 QAIATAGLQVAVLTPKRSMAIGGGTYLGEAGYAIIGYSSISAGGNMIIKGTASGNSRGHG 532  
DB 526 QAIATAGLQVAVLTPKRSMAIGGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHG 585  
QY 533 ASASVGYOW 541  
DB 586 ASASVGYOW 594

RESULT 11  
US-09-377-155-9  
Sequence 9, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 9  
LENGTH: 594  
TYPE: PR  
ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 87.9%; Score 2404.5; DB 3; Length 594;  
Best Local Similarity 88.7%; Pred. No. 7.7e-182;  
Matches 487; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 1 TDEEELESVOR-SVVGSIQASMEGSVELETISLSMTNDS-----KEFVDPIYVT 52  
DB 51 TTDDDDLYLEPVQRTAVVLSFRSDKEGTEKE-----VTEDSNMGYVEPKKGVLTAGIT 105  
QY 53 LKAGNLKIKONTNENTNASSFTYSLKDLTGLINVEFEKLSFGANGKRVNIISPTKGLN 112  
DB 106 LKAGNLKIKONTNENTNASSFTYSLKDLTGLTDLTSVGEFEKLSFGANGKRVNIISPTKGLN 165  
QY 113 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDNVTDDEKRAASVADVLNMG 172  
DB 166 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDNVTDDEKRAASVADVLNMG 225  
QY 173 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKTEVYKIGAKTSVKE 232  
DB 226 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKTEVYKIGAKTSVKE 285  
QY 233 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAARMKTTTANGOTGADKFEYVT 292  
DB 286 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAARMKTTTANGOTGADKFEYVT 345  
QY 293 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 352  
DB 346 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 405  
QY 353 VTSGNVSPSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSV 412  
DB 406 VTSGNVSPSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSV 465  
QY 413 DDEGALNNGSKDANKPVRTITNVAPEVKEDVTNVQOLKVAONLNRRIDNVGNARAGIA 472  
DB 466 DDEGALNNGSKDANKPVRTITNVAPEVKEDVTNVQOLKVAONLNRRIDNVGNARAGIA 525  
QY 473 QAIATAGLQVAVLTPKRSMAIGGGTYLGEAGYAIIGYSSISAGGNMIIKGTASGNSRGHG 532  
DB 526 QAIATAGLQVAVLTPKRSMAIGGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHG 585  
QY 533 ASASVGYOW 541  
DB 586 ASASVGYOW 594

RESULT 12  
US-09-669-974-9  
Sequence 9, Application US/09669974  
Patent No. 6333173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974







10	2451.5	94.2	598	22	AAV006178	N. meningitidis BZ
11	2448.5	94.1	594	20	AAV23739	A surface protein
12	2448.5	94.1	594	22	AAU06179	N. meningitidis BZ
13	2409.5	92.6	594	20	AAV23740	A surface protein
14	2409.5	92.6	594	21	AAV57044	BASB029 amino acid
15	2409.5	92.6	594	22	AAU06174	N. meningitidis BZ
16	2408	92.5	591	21	AAV57045	BASB029 amino acid
17	2407	92.5	591	20	AAV72202	Amino acid sequenc
18	2407	92.5	591	20	AAV23746	A surface protein
19	2407	92.5	591	22	AAU06171	N. meningitidis BZ
20	2402.5	92.3	592	20	AAU23737	N. meningitidis BZ
21	2395	92.0	591	20	AAV23741	A surface protein
22	2395	92.0	591	22	AAU06175	N. meningitidis BZ
23	2351.5	90.4	592	22	AAU06180	N. meningitidis BZ
24	2315.5	89.0	592	20	AAV27203	Amino acid sequenc
25	2314	88.9	589	20	AAV23745	A surface protein
26	2314	88.9	589	22	AAU06186	N. meningitidis BZ
27	2255.5	86.7	502	22	AAU06186	N. meningitidis BZ
28	2106.5	81.0	604	22	AAU06181	N. meningitidis BZ
29	2055	79.0	433	22	AAU06185	N. meningitidis BZ
30	1909	73.4	407	22	AAU06184	A surface protein
31	981.5	37.7	1094	21	AAAB23858	N. meningitidis BZ
32	966.5	37.1	1098	17	AAAB9392	Haemophilus influ
33	941.5	36.2	2411	21	AAAB23860	Haemophilus adhe
34	939.5	36.1	2353	17	AAAB9393	Haemophilus influ
35	761	29.2	679	17	AAAB9394	Haemophilus adhe
36	761	29.2	679	21	AAAB23855	Haemophilus influ
37	728.5	26.0	245	20	AAV72201	Amino acid sequenc
38	685.5	28.3	1002	21	AAAB23854	Haemophilus influ
39	668.5	25.7	1004	21	AAAB23857	Haemophilus influ
40	580	22.3	116	21	AAAB37832	Neisseria conserv
41	562.5	21.6	1104	21	AAAB23856	Haemophilus influ
42	562.5	21.6	1104	21	AAAB23859	Haemophilus influ
43	526.5	20.2	298	24	AAE63047	Haemophilus influ
44	379	14.6	2314	22	AAAB69136	M. catarrhalis les
45	378.5	14.5	2139	24	ABP71294	M. catarrhalis su
ALIGNMENTS						
RESULT 1						
AAU06183	AAU06183 standard; Protein; 513 AA.					
AAU06183;						
24-OCT-2001	(first entry)					
N. meningitidis H41	NhaA deletion mutant.					
Surface antigen NhaA;	meningococcal disease; meningitis vaccine;					
mutant; muten.						
Neisseria meningitidis strain H41.						
Synthetic.						
Key	Location/Qualifiers					
Peptide	1..51					
Protein	/label= Signal_peptide					
	52..513					
	/label= Mature_NhaA_deletion_mutant					
	/note= "Predicted mature protein, specifically					
	claimed in claim 12"					
WO200155182-A1.						
02-AUG-2001.						
25-JAN-2001;	2001WO-AU00069.					
25-JAN-2000;	2000US-0177917.					

PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
DR N-PSDB; AAS09173.  
XX  
XX New Nhma surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 12; Fig 6; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhma  
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain H41 surface  
CC antigen Nhma deletion mutant.  
CC  
XX  
SQ Sequence 513 AA;  
  
Query Match 100.0%; Score 2602; DB 22; Length 513;  
Best Local Similarity 100.0%; Pred. No. 4.7e-153;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNKIYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFAIVQANATDEGLIN 60  
DB 1 MNKIYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFAIVQANATDEGLIN 60  
QY 61 ETEKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLNIGSTLMDLNTGATTV 120  
DB 61 ETEKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLNIGSTLMDLNTGATTV 120  
QY 121 TNDNVTDDEKKRAASKVDYLNAGMNIKGVKPGTTASNDVFVETVDFEFLSADTKTV 180  
DB 121 TNDNVTDDEKKRAASKVDYLNAGMNIKGVKPGTTASNDVFVETVDFEFLSADTKTV 180  
QY 181 NVESKDNKGKTEYKIGAKTSVIREKDKLVTGKKGENGSSTEDEGLVTAKEVIDAVNK 240  
DB 181 NVESKDNKGKTEYKIGAKTSVIREKDKLVTGKKGENGSSTEDEGLVTAKEVIDAVNK 240  
QY 241 AGRRMKTTPANGTGADKFEYTSCTKVTFAFGNGTTATVSKDDGNIITVKYDVNVGDA 300  
DB 241 AGRRMKTTPANGTGADKFEYTSCTKVTFAFGNGTTATVSKDDGNIITVKYDVNVGDA 300  
QY 301 LANNQLONSGWNIDSLAAGSSSGKVISGNVSPSKGMDETVNINAGNNIEITRNKNIDI 360  
DB 301 LANNQLONSGWNIDSLAAGSSSGKVISGNVSPSKGMDETVNINAGNNIEITRNKNIDI 360  
QY 361 AFSMTPOFSSSVSLGAGADAPTLISVDEGALNVGSKDANKPVRTTNVAPGVKEGDVTVAQ 420  
DB 361 AFSMTPOFSSSVSLGAGADAPTLISVDEGALNVGSKDANKPVRTTNVAPGVKEGDVTVAQ 420  
QY 421 LKGVANQNLNRIDNVGNARAGIAQALATAGLVQATLPKGSMAIGGGITVLSAGTAIGY 480  
DB 421 LKGVANQNLNRIDNVGNARAGIAQALATAGLVQATLPKGSMAIGGGITVLSAGTAIGY 480  
QY 481 SSISAGNNIITKGTASGNSRGHFGASASVGYOM 513  
DB 481 SSISAGNNIITKGTASGNSRGHFGASASVGYOM 513  
  
RESULT 2  
AA23744  
ID AAY23744 standard; protein; 592 AA.  
XX

AC AAY23744;  
XX  
XX 08-SEP-1999 (first entry)  
DT  
XX  
XX A surface protein of Neisseria meningitidis.  
DE  
XX  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW Immunoreactive peptide.  
XX  
XX Neisseria meningitidis.  
OS  
XX  
XX WO931132-A1.  
PN  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
XX 12-DEC-1997; 97GB-0026398.  
PR  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
PI  
XX  
XX WPI: 1999-418754/35.  
DR N-PSDB; AAX85796.  
DR  
XX  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PT  
PS Claim 1; Page 118-120; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
CC  
XX  
SQ Sequence 592 AA;  
  
Query Match 98.1%; Score 2552.5; DB 20; Length 592;  
Best Local Similarity 86.7%; Pred. No. 6.4e-150;  
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;  
  
QY 1 MNKIYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFAIVQANATDE----- 54  
DB 1 MNKIYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFAIVQANATDEDEEEL 60  
QY 55 ----- 54  
DB 55 ----- 54  
QY 61 ESQORSVGSIQASMEGSVELETISLMTNDSKEFVDPPIVTVLKAQDNLIKQNTNENT 120  
DB 61 ESQORSVGSIQASMEGSVELETISLMTNDSKEFVDPPIVTVLKAQDNLIKQNTNENT 120  
QY 55 -----TGLINVETKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLN 101  
DB 55 -----TGLINVETKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLN 101  
QY 102 GIGSTLTDMLNTGATTNTNDVNTDDEKKRAASVDYLNAGNNIKGVKPGTTASNDVF 161  
DB 102 GIGSTLTDMLNTGATTNTNDVNTDDEKKRAASVDYLNAGNNIKGVKPGTTASNDVF 161  
QY 181 GIGSTLTDMLNTGATTNTNDVNTDDEKKRAASVDYLNAGNNIKGVKPGTTASNDVF 240  
DB 181 GIGSTLTDMLNTGATTNTNDVNTDDEKKRAASVDYLNAGNNIKGVKPGTTASNDVF 240  
QY 162 VRTYDVEFLSADTKTTPVNVESKDNKGKTEYKIGAKTSVIREKDKLVTGKKGENGSS 221  
DB 162 VRTYDVEFLSADTKTTPVNVESKDNKGKTEYKIGAKTSVIREKDKLVTGKKGENGSS 221  
QY 241 VRTYDVEFLSADTKTTPVNVESKDNKGKTEYKIGAKTSVIREKDKLVTGKKGENGSS 300  
DB 241 VRTYDVEFLSADTKTTPVNVESKDNKGKTEYKIGAKTSVIREKDKLVTGKKGENGSS 300  
QY 222 TDEGEGLVTAKEVIDAVNKRGMKTTTANGTGADKFEYTSCTKVTFAFGNGTTATV 281  
DB 222 TDEGEGLVTAKEVIDAVNKRGMKTTTANGTGADKFEYTSCTKVTFAFGNGTTATV 281  
QY 301 TDEGEGLVTAKEVIDAVNKRGMKTTTANGTGADKFEYTSCTKVTFAFGNGTTATV 360  
DB 301 TDEGEGLVTAKEVIDAVNKRGMKTTTANGTGADKFEYTSCTKVTFAFGNGTTATV 360  
QY 282 SKDDQGNITVYKIVNVGDALNVQLONSGWNIDSKAAGSSGKVISGNVSPSKGMDETV 341  
DB 282 SKDDQGNITVYKIVNVGDALNVQLONSGWNIDSKAAGSSGKVISGNVSPSKGMDETV 341

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DB      361 SKDDGNTVYKDYVNVGDLNVNQLONGSGWNLDSKAVAGSSGKVISGNVSPSKGMDPTV 420
OY      342 NINAGNNIEITRNGKNIDIAITSMTPOFSSVSLGAGADAPTLSVDEGALNYSKRAKPV 401
DB      421 NINAGNNIEITRNGKNIDIAITSMTPOFSSVSLGAGADAPTLSVDEGALNYSKRAKPV 480
OY      402 RITNVAPGVKGGDYTNVAQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAYLPKGS 461
DB      481 RITNVAPGVKGGDYTNVAQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAYLPKGS 540
OY      462 MAAIGGTYLGBAGYAIGYSSISAGGNMIIRKGTASGNSRGHFGASASVGYQM 513
DB      541 MAAIGGTYLGBAGYAIGYSSISAGGNMIIRKGTASGNSRGHFGASASVGYQM 592

RESULT 3
AAU06172
ID      AAU06172 standard: Protein: 592 AA.
AC      AAU06172;
XX      24-OCT-2001 (first entry)
DE      N. meningitidis H41 surface antigen Noha polypeptide sequence.
XX      Surface antigen Noha; meningococcal disease; meningitis vaccine.
XX      Neisseria meningitidis strain H41.
XX      Key
FH      Location/Qualifiers
FT      Peptide
FT      1..51
FT      /label= Signal_peptide
FT      1..50
FT      /label= C1
FT      /note= "Conserved region 1"
FT      51..102
FT      /label= V1
FT      /note= "Variable region 1"
FT      52..592
FT      /label= Mature_Noha
FT      /note= "Predicted mature protein, specifically
FT      claimed in claim 12"
FT      103..114
FT      /label= C2
FT      /note= "Conserved region 2"
FT      115..124
FT      /label= V2
FT      /note= "Variable region 2"
FT      125..188
FT      /label= C3
FT      /note= "Conserved region 3"
FT      189..210
FT      /label= V3
FT      /note= "Variable region 3"
FT      211..229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..592
FT      /label= C5
FT      /note= "Conserved region 5"
XX      WO20015182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX
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PA      (UYU ) UNIV QUEENSLAND.
XX      PI      Peak IRA, Jennings MP;
XX      DR      WPI: 2001-488774/53.
XX      N-PSDB: AAS09162.
XX      PT      New Noha surface antigen polypeptides and polynucleotides from
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      preventing broad spectrum of Neisseria meningitidis -
XX      Claim 9; Fig 1; 91pp; English.
XX      PS      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Noha
XX      (AAU06182-AAU06186). The modified or mutant Noha polypeptides are
XX      characterised by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      medicaments. The mutant proteins when used as a vaccine can effectively
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      would be expected from a corresponding wild-type surface antigen.
XX      CC      The present sequence representing the wild type surface antigen Noha
XX      from N. meningitidis strain H41 is 1 of 10 Noha polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
XX      SQ      Sequence 592 AA:
XX
XX      Query Match 98.1%; Score 2552.5; DB 22; Length 592;
XX      Best Local Similarity 86.7%; Pred. No. 6.4e-150;
XX      Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
OY      1 MNKIYRIIWSNALNMAVAVSELTRNHRKASATVTAVALTLFATVOANATDF----- 54
DB      1 MNKIYRIIWSNALNMAVAVSELTRNHRKASATVTAVALTLFATVOANATDFEEBEL 60
OY      55 ----- 54
DB      61 ESVQSRVYVGSIQASMEGSEVELETISLSMTNDSKEVPDPIYVTLKAGNLKIKONTNENT 120
OY      55 -----TGLINVEETEKLSEFGANGKRVNIISDTKGLNFAKETAAGTNGDTVHLN 101
DB      121 NASSFTYSLEKKDLDTGLINVEETEKLSEFGANGKRVNIISDTKGLNFAKETAAGTNGDTVHLN 180
OY      102 GIGSTLTDMLNTGATVNTVDNDVTDDEKKRAASVKDVLAAGWNIKGVKPGTTASDNDVF 161
DB      181 GIGSTLTDMLNTGATVNTVDNDVTDDEKKRAASVKDVLAAGWNIKGVKPGTTASDNDVF 240
OY      162 VRTYDTVEFLSADPTTIVNVESKNGKTEYKIGAKSVIKERKGLVTKGGENSS 221
DB      241 VRTYDTVEFLSADPTTIVNVESKNGKTEYKIGAKSVIKERKGLVTKGGENSS 300
OY      222 TDEGGLYTAKEVIDAVNKAQWPKTKTANGQTGADRFETVTSCTKYTFASGNGTATV 281
DB      301 TDEGGLYTAKEVIDAVNKAQWPKTKTANGQTGADRFETVTSCTKYTFASGNGTATV 360
OY      282 SKDDGNTVYKDYVNVGDLNVNQLONGSGWNLDSKAVAGSSGKVISGNVSPSKGMDPTV 341
DB      361 SKDDGNTVYKDYVNVGDLNVNQLONGSGWNLDSKAVAGSSGKVISGNVSPSKGMDPTV 420
OY      342 NINAGNNIEITRNGKNIDIAITSMTPOFSSVSLGAGADAPTLSVDEGALNYSKRAKPV 401
DB      421 NINAGNNIEITRNGKNIDIAITSMTPOFSSVSLGAGADAPTLSVDEGALNYSKRAKPV 480
OY      402 RITNVAPGVKGGDYTNVAQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAYLPKGS 461
DB      481 RITNVAPGVKGGDYTNVAQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAYLPKGS 540
OY      462 MAAIGGTYLGBAGYAIGYSSISAGGNMIIRKGTASGNSRGHFGASASVGYQM 513
DB      541 MAAIGGTYLGBAGYAIGYSSISAGGNMIIRKGTASGNSRGHFGASASVGYQM 592
```

ID	AA	Score	DB	Length	599
XX	AAAY23743	standard; Protein; 599 AA.			
XX	AAAY23743				
XX	AAAY23743				
XX	08-SEP-1999	(first entry)			
XX	A	surface protein of Neisseria meningitidis.			
XX	Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.				
XX	Neisseria meningitidis.				
XX	MO9931132-A1.				
XX	24-JUN-1999.				
XX	14-DEC-1998;	98WO-AU01031.			
XX	12-DEC-1997;	97GB-0026398.			
XX	(ISIS-) ISIS INNOVATION LTD.				
XX	(UYOU) UNIV QUEENSLAND.				
XX	Jennings MP, Moxon ER, Peak IRA;				
XX	WPI: 1999-418754/35.				
XX	N-PSDB; AAX85795.				
XX	Neisseria meningitidis surface proteins useful for treating N. meningitidis infections				
XX	Claim 1; Page 114-115; 132pp; English.				
XX	The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.				
XX	Sequence	599 AA;			
XX	Query Match	95.0%; Score 2472; DB 20;			
XX	Best Local Similarity	83.1%; Pred. No. 6.2e-145;			
XX	Matches 498; Conservative	5; Mismatches 10; Indels 86; Gaps 1			
XX	1 MNKIYRIIWNALNVAVASELTRNHTKRASATVTAVALATLFFATVQANATDE-----	54			
XX	1 MNKIYRIIWNALNVAVASELTRNHTKRASATVTAVALATLFFATVQANATDE-----	54			
XX	1 MNKIYRIIWNALNVAVASELTRNHTKRASATVTAVALATLFFATVQANATDE-----	54			
XX	55 -----	54			
XX	61 EPVVSALVLOFMIDKEGNGENESTGNIWISYIDNHTLHGATVTLKAGDNLIKQNTN	120			
XX	55 -----	94			
XX	121 KNTVENINDDSFYSLAKDLTDLVSETEKUSFGANGKKNITSDTKGLNFAKETAGTNG	180			
XX	95 DTFVHLNIGSLTDLMLNTGATTVNTDNYVDLDDKKRAASVYDVLNAGWNLIKGVKPGTT	154			
XX	181 DTFVHLNIGSLTDLMLNTGATTVNTDNYVDLDDKKRAASVYDVLNAGWNLIKGVKPGTT	240			
XX	155 ASDNVADPRDYDYEFSLADPKRTTVNVEKDNKKTEVKIGAKSVIKERKGLVTGKG	214			
XX	241 ASDNVADPRDYDYEFSLADPKRTTVNVEKDNKKTEVKIGAKSVIKERKGLVTGKG	300			

OY		215	KGENGSTEGCEBELVIAKAVIDAIVNKKAGRMKTATTANGOTGOADKEFTVTSGTKVPASG	274
Dd		301	KGENGSSTBGBELVIAKEVIDAIVNKAKGRMKTATTANQOTGOADKEFTVTSGETVWTPASG	360
OY		275	NGTTATVSKDDOGNITVKYDVNVGDALVNYNOJNSGMWLDSKAVAGSSGVISGNVSPSK	334
OY		395	KDANKRPVRTNNAPGVKEGDYTNNVAOLKGVAONLNRRIDNTNGNARAGIAQAITYAGLYQ	454
Dd		481	KDANKRVRRTNNAPGVKEGDYTNNVAOLKGVAONLNRRIDNTDGNARRAGIAQAITYAGLYQ	540
OY		335	GKMDEVNINAGNNIEITPENGKNIDIAIYSMPQESSVSLGAGADAPTLSVDDEGALVGS	394
Dd		421	GKMDDEVNINAGNNIEITRNENKNIDIASMTPOFSSVSILGAGADAPTLSVDKGLNVGS	480
OY		455	AYLPGKSMAIGGGTYLGAGYAIGVSSISAGNMIIKGTASGNSRGHFGASASVGYYQW	513
Dd		541	AYLPGKSMAIGGGTYRGAGYAIGVSSISDGNMIIKGTASGNSRGHFGASASVGYYQW	599
 RESULT 5 AAU06176 standard; Protein; 599 AA.				
XX	AC	AAU06176;		
XX	DT	24-OCT-2001 (first entry)		
XX	XX	N. meningitidis H38 surface antigen NhbA polypeptide sequence.		
DE	XX	Surface antigen NhbA; meningococcal disease; meningitis vaccine.		
XX	OS	Neisseria meningitidis strain H38.		
XX	Key	Location/Qualifiers		
FH	Region	/label= C1		
FT	Region	/note= "Conserved region 1"		
FT	Region	/label= V1		
FT	Region	/note= "Variable region 1"		
FT	Region	/label= C2		
FT	Region	/note= "Conserved region 2"		
FT	Region	/label= V2		
FT	Region	/note= "Variable region 2"		
FT	Region	/label= C3		
FT	Region	/note= "Conserved region 3"		
FT	Region	/label= V3		
FT	Region	/note= "Variable region 3"		
FT	Region	/label= C4		
FT	Region	/note= "Conserved region 4"		
FT	Region	/label= V4		
FT	Region	/note= "Variable region 4"		
FT	Region	/label= C5		
FT	Region	/note= "Conserved region 5"		
XX	PN	WO200155182-A1.		
XX	PD	02-AUG-2001.		
XX	PE	25-JAN-2001; 2001MO-AAU00069.		
XX	PR	25-JAN-2000; 2000US-0177917.		

PA (UYOU ) UNIV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
DR  
DR N-PSDB: AAS09166.  
XX  
XX  
XX New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
XX Claim 9, Fig 1; 91pp; English.  
XX  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
XX  
SQ Sequence 599 AA:  
Query Match 95.0%; Score 2472; DB 22; Length 599;  
Best Local Similarity 83.1%; Pred. No. 6-2e-145;  
Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;  
QY 1 MNKIYRIIWSALNMAVAVSELTRNHRTRASATVATVATLLEFATVOANATDE----- 54  
DB 1 MNKIYRIIWSALNMAVAVSELTRNHRTRASATVATVATLLEFATVOANATDEDEEEL 60  
QY 55 ----- 54  
DB 61 EPPVRSALVLOPMIDKEGNGENESGNGISYIYNHNTLGCATVYTLKAGDNLKIKQNTN 120  
QY 55 -----TGLINVEETEKLSPGANGKRVNIISDTKGLNFAKETAGTNG 94  
DB 121 KNTNENTNDSSEFTYSLKKDLFDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNG 180  
QY 95 DTYHLNGIGSTLIDMLNTGATTNTVNDVNTDDEKRAASVYKDVLANGMNKGVPETT 154  
DB 181 DTYHLNGIGSTLIDMLNTGATTNTVNDVNTDDEKRAASVYKDVLANGMNKGVPETT 240  
QY 155 ASDNVDFTVRYDYVEFLSADTKRTTNTVNESKONGKKEVKGAKTSVIREKDGKLVTKG 214  
DB 241 ASDNVDFTVRYDYVEFLSADTKRTTNTVNESKONGKKEVKGAKTSVIREKDGKLVTKG 300  
QY 215 KGENSSSTDEEGGLTAKEVIDAVNKAQMRKTTTANGQTGOADKFETVTSQTVTFASG 274  
DB 301 KGENSSSTDEEGGLTAKEVIDAVNKAQMRKTTTANGQTGOADKFETVTSQTVTFASG 360  
QY 275 NGTATVSKDQGNITVYDVNVDALVNOLNSGMULDSKAAVAGSSGKVIISGVNPSK 334  
DB 361 KGTATVSKDQGNITVYDVNVDALVNOLNSGMULDSKAAVAGSSGKVIISGVNPSK 420  
QY 335 GKMDFTVINAGNNNEITRNCKNIDIASMTPOFSVSLGAGADAPTLSPVDEGLANGS 394  
DB 421 GKMDFTVINAGNNNEITRNCKNIDIASMTPOFSVSLGAGADAPTLSPVDEGLANGS 480  
QY 395 KDANKPVRITNVAPGVEKGYTNTVAQLKVAONLNRRIDNVNGNARAGIAAIAATAGLVQ 454  
DB 481 KDANKPVRITNVAPGVEKGYTNTVAQLKVAONLNRRIDNVNGNARAGIAAIAATAGLVQ 540  
QY 455 AYLPEKSMATIGGGYLGEGAGYAGYSSISAGGNMIIKGTASGNSRGHFGASASVGYOM 513  
DB 541 AYLPEKSMATIGGGYLGEGAGYAGYSSISAGGNMIIKGTASGNSRGHFGASASVGYOM 599

RESULT 6  
AAV23742  
ID AAV23742 standard; Protein; 598 AA.  
XX  
XX AAV23742;  
AC  
XX 08-SEP-1999 (first entry)  
XX  
XX A surface protein of Neisseria meningitidis.  
DE  
XX Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX  
XX Neisseria meningitidis.  
OS  
XX WO931132-A1.  
XX  
XX 24-JUN-1999.  
PD  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
XX 12-DEC-1997; 97GB-0026398.  
PR  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
PI  
DR WPI: 1999-418754/35.  
DR N-PSDB: AAX85794.  
XX  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
XX Claim 1; Page 108-110; 132pp; English.  
XX  
XX  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX  
SQ Sequence 598 AA:  
Query Match 94.6%; Score 2460.5; DB 20; Length 598;  
Best Local Similarity 82.9%; Pred. No. 3.2e-144;  
Matches 496; Conservative 4; Mismatches 13; Indels 85; Gaps 1;  
QY 1 MNKIYRIIWSALNMAVAVSELTRNHRTRASATVATVATLLEFATVOANATDE----- 54  
DB 1 MNKIYRIIWSALNMAVAVSELTRNHRTRASATVATVATLLEFATVOANATDDDDLLLE 60  
QY 55 ----- 54  
DB 61 PVQRTAVVLSFRSDEKGTGEKEGTEDSNMVAVFDEKRVYLKAGATLTLKAGDNLKIKQNTNE 120  
QY 55 -----TGLINVEETEKLSPGANGKRVNIISDTKGLNFAKETAGTNGD 95  
DB 121 KNTNENTNDSSEFTYSLKKDLFDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGD 180  
QY 96 TTYHLNGIGSTLIDMLNTGATTNTVNDVNTDDEKRAASVYKDVLANGMNKGVPETT 155  
DB 181 PTVHLNGIGSTLIDMLNTGATTNTVNDVNTDDEKRAASVYKDVLANGMNKGVPETT 240  
QY 156 SDNVDFTVRYDYVEFLSADTKRTTNTVNESKONGKKEVKGAKTSVIREKDGKLVTKGK 215  
DB 241 SDNVDFTVRYDYVEFLSADTKRTTNTVNESKONGKKEVKGAKTSVIREKDGKLVTKGK 300



RESULT 8
ID AAU06182 standard; Protein; 512 AA.
XX AAU06182;
AC XX
DT 24-OCT-2001 (first entry)
XX N. meningitidis PMC21 Nhba deletion mutant #1.
DE XX Surface antigen Nhba; meningococcal disease; meningitis vaccine;
KW mutant; muten.
XX Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..51
FT /label= Signal_peptide
FT Protein 52..512
FT /label= Mature_Nhba_deletion_mutant_#1
FT /note= "Predicted mature protein, specifically claimed in claim 12"
FT
XX W020015182-A1.
PN
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEBENSLAND.
PA
PI Peak IRA, Jennings MP;
XX WP1: 2001-488774/53.
DR N-PSDB; AAS09172.
PT New Nhba surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 12; Fig 5; 91pp; English.
PS The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhba
CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhba deletion mutant #1.
XX
SQ Sequence 512 AA;
Query Match 94.4%; Score 2456.5; DB 22; Length 512;
Best Local Similarity 95.3%; Pred. No. 4.6e-144;
Matches 489; Conservative 5; Mismatches 18; Indels 1; Gaps 1
QY 1 MNKYIRIIMNSALNAMYAVSELTRNHTRKRAATVKTAYLATLLEFATVOANATDETGLINV 60
Db 1 MNKYIRIIMNSALNAMYAVSELTRNHTRKRAATVKTAYLATLLEFATVOASANNENDLSV 60
61 ETEKLSSGANGKKNIISDTRYGLNFAKTAAGTNGDTYTHVLNGIGSTLDMLNCATTVN 120
61 GTEKLSSGANGKKNIISDTRYGLNFAKTAAGTNGDTYTHVLNGIGSTLDMLNCATTVN 120

QY	121	INDNTDDEKKRAASVRYVLNAGNMIKGVKPGCTTASDNDDPFRKYDTYVEFLSADTKTTTY	180
QY	121	INDNTDDEKKRAASVRYVLNAGNMIKGVKPGCTTASDNDDPFRKYDTYVEFLSADTKTTTY	180
QY	181	NVESKONGKKTVEKIGAKTSVTKERKDGKLVTKGKGENGSSPDEGGGLVTAKEVIDAVNK	240
QY	181	NVESKONGKKTVEKIGAKTSVTKERKDGKLVTKGKGENGSSPDEGGGLVTAKEVIDAVNK	240
QY	181	NVESKONGKKTVEKIGAKTSVTKERKDGKLVTKGKGENGSSPDEGGGLVTAKEVIDAVNK	240
QY	241	AGWRKTTTJANGQOTGOADKFEYTVTSCTKVTFASSGNGTTATVASKDDGNTTVKYDVNVGDA	300
QY	241	AGWRKTTTJANGQOTGOADKFEYTVTSCTKVTFASSGNGTTATVASKDDGNTTVKYDVNVGDA	300
QY	241	AGWRKTTTJANGQOTGOADKFEYTVTSCTKVTFASSGNGTTATVASKDDGNTTVKYDVNVGDA	300
QY	301	LNVNOLONGSNWLDKRAVAGSSGKATYISGVNPSFKGKMDTVINAGNNTIETFRNGKNIDI	360
QY	301	LNVNOLONGSNWLDKRAVAGSSGKATYISGVNPSFKGKMDTVINAGNNTIETFRNGKNIDI	360
QY	301	LNVNOLONGSNWLDKRAVAGSSGKATYISGVNPSFKGKMDTVINAGNNTIETFRNGKNIDI	360
QY	361	ATSMTPORSVSLGAGADAPLTSLVDEGLANVSGSDANKPVITITNAPVPEVKEDDVNVAQ	420
QY	361	ATSMTPORSVSLGAGADAPLTSLVDEGLANVSGSDANKPVITITNAPVPEVKEDDVNVAQ	420
QY	361	ATSMTPORSVSLGAGADAPLTSLVDEGLANVSGSDANKPVITITNAPVPEVKEDDVNVAQ	420
QY	421	LKGAQAQNNLRIDNVNNGNARAGIADAITAGLVQAQVLPKPSMAIATGGCTYLGEEAGYAIG	480
QY	421	LKGAQAQNNLRIDNVNNGNARAGIADAITAGLVQAQVLPKPSMAIATGGCTYLGEEAGYAIG	480
QY	421	LKGAQAQNNLRIDNVNNGNARAGIADAITAGLVQAQVLPKPSMAIATGGCTYLGEEAGYAIG	480
QY	481	SSISAGGWIITKGTASGNSRGHFGASASVGYOW	513
QY	481	SSISAGGWIITKGTASGNSRGHFGASASVGYOW	513
QY	481	SSISAGGWIITKGTASGNSRGHFGASASVGYOW	513

RESULT 9	
AA123738	
ID	AA123738 standard; Protein: 598 AA.
XX	
AC	
XX	AA123738:
DT	08-SEP-1999 (first entry)
XX	
DE	A surface protein of <i>Neisseria meningitidis</i> .
XX	
KM	Surface protein: surface glycoprotein; infection; vaccine;
XX	immunoreactive peptide.
XX	
OS	<i>Neisseria meningitidis</i> .
XX	
PN	W09931132-A1.
PD	
XX	24-JUN-1999.
PF	
XX	14-DEC-1998: 98WO-AU01031.
FR	
XX	12-DEC-1997: 97GB-0026398.
PA	(ISIS-) ISIS INNOVATION LTD.
XX	(UYOU ) UNIV QUEENSLAND.
PI	
XX	Jennings MP, Moxon ER, Peak IRA;
DR	
DR	WPI; 1999-418754/35.
DR	N-PSDB; AAX85790.
XX	
PT	<i>Neisseria meningitidis</i> surface proteins useful for treating <i>N.</i>
XX	<i>meningitidis</i> infections
PS	
XX	Claim 1; Page 91-93; 132pp; English.
CC	
CC	The present sequence represents a surface protein of <i>Neisseria</i>
CC	<i>meningitidis</i> which is approximately 62 kDa. The <i>N. meningitidis</i>
CC	surface glycoproteins, nucleic acids, the primers and optionally
CC	a thermostable polymerase, or antibodies are useful in a kit for
CC	the detection or diagnosis of <i>N. meningitidis</i> infection in humans
CC	The <i>N. meningitidis</i> surface glycoproteins can also be used to
CC	prevent or treat <i>N. meningitidis</i> infection in humans, especially





```

QY 96 TTVHLNGIGSTLTDLMLNTGATTNTNDNVTDEDEKKRAASVDVNLNAGNINIGVPGTTA 155
    |||||
Db 181 PTVHLNGIGSTLTDLMLNTGATTNTNDNVTDEDEKKRAASVDVNLNAGNINIGVPGTTA 240
QY 156 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVIGAKTSVIREKDGKLVYTGK 215
    |||||
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVIGAKTSVIREKDGKLVYTGK 300
QY 216 GENSGSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGTGQADKEFTVSGTKVTFASGN 275
    |||||
Db 301 GENSGSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGTGQADKEFTVSGTKVTFASGN 360
QY 276 GTTATVSKDQGNITVYKDVVNGDALNVNOLNSGWNLSKRAVAGSSGKVISGNVSPSKG 335
    |||||
Db 361 GTTATVSKDQGNITVYKDVVNGDALNVNOLNSGWNLSKRAVAGSSGKVISGNVSPSKG 420
QY 336 KMDFTVNINAGNNIETTRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 395
    |||||
Db 421 KMDFTVNINAGNNIETTRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
QY 396 DANKPVRTTNVAPGVKEGDTVNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLYQA 455
    |||||
Db 481 DANKPVRTTNVAPGVKEGDTVNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLYQA 540
QY 456 YLPGRKSMAAIGGCTYLGEGYGAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQM 513
    |||||
Db 541 YLPGRKSMAAIGGCTYRGEGYGAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 598

```

## RESULT 11

AAV23739

ID AAV23739 standard; Protein: 594 AA.

AAV23739;

08-SEP-1999 (first entry)

A surface protein of Neisseria meningitidis.

Surface protein; surface glycoprotein; infection; vaccine;

Immunoreactive peptide.

Neisseria meningitidis.

W09931132-A1.

24-JUN-1999.

14-DEC-1998; 98MO-AU01031.

12-DEC-1997; 97GB-0026398.

(ISIS-) ISIS INNOVATION LTD.

(UYOU ) UNIV QUEBENSLAND.

Jennings MP, Moxon ER, Peak IRA;

WPI: 1999-418754/35.

N-PSDB; AAX85791.

Neisseria meningitidis surface proteins useful for treating N.

meningitidis infections

Claim 1: Page 95-97; 132pp: English.

CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

SQ Sequence 594 AA:

Query Match 94.1%; Score 2448.5; DB 20; Length 594;  
 Best Local Similarity 83.2%; Pred. No. 1.7e-143;  
 Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

```

QY 1 MNKIRIITNSALNVAVSELTNRHTRASTVTAVALTLTFVQANATDE----- 54
    |||||
Db 1 MNKIRIITNSALNVAVSELTNRHTRASTVTAVALTLTFVQANATDDDLYLE 60
QY 55 ----- 54
Db 61 PVQRTAVVLSFRSDKEGTEGKEDSDSMWAVYFDEKRVLKACATILKAGDNLIKQNTNE 120
QY 55 -----TGLINMETEKLSEGANCKVNIISDTRKGLNFAKETAGTNGDTTVH 99
    |||||
Db 121 NTNDSFTYSLKKDLTLTSVETELSFGANCKVNIISDTRKGLNFAKETAGTNGDPTVH 180
QY 100 LMGISTLTDLMLNTGATTNTNDNVTDEDEKKRAASVDVNLNAGNINIGVPGTTASDNV 159
    |||||
Db 181 LMGISTLTDLMLNTGATTNTNDNVTDEDEKKRAASVDVNLNAGNINIGVPGTTASDNV 240
QY 160 DFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVIGAKTSVIREKDGKLVYTGKKGENG 219
    |||||
Db 241 DFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVIGAKTSVIREKDGKLVYTGKKGENG 300
QY 220 SSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGTGQADKEFTVSGTKVTFASGNGTTA 279
    |||||
Db 301 SSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGTGQADKEFTVSGTKVTFASGNGTTA 360
QY 280 TVSKDQGNITVYKDVVNGDALNVNOLNSGWNLSKRAVAGSSGKVISGNVSPSKGKDE 339
    |||||
Db 361 TVSKDQGNITVYKDVVNGDALNVNOLNSGWNLSKRAVAGSSGKVISGNVSPSKGKDE 420
QY 340 TVNINAGNNIETTRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 399
    |||||
Db 421 TVNINAGNNIETTRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480
QY 400 PVRTTNVAPGVKEGDTVNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLYQALPG 459
    |||||
Db 481 PVRTTNVAPGVKEGDTVNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLYQALPG 540
QY 460 KSMAAIGGCTYLGEGYGAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQM 513
    |||||
Db 541 KSMAAIGGDTYRGEGYGAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 594

```

## RESULT 12

AAU06179

ID AAU06179 standard; Protein: 594 AA.

AAU06179;

24-OCT-2001 (first entry)

N. meningitidis B2198 surface antigen Nhma polypeptide sequence.

Surface antigen Nhma; meningococcal disease; meningitis vaccine.

Neisseria meningitidis strain B2198.

Key Location/Qualifiers

FH Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..104

FT /label= V1

FT /note= "Variable region 1"

FT Region 105..116

FT /label= C2

[illegible]

QY	100	LNIGSGFLPDLMLNTCATNTNVINDNTDEKKRAASVDVYNAGNNIGVAPGTTASDNV	1599
Db	181	LNIGSLTDLTDLTLNLTGATNTNVINDNTDEKKRAASVDVYNAGNNIGVAPGTTASDNV	2404
QY	160	DFVRYDYVEFLSADTKRTTNTVNESKDNCKTEVKGAKTSVIREKDKLVTGKGKNG	2194
Db	241	DFVRYDYVEFLSADTKRTTNTVNESKDNCKTEVKGAKTSVIREKDKLVTGKGKNG	3000
QY	220	SSPDEBGLVTAKEVEIDAVNKAQWRKRTTANGQTGGADKREYTSQTKVTFASGNQTTA	2797
Db	301	SSPDEBGLVTAKEVEIDAVNKAQWRKRTTANGQTGGADKREYTSQTKVTFASGNQTTA	3600
QY	280	TVSKDDOQNTTVYDVNVGDALNVNOLQNSGNLDSKVAASSSGKVISGNVSPSKGKME	3399
Db	361	TVSKDDOQNTTVYDVNVGDALNVNOLQNSGNLDSKVAASSSGKVISGNVSPSKGKME	4200
QY	340	TVNINAGNNIEITRNKNKIDIAITSMPTQESSVSLGAGADAPTLVSDEGALNVGSKDANK	3999
Db	421	TVNINAGNNIEITRNKNKIDIAITSMPTQESSVSLGAGADAPTLVSDEGALNVGSKDANK	4800
QY	400	PVRITTVNVAQGVKEGDTVTNNAQLKGYAQNLNRRIDNVNNGNARAGIAQAATAGLVQAALPG	4599
Db	481	PVRITTVNVAQGVKEGDTVTNNAQLKGYAQNLNRRIDNVNNGNARAGIAQAATAGLVQAALPG	5400
QY	460	KSMMAIGGGYLYCEAGYVIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW	513
Db	541	KSMMAIGGGYLYCEAGYVIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW	594
RESULT 13			
ID	AAV23740	standard; protein; 594 AA.	
AC	AAV23740;		
XX			
DT	08-SEP-1999	(first entry)	
XX			
DE	A surface protein of Neisseria meningitidis.		
XX			
KM	Surface protein; surface glycoprotein; infection; vaccine;		
XX			
OS	Neisseria meningitidis.		
XX			
PN	WO9931132-A1.		
XX			
PD	24-JUN-1999.		
XX			
PF	14-DEC-1998;	98WO-AU01031.	
XX			
PR	12-DEC-1997;	97GB-0026398.	
XX			
PA	(ISIS-) ISIS INNOVATION LTD.		
XX	(UYOU) UNIV QUEENSLAND.		
XX			
P1	Jennings MP, Moxon ER, Peak IRA;		
DR	WPI, 1999-418754/35.		
XX			
DR	N-PSDB; AAB5792.		
PT	Neisseria meningitidis surface proteins useful for treating N.		
XX	meningitidis infections		
ES	Claim 1; Page 100-101; 132pp; English.		
CC	The present sequence represents a surface protein of Neisseria		
CC	meningitidis which is approximately 62 kDa. The N. meningitidis		
CC	surface glycoproteins, nucleic acids, the primers and optionally		
CC	a thermostable polymerase, or antibodies are useful in a kit for		
CC	the detection or diagnosis of N. meningitidis infection in humans.		
CC	The N. meningitidis surface glycoproteins can also be used to		
CC	prevent or treat N. meningitidis infection in humans, especially		



Db 421 TVNINAGNNIETIRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNNGSKDANK 480  
 QY 400 PVRITNVAPGKEDGYTNVAQLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPG 459  
 Db 481 PVRITNVAPGKEDGYTNVAQLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPG 540  
 QY 460 KSMMAIGGGTYLGEAGYATGYSISAGGNNIIGTASGNSRGHFGASASVGYOW 513  
 Db 541 KSMMAIGGGTYLGEAGYATGYSISAGGNNIIGTASGNSRGHFGASASVGYOW 594  
 RESULT 15  
 AAU06174  
 ID AAU06174 standard; protein: 594 AA.  
 AC AAU06174;  
 XX  
 DE 24-OCT-2001 (first entry)  
 DE N. meningitidis EG327 surface antigen Nhma polypeptide sequence.  
 KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain EG327.  
 XX  
 FH Key  
 FH Location/Qualifiers  
 FT 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..104  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 105..116  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 117..126  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT 127..190  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 191..212  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 213..231  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 232..238  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 239..594  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 FT  
 FT  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI; 2001-488774/53.  
 DR N-PSDB; AAS09164.  
 XX  
 PT New Nhma surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9; Fig 1; 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhma  
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhma  
 CC from N. meningitidis strain EG327 is 1 of 10 Nhma polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX  
 SQ Sequence 594 AA;  
 Query Match 92.6%; Score 2409.5; DB 22; Length 594;  
 Best Local Similarity 82.0%; Pred. No. 4.5e-141;  
 Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;  
 QY 1 MNKIRIYNSALNANVAVSELTRNHTKRASATVAATLTFATVQANATDE----- 54  
 Db 1 MNKIRIYNSALNANVAVSELTRNHTKRASATVAATLTFATVQASTDDDDLYLE 60  
 QY 55 ----- 54  
 Db 61 PVORTAVVLSFRBDEKGTGKEVTEDSNMGVYRDKKGVLTAGTITLTKAGDNLIKONTNE 120  
 QY 55 -----TGLINVEETKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTYVH 99  
 Db 121 NTNASSFTYSLKRDLDLTSVGTETKLSFSANSKVNITSDTKGLNFAKKAETRNGDTYVH 180  
 QY 100 LINGISTLTPMLNTGATTWTDNTYDDEKRAAAYKDYLANGNINIKYKPGTTASDNY 159  
 Db 181 LINGISTLTPMLNTGATTWTDNTYDDEKRAAAYKDYLANGNINIKYKPGTTASDNY 240  
 QY 160 DFRVTDYVEFLSADRTTIVNESKDKNGKKTVEKIGAKTSVIREKDGKLVTKGGENG 219  
 Db 241 DFRVTDYVEFLSADRTTIVNESKDKNGKKTVEKIGAKTSVIREKDGKLVTKGGEND 300  
 QY 220 SSTDEGEGLYTAKEVIDAVNKAAGRMKTTANGOTQADKFEVTSCTVTFASNGGTGA 279  
 Db 301 SSTDEGEGLYTAKEVIDAVNKAAGRMKTTANGOTQADKFEVTSCTVTFASNGGTGA 360  
 QY 280 TVSKDDOGNTTVKYDVNVDGALVNOLONGNMLDSKAVSGSGXYISGNVSPSKGKME 339  
 Db 361 TVSKDDOGNTTVKYDVNVDGALVNOLONGNMLDSKAVSGSGXYISGNVSPSKGKME 420  
 QY 340 TVNINAGNNIETIRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNNGSKDANK 399  
 Db 421 TVNINAGNNIETIRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNNGSKDANK 480  
 QY 400 PVRITNVAPGKEDGYTNVAQLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPG 459  
 Db 481 PVRITNVAPGKEDGYTNVAQLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPG 540  
 QY 460 KSMMAIGGGTYLGEAGYATGYSISAGGNNIIGTASGNSRGHFGASASVGYOW 513  
 Db 541 KSMMAIGGGTYLGEAGYATGYSISAGGNNIIGTASGNSRGHFGASASVGYOW 594

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 Job time : 46.0542 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 13.7186 Seconds  
(without alignments)  
1582.188 Million cell updates/sec

Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKIRIIMNSALNMAVAVS.....TASGNSRCHFGASASVGYQW 513

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCtUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2552.5	98.1	592	US-09-377-155-17	Sequence 17, Appl
2	2552.5	98.1	592	US-09-669-974-17	Sequence 17, Appl
3	2472	95.0	599	US-09-377-155-15	Sequence 15, Appl
4	2472	95.0	599	US-09-669-974-15	Sequence 15, Appl
5	2460.5	94.6	598	US-09-377-155-13	Sequence 13, Appl
6	2460.5	94.6	598	US-09-669-974-13	Sequence 13, Appl
7	2451.5	94.2	598	US-09-377-155-5	Sequence 5, Appl
8	2451.5	94.2	598	US-09-669-974-5	Sequence 5, Appl
9	2448.5	94.1	594	US-09-377-155-7	Sequence 7, Appl
10	2448.5	94.1	594	US-09-669-974-7	Sequence 7, Appl
11	2409.5	92.6	594	US-09-377-155-9	Sequence 9, Appl
12	2409.5	92.6	594	US-09-669-974-9	Sequence 9, Appl
13	2407	92.5	591	US-09-377-155-21	Sequence 21, Appl
14	2407	92.5	591	US-09-669-974-21	Sequence 21, Appl
15	2402.5	92.3	592	US-09-377-155-2	Sequence 2, Appl
16	2402.5	92.3	592	US-09-669-974-2	Sequence 2, Appl
17	2395	92.0	591	US-09-377-155-11	Sequence 11, Appl
18	2395	92.0	591	US-09-669-974-11	Sequence 11, Appl
19	2314	88.9	589	US-09-377-155-19	Sequence 19, Appl
20	2314	88.9	589	US-09-669-974-19	Sequence 19, Appl
21	981.5	37.7	1094	US-09-268-347-32	Sequence 32, Appl
22	966.5	37.1	1098	US-08-409-995-2	Sequence 2, Appl
23	966.5	37.1	1098	US-08-685-467-2	Sequence 2, Appl
24	966.5	37.1	1098	US-09-377-155-32	Sequence 32, Appl
25	966.5	37.1	1098	US-08-913-942-2	Sequence 2, Appl
26	966.5	37.1	1098	US-09-669-974-32	Sequence 32, Appl
27	966.5	37.1	1098	US-09-268-347-44	Sequence 44, Appl

28	963.5	37.0	658	US-08-409-995-5	Sequence 5, Appl
29	963.5	37.0	658	US-08-685-467-5	Sequence 5, Appl
30	963.5	37.0	658	US-08-913-942-5	Sequence 5, Appl
31	941.5	36.2	2411	US-09-268-347-36	Sequence 36, Appl
32	939.5	36.1	2353	US-09-377-155-33	Sequence 33, Appl
33	939.5	36.1	2353	US-08-913-942-4	Sequence 4, Appl
34	939.5	36.1	2353	US-09-669-974-33	Sequence 33, Appl
35	938.5	36.1	2354	US-09-268-347-47	Sequence 47, Appl
36	882	33.9	607	US-08-409-995-6	Sequence 6, Appl
37	882	33.9	607	US-08-685-467-6	Sequence 6, Appl
38	882	33.9	607	US-08-913-942-6	Sequence 6, Appl
39	882	33.9	1912	US-08-409-995-4	Sequence 4, Appl
40	882	33.9	1912	US-08-685-467-4	Sequence 4, Appl
41	761	29.2	679	US-08-913-942-15	Sequence 15, Appl
42	761	29.2	679	US-09-268-347-26	Sequence 26, Appl
43	685.5	26.3	1002	US-09-268-347-24	Sequence 24, Appl
44	668.5	25.7	1004	US-09-268-347-30	Sequence 30, Appl
45	562.5	21.6	1104	US-09-268-347-28	Sequence 28, Appl

## ALIGNMENTS

RESULT 1					
US-09-377-155-17					
Sequence 17, Application US/09377155					
Patent No. 6197312					
GENERAL INFORMATION:					
APPLICANT: PEAK, Ian Richard Anselm					
APPLICANT: JENNINGS, Michael Paul					
APPLICANT: MOXON, E. Richard					
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN					
FILE REFERENCE: 065064/0128					
CURRENT APPLICATION NUMBER: US/09/377,155					
CURRENT FILING DATE: 1999-08-19					
PRIOR APPLICATION NUMBER: PCT/AU98/01031					
PRIOR FILING DATE: 1998-12-14					
PRIOR APPLICATION NUMBER: GB 9726398.2					
PRIOR FILING DATE: 1997-12-12					
NUMBER OF SEQ ID NOS: 33					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 17					
LENGTH: 592					
TYPE: PRT					
ORGANISM: Neisseria meningitidis					
US-09-377-155-17					
Query Match					
Best Local Similarity 98.1%; Score 2552.5; DB 3; Length 592;					
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;					
QY	1	MNKIRIIMNSALNMAVAVSELTRNHTKRASTVTAVALTLLEFVQANATDE-----	54		
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QY	55	-----TGLINVEFEKLSFGANGKRVNIISDTKGLNFAKTAGTNGDTTHLN	101		
DB	61	ESVQSVYGSIOASMEGSEVELETTLSMTNDSKEVDYIYVTLAKAGDNLTAKONTNENT	120		
QY	55	-----TGLINVEFEKLSFGANGKRVNIISDTKGLNFAKTAGTNGDTTHLN	101		
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QY	102	GIGSLTTLMLNTGATTTVNDVYDDEKRRASVKDVLNMGWNIKGVKPGTTASDNDVF	161		
DB	181	GIGSLTTLMLNTGATTTVNDVYDDEKRRASVKDVLNMGWNIKGVKPGTTASDNDVF	240		
QY	162	VRTYTVFELSDTFTTVNVEKNGKTEKIGAKTSVIEKDGKLVYTGKGENSS	221		
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QY	222	TDEGGLVTAAEVIDAVKAGWRMTTANGQTGADFEFVYTSQTKVTFASGNGTATV	281		

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Db 361 SKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGKDETV 420
Qy 342 NINAGNNIETRRGNKIDATSMTPQFSSVSLGAGADAPLTVDDGALNVGSKDANKPV 401
Db 421 NINAGNNIETRRGNKIDATSMTPQFSSVSLGAGADAPLTVDDGALNVGSKDANKPV 480
Qy 402 RINNVAPGVKEGVDVTVNAOLKGVAQNLNRRIDNVNNGNARAGIAQALATATAGLYVAPLPGKS 461
Db 481 RINNVAPGVKEGVDVTVNAOLKGVAQNLNRRIDNVNNGNARAGIAQALATAGLYVAPLPGKS 540
Qy 462 MMAIGGTYLGEAGVAIGYSSISAGGNWIIKGTASGNSRCHFGASASVGYOW 513
Db 541 MMAIGGTYLGEAGVAIGYSSISAGGNWIIKGTASGNSRCHFGASASVGYOW 592
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RESULT 2
US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 592
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-669-974-17
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Query Match 98.1%; Score 2552.5; DB 4; Length 592;
Best Local Similarity 86.7%; Pred. No. 8.8e-196;
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
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Qy 55 ----- 54
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Db 121 MASSFTYSLKDKLTGLINVEETKLSFGANGKKNYIISDTKGLNFAKETAGTNGDTVHLN 180
Qy 102 GIGSTLTDLMLNTGATTNTNDVTDDEKKRAASVYKDVYLNAGNNIKGVPKGTJASDNVDF 161
Db 181 GIGSTLTDLMLNTGATTNTNDVTDDEKKRAASVYKDVYLNAGNNIKGVPKGTJASDNVDF 240
Qy 162 VRTYDVEEFLSADTKTTTVNVESEKDKGKTEYKIGAKTSVIREKDGKLVYTGKKGENGSS 221
Db 241 VRTYDVEEFLSADTKTTTVNVESEKDKGKTEYKIGAKTSVIREKDGKLVYTGKKGENGSS 300
Qy 222 TDGEGELVTAKEVIDAVNKAQRMKTTTANGOTGQADKFEFTVSGTKVTFASNGTTATV 281
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Qy 342 NINAGNNIETRRGNKIDATSMTPQFSSVSLGAGADAPLTVDDGALNVGSKDANKPV 401
Db 421 NINAGNNIETRRGNKIDATSMTPQFSSVSLGAGADAPLTVDDGALNVGSKDANKPV 480
Qy 402 RINNVAPGVKEGVDVTVNAOLKGVAQNLNRRIDNVNNGNARAGIAQALATATAGLYVAPLPGKS 461
Db 481 RINNVAPGVKEGVDVTVNAOLKGVAQNLNRRIDNVNNGNARAGIAQALATAGLYVAPLPGKS 540
Qy 462 MMAIGGTYLGEAGVAIGYSSISAGGNWIIKGTASGNSRCHFGASASVGYOW 513
Db 541 MMAIGGTYLGEAGVAIGYSSISAGGNWIIKGTASGNSRCHFGASASVGYOW 592
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US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 15
; LENGTH: 599
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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Query Match 95.0%; Score 2472; DB 3; Length 599;
Best Local Similarity 83.1%; Pred. No. 2.4e-189;
Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;
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Qy 55 ----- 54
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Qy 55 -----TGLINVEETKLSFGANGKKNYIISDTKGLNFAKETAGTNG 94
Db 121 KNTNENTNDSFTYSLKDKLTDLTSVETKLSFGANGKKNYIISDTKGLNFAKETAGTNG 180
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Db 181 DTTVHLNGTSTLTDLMLNTGATTNTNDVTDDEKKRAASVYKDVYLNAGNNIKGVPKGTJ 240
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Db	481	KDANKPVITVNAFVGKEDVTVNAOLGVANOLNRIIDVNGNRAIGIAIATAGLVQ	540
QY	455	AYLPKSSMAAIGGGTYLGEAGYATGYSISAGNWIIGTASGNSRGHFGASASVGYOM	513
Db	541	AYLPKSSMAAIGGGTYRREAGYATGYSISIDSGNMWIKGTASGNSRGHFGASASVGYOM	599
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US-09-669-974-15			
; Sequence 15, Application US/09669974			
; Patent No. 6333173			
GENERAL INFORMATION:			
; APPLICANT: PEAK, Ian Richard Anselm			
; APPLICANT: JENNINGS, Michael Paul			
; APPLICANT: MOXON, E. Richard			
; TITLE OF INVENTION: NOVEL SUDFACE ANTIGEN			
; FILE REFERENCE: 065064/0128			
; CURRENT APPLICATION NUMBER: US/09/669, 974			
; CURRENT FILING DATE: 2000-09-26			
; PRIOR APPLICATION NUMBER: US 09/377,155			
; PRIOR FILING DATE: 1999-08-19			
; PRIOR APPLICATION NUMBER: PCT/AU98/01031			
; PRIOR FILING DATE: 1998-12-14			
; PRIOR APPLICATION NUMBER: GB 9726398.2			
; PRIOR FILING DATE: 1997-12-12			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 15			
; LENGTH: 599			
; TYPE: PRT			
; ORGANISM: Neisseria meningitidis			
US-09-669-974-15			
Query Match 95.0%; Score 2472; DB 4; Length 599;			
Best Local Similarity 83.1%; Pred. No. 2.4e-189;			
Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;			
QY	1	MNKYIRIIMNSALNMAVAVSELRNHRNRKASATYKTAVALATLLEFATVOANATDE-----	54
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QY	55	-----TGLINVERTEKLSFGANGKRVNIIISPTKRLNFAKETAGNG	94
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QY	95	DTVHALNGISLTLDMLNTGATTNVTNDNTYDDEKKRAASVKYDLNAGWNLIKGVPGTT	154
Db	181	DTVHALNGISLTLDMLNTGATTNVTNDNTYDDEKKRAASVKYDLNAGWNLIKGVPGTT	240
QY	155	ASDNVDFRITDYVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVIREKDGKLVYGG	214
Db	241	ASDNVDFRITDYVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVIREKDGKLVYGG	300
QY	215	KGENSSSTDEGGIYTAKEVIDAVNKAAGMRKTTTANGOTQADKEFTVTSGTNTPFASG	274
Db	301	KGENSSSTDEGGIYTAKEVIDAVNKAAGMRKTTTANGOTQADKEFTVTSGTNTPFASG	360
QY	275	NGTATVSKDQGNITTVYDVNVGDLVNVNOLONGNMLDLSKAVNGSSGKYISGNVSPSK	334
Db	361	KGTATVSKDQGNITTVYDVNVGDLVNVNOLONGNMLDLSKAVNGSSGKYISGNVSPSK	420
QY	335	GKMDFTVINAGNNIETIRNRGNKNDIDATSMTPPOSSVSLGAGADAPTLVSUDEGALNVS	394

Db	421	GKMDETVINAGANNIETTRNGKNIDIAISMTPESSSVSLGACADAPTLISVDDKALNWS	480
Qy	395	KDANKPVRITTNVAPGVEKGEVDYTNVAQLKGVANQLNNRIDNWNGNARAGIAQAIATAGLVQ	454
Db	481	KDANKPVRITTNVAPGVEKGEVDYTNVAQLKGVANQLNNRIDNWDGNARAGIAQAIATAGLVQ	540
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US-09-377-155-13			
; Sequence 13, Application US/09377155			
; Patent No. 6197312			
GENERAL INFORMATION:			
; APPLICANT: PEAK, Ian Richard Anselm			
; APPLICANT: JENNINGS, Michael Paul			
; APPLICANT: MOXON, E. Richard			
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN			
; FILE REFERENCE: 065064/0128			
; CURRENT APPLICATION NUMBER: US/09/377, 155			
; CURRENT FILING DATE: 1999-08-19			
; PRIOR APPLICATION NUMBER: PCT/AU98/01031			
; PRIOR FILING DATE: 1998-12-14			
; PRIOR APPLICATION NUMBER: GB 9726398.2			
; PRIOR FILING DATE: 1997-12-12			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 13			
; LENGTH: 598			
; TYPE: PRT			
; ORGANISM: Neisseria meningitidis			
US-09-377-155-13			
Query Match	94.6%;	Score 2460.5;	DB 3; Length 598;
Best Local Similarity	82.9%;	Pred. No. 2e-188;	
Matches 496;	Conservative 4;	Mismatches 13;	Indels 85; Gaps 1.
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Db	1	MNKIYRIIWSALNMAVAVSELTTRNHTKRASATYKTAVALATLLFATVOANATDDDDLYLE	60
Qy	55	-----	54
Db	61	PVQRTAAVVLSPRSDEGTGEGKCTEDSMWAVYFDEKRYLKKAGIITLAKGDNLIKONTNE	120
Qy	55	-----TGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGD	95
Db	121	NTNENTNDSFPTYSLKDKLTDLTLSVETEKLSFGANGKNVNIISDPTKGLNFAKETAGTNGD	180
Qy	96	TTVHNLNGISPTLTDKLLMTNGATTNTNTNNVTDDEKKRAASVADVILNAGNNIKGVAPGTTA	155
Db	181	PTVHLNGISPTLTDKLLMTNGATTNTNDVTDDEKKRAASVADVILNAGNNIKGVAPGTTA	240
Qy	156	SDNVDFVPTYDYVEFLSADFTKTTYNVESKDKNGKTEYKIGAKTSVIREKDGKLTVYGKX	215
Db	241	SDNVDFVPTYDYVEFLSADFTKTTYNVESKDKNGKTEYKIGAKTSVIREKDGKLTVYGKX	300
Qy	216	GENGSSTDEGBEGLVAKEVIDAVNRKAGRMKTTTANGOTGADKFEYVTSGTVFPASGN	275
Db	301	DENGSSSTDEGBEGLVAKEVIDAVNRKAGRMKTTTANGOTGADKFEYVTSGTVFPASGN	360
Qy	276	GTTAAVSKDDGNTIVKVDVNVGDLANNQNLONSSMNLDISKVAASSGKVVISGNVSPSGK	335
Db	361	GTTAAVSKDDGNTIVKVDVNVGDLANNQNLONSSMNLDISKVAASSGKVVISGNVSPSGK	420
Qy	336	KMDETVNINAGNNIEITRNGKNIDIAISMTPESSSVSLGACADAPTLISVDDGALNWSGK	395
Db	421	KMDETVNINAGNNIEITRNGKNIDIAISMTPESSSVSLGACADAPTLISVDDGALNWSGK	480
Qy	396	DANKPVRITTNVAPGVEKGEVDYTNVAQLKGVANQLNNRIDNWNGNARAGIAQAIATAGLVQ	455

Db 481 DANKPVRTINVAAGVEGDTYNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 540  
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Db 541 YLPKSMMAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 6  
US-09-669-974-13  
; Sequence 13, Application US/0966974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; LENGTH: 598  
; TYPE: PRM  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 94.6%; Score 2460.5; DB 4; Length 598;  
Best Local Similarity 82.9%; Pred. No. 2e-188;  
Matches 496; Conservative 4; Mismatches 13; Indels 85; Gaps 1;

QY 1 MNKIYRIIMNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDE----- 54  
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Db 61 PVORTAVVLSFRSDEKGEKTEGEDSNNVAVFDEKRVLKAGAITLKAGDNLIKONTNE 120  
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Db 121 NTNENTNDSSFTYSLKRDLDLTSVETEKLSFGANGKVNIIISDTGKLNPAKETAAGTNGD 180  
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Db 181 PTVHLNGIGSTLTDLTLNLTGATTNVTNDVNTDDEKKRAASVKDVLNAGNMNIKGVKPGTTA 240  
QY 156 SDNVDFVRRTDYVEFLSADTKTTTVNVEESKDNKTEVKGAKTSYIKERDGLVYGK 215  
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Db 241 SDNVDFVRRTDYVEFLSADTKTTTVNVEESKDNKTEVKGAKTSYIKERDGLVYGK 300  
QY 216 GENGSSTDEBEGVLTAKEVIDAVNKAQWRRKTTTANGQTQADKFEFTVSGTVTFASGN 275  
|||||  
Db 301 DENGSSTDEBEGVLTAKEVIDAVNKAQWRRKTTTANGQTQADKFEFTVSGTVTFASGN 360  
QY 276 GTTATVSKDDQGNITVKYDVNVDALNVNOLQNSGNNLDSKAVAGSSGKVISGNVSPSKG 335  
|||||  
Db 361 GTTATVSKDDQGNITVKYDVNVDALNVNOLQNSGNNLDSKAVAGSSGKVISGNVSPSKG 420  
QY 336 KMEETVNNAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDDEGALNVGSK 395  
|||||  
Db 421 KMEETVNNAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDDEGALNVGSK 480  
QY 396 DANKPVRTINVAAGVEGDTYNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 455  
|||||  
Db 481 DANKPVRTINVAAGVEGDTYNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 540

QY 456 YLPKSMMAIGGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVGYQW 513  
Db 541 YLPKSMMAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 7  
US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377, 155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; LENGTH: 598  
; TYPE: PRM  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 94.2%; Score 2451.5; DB 3; Length 598;  
Best Local Similarity 82.6%; Pred. No. 1e-187;  
Matches 494; Conservative 5; Mismatches 14; Indels 85; Gaps 1;

QY 1 MNKIYRIIMNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDE----- 54  
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Db 1 MNKIYRIIMNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDDDLYLE 60  
55 ----- 54  
Db 61 PVORTAVVLSFRSDEKGEKTEGEDSNNVAVFDEKRVLKAGAITLKAGDNLIKONTNE 120  
QY 55 -----TGLINVEETEKLSFGANGKVNIIISDTGKLNPAKETAAGTNGD 95  
|||||  
Db 121 NTNENTNDSSFTYSLKRDLDLTSVETEKLSFGANGKVNIIISDTGKLNPAKETAAGTNGD 180  
QY 96 TTVHLNGIGSTLTDMNLNLTGATTNVTNDVNTDDEKKRAASVKDVLNAGNMNIKGVKPGTTA 155  
|||||  
Db 181 PTVHLNGIGSTLTDLTLNLTGATTNVTNDVNTDDEKKRAASVKDVLNAGNMNIKGVKPGTTA 240  
QY 156 SDNVDFVRRTDYVEFLSADTKTTTVNVEESKDNKTEVKGAKTSYIKERDGLVYGK 215  
|||||  
Db 241 SDNVDFVRRTDYVEFLSADTKTTTVNVEESKDNKTEVKGAKTSYIKERDGLVYGK 300  
QY 216 GENGSSTDEBEGVLTAKEVIDAVNKAQWRRKTTTANGQTQADKFEFTVSGTVTFASGN 275  
|||||  
Db 301 GENGSSTDEBEGVLTAKEVIDAVNKAQWRRKTTTANGQTQADKFEFTVSGTVTFASGN 360  
QY 276 GTTATVSKDDQGNITVKYDVNVDALNVNOLQNSGNNLDSKAVAGSSGKVISGNVSPSKG 335  
|||||  
Db 361 GTTATVSKDDQGNITVKYDVNVDALNVNOLQNSGNNLDSKAVAGSSGKVISGNVSPSKG 420  
QY 336 KMEETVNNAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDDEGALNVGSK 395  
|||||  
Db 421 KMEETVNNAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDDEGALNVGSK 480  
QY 396 DANKPVRTINVAAGVEGDTYNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 455  
|||||  
Db 481 DANKPVRTINVAAGVEGDTYNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 540  
QY 456 YLPKSMMAIGGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVGYQW 513  
|||||  
Db 541 YLPKSMMAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYQW 598



RESULT 8  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRF  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 94.2%; Score 2451.5; DB 4; Length 598;  
Best Local Similarity 82.6%; Pred. No. 1e-187;  
Matches 494; Conservative 5; Mismatches 14; Indels 85; Gaps 1;  
QY 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVATATLTLFATVOANATDE----- 54  
DB 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVATATLTLFATVOANATDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVORTAVLSRSDKEGEGEKEGEDSMMNAVYFDEKRVLKAGATILKAGDMLKIKONTNE 120  
QY 55 ----- 54  
DB 121 NTNDSFTYSLKDDTLDTLTSVEFEKLSFGANGKNVNITSDTKGLNFAKETAGTNDP 180  
QY 96 TTVHANGISLTDLMLNTGATNTVNDVNDYDDEKRRASVADVLNAGMNKGVKPGTTA 155  
DB 181 PTVHANGISLTDLMLNTGATNTVNDVNDYDDEKRRASVADVLNAGMNKGVKPGTTA 240  
QY 156 SDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTEYKIGAKTSVIREKDKLVTKGK 215  
DB 241 SDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTEYKIGAKTSVIREKDKLVTKGK 300  
QY 216 GENSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTKYTFASGN 275  
DB 301 GENSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTKYTFASGN 360  
QY 276 GTTAVSKDDGNTTVKTDVNVGDLANNQLONSGMNDSKAVASSSGKVISGNVSPK 335  
DB 361 GTTAVSKDDGNTTVKTDVNVGDLANNQLONSGMNDSKAVASSSGKVISGNVSPK 420  
QY 336 KMDFTVINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 395  
DB 421 KMDFTVINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 480  
QY 396 DANKPVRTTNVAPGVKBEVDVNVQOLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQA 455  
DB 481 DANKPVRTTNVAPGVKBEVDVNVQOLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQA 540  
QY 456 YLPKSMMAIGGTYLGEAGYAGYSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 513  
DB 541 YLPKSMMAIGGTYLGEAGYAGYSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 598

RESULT 9

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRF  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 94.1%; Score 2448.5; DB 3; Length 594;  
Best Local Similarity 83.2%; Pred. No. 1.8e-187;  
Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;  
QY 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVATATLTLFATVOANATDE----- 54  
DB 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVATATLTLFATVOANATDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVORTAVLSRSDKEGEGEKEGEDSMMNAVYFDEKRVLKAGATILKAGDMLKIKONTNE 120  
QY 55 ----- 54  
DB 121 NTNDSFTYSLKDDTLDTLTSVEFEKLSFGANGKNVNITSDTKGLNFAKETAGTNDP 180  
QY 100 LNGISLTDLMLNTGATNTVNDVNDYDDEKRRASVADVLNAGMNKGVKPGTTASNV 159  
DB 181 LNGISLTDLMLNTGATNTVNDVNDYDDEKRRASVADVLNAGMNKGVKPGTTASNV 240  
QY 160 DFVRYDTVEFLSADTKTTTVNVEKDKNGKTEYKIGAKTSVIREKDKLVTKGKENG 219  
DB 241 DFVRYDTVEFLSADTKTTTVNVEKDKNGKTEYKIGAKTSVIREKDKLVTKGKENG 300  
QY 220 SSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTKYTFASGN 279  
DB 301 SSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTKYTFASGN 360  
QY 280 TVSKDDGNTTVKTDVNVGDLANNQLONSGMNDSKAVASSSGKVISGNVSPK 339  
DB 361 TVSKDDGNTTVKTDVNVGDLANNQLONSGMNDSKAVASSSGKVISGNVSPK 420  
QY 340 TVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 399  
DB 421 TVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 480  
QY 400 PVRTTNVAPGVKBEVDVNVQOLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQAYLPG 459  
DB 481 PVRTTNVAPGVKBEVDVNVQOLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQAYLPG 540  
QY 460 KSMMAIGGTYLGEAGYAGYSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 513  
DB 541 KSMMAIGGTYLGEAGYAGYSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 10  
US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 594  
TYPE: PRN  
ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 94.1%; Score 2448.5; DB 4; Length 594;  
Best Local Similarity 83.2%; Pred. No. 1.8e-187;  
Matches 444; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

QY 1 MNKIRIIMNSALNMAVAVSELTNRHTKRASATVKTAVLATILFATVOANATDE----- 54  
DB 1 MNKIRIIMNSALNMAVAVSELTNRHTKRASATVKTAVLATILFATVOANATDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVQRTAVVLSFSDKEGTEGKEGEDSNNMAYFDEKRVLAKAGITLAKADNLKIKONTNE 120  
QY 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 99  
DB 121 NTNASSFTYSLKKDLTLDSVTEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 180  
QY 100 LNCIGSTLMDLNTGATNTVNDVNTDDEKRAASVKDVLNAGNMIKGVKPGTASDNV 159  
DB 181 LNCIGSTLMDLNTGATNTVNDVNTDDEKRAASVKDVLNAGNMIKGVKPGTASDNV 240  
QY 160 DFRRTDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKEDGKLVYTGKGEENG 219  
DB 241 DFRRTDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKEDGKLVYTGKGEENG 300  
QY 220 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVYSGTFTFASGNGTGA 279  
DB 301 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVYSGTFTFASGNGTGA 360  
QY 280 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLSKAVAGSSGKVISGNVSPSKGKMD 339  
DB 361 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLSKAVAGSSGKVISGNVSPSKGKMD 420  
QY 340 TVNINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNVSCKDANK 399  
DB 421 TVNINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNVSCKDANK 480  
QY 400 PVRTNVAVGVEGDTNVNVAOLKGVQNONNRIIDNVNNGARAGIAQAITAGIYQAYLPG 459  
DB 481 PVRTNVAVGVEGDTNVNVAOLKGVQNONNRIIDNVNNGARAGIAQAITAGIYQAYLPG 540  
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGNMIKGTASGNSRGHFGASASVGYOW 513  
DB 541 KSMMAIGGTYLGEAGYAIGYSSISAGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 11  
US-09-377-155-9  
Sequence 9, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 594  
TYPE: PRN  
ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 92.6%; Score 2409.5; DB 3; Length 594;  
Best Local Similarity 82.0%; Pred. No. 2.3e-184;  
Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

QY 1 MNKIRIIMNSALNMAVAVSELTNRHTKRASATVKTAVLATILFATVOANATDE----- 54  
DB 1 MNKIRIIMNSALNMAVAVSELTNRHTKRASATVKTAVLATILFATVOASTTDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVQRTAVVLSFSDKEGTEGKEGEDSNNMAYFDEKRVLAKAGITLAKADNLKIKONTNE 120  
QY 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 99  
DB 121 NTNASSFTYSLKKDLTLDSVTEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 180  
QY 100 LNCIGSTLMDLNTGATNTVNDVNTDDEKRAASVKDVLNAGNMIKGVKPGTASDNV 159  
DB 181 LNCIGSTLMDLNTGATNTVNDVNTDDEKRAASVKDVLNAGNMIKGVKPGTASDNV 240  
QY 160 DFRRTDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKEDGKLVYTGKGEENG 219  
DB 241 DFRRTDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKEDGKLVYTGKGEENG 300  
QY 220 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVYSGTFTFASGNGTGA 279  
DB 301 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVYSGTFTFASGNGTGA 360  
QY 280 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLSKAVAGSSGKVISGNVSPSKGKMD 339  
DB 361 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLSKAVAGSSGKVISGNVSPSKGKMD 420  
QY 340 TVNINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNVSCKDANK 399  
DB 421 TVNINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALNVSCKDANK 480  
QY 400 PVRTNVAVGVEGDTNVNVAOLKGVQNONNRIIDNVNNGARAGIAQAITAGIYQAYLPG 459  
DB 481 PVRTNVAVGVEGDTNVNVAOLKGVQNONNRIIDNVNNGARAGIAQAITAGIYQAYLPG 540  
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGNMIKGTASGNSRGHFGASASVGYOW 513  
DB 541 KSMMAIGGTYLGEAGYAIGYSSISAGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 12  
US-09-669-974-9  
Sequence 9, Application US/09669974  
Patent No. 6333173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974

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; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 21
; LENGTH: 591
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
; US-09-377-155-21

```

Query Match	92.5%	Score 2407;	DB 3;	length 591;
Best Local Similarity	82.6%;	Pred. No. 3.7e-184;		
Matches 489; Conservative	5;	Mismatches 18;	Indels 80;	Gaps 2

QY 55 ----- 54

0Y 55 -----TGLINVETEKISFGANGKVNISDTKGLINFAKETAGTNGDTVHLN 101

Db 121 NGTFYSLKLDLDLTSVCTEKLSFSANCKVNTSDTGLNFAKETAGTNGDTVHLN 180

102 GIGSTLTDMLLNMGATTNVTNDNVTDDDEKKRAASYKVDVLNAGWNIKGVKPGTTASDNVDF 161

Db 181 GIGSTLDTLLNTGATTNNTNDNTDDEKKRAASYKVDYLNAGWNIKGVKPGTTASDNDVF 240

QY 162 VRFYDVEELSDPTKTTTVNVEESKNGKTEVRIKAKTSVIKERDGLVTGKGKENGSS 221

Db 241 VRTYDIVEELSDADTKTTTVNVEKDKGKTEVIGAKTSVIAKEKDKLVTKGDKGNGSS 300

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0Y      222 TDEBGLTAKEVDAVNKAGWRKTTTANGQTGQADKEVTSTKVFASGNITTAFV 281
|||||
0Y      TDEBGLTAKEVDAVNKAGWRKTTTANGQTGQADKEVTSTKVFASGNITTAFV 280
|||||

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283 SKDDOGNTVMKVDNVGDAI NMINOT ONSGNI DSKAVAGSSGKYV SCNVSSDSKGMDETV 341  
DB 301 TDEEGELVAKELDAVAVNKGWRMKTTTANGQIQADKEETVIGSTNVIFASGKTTAV 360

Db 361 SKDDSGITVYMDVNNKDALNVMOLNDSGNINLDSRAVAGSSSGKVIISGVNPSRSGKMDFTV 420

342 NINAGNNIETTRNGCNIDATSMPOFSSVSLGAGADAPTLVSUDEGALVNGSKDANKPV 401

Db 421 NINAGNIETFRGNIDITATSMTPQFSSVSLGACADAPTLSVDGD-ALNWGSKKDNKPV 479

402 RITNPAPGYKEGDVTNVAQLKGVAQNLRNRIDNTNGNARAGIAQAIAATAGLVQAYLPKGS 461

Db  
480 RITNVPGVKEGDVTNVAQLKGVANLNRRIDNVNMGNARAGIAQAIATAGLVQAYLPGKS 539

462 MMAIGGCTYLGEAGYALCYSSISAGCNWITKGTASGNSRCHFGASASVGYW 513

Db 540 MMALGGGTYRGEAGYAIGSYSSIDSGNNWIKGFGSGNSRKHFGASASVGIQW 591

## RESULT 14

US-09-669-974-21  
; Sequence 21, Application US/09669974

; Patent No. 6333173  
; GENERAL INFORMATION:  
; INFORMATION FROM THE PUBLISHED INVENTION

APPLICANT: PEAN, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
ADDITIONAL: MOYON R Richard

FILE REFERENCE: 065064/0128

: CURRENT APPLICATION NUMBER: US/09/669,974  
 :  
 : CURRENT FILING DATE: 2000-09-26  
 :

; PRIOR APPLICATION NUMBER: US 09/377,155  
 ; PRIOR FILING DATE: 1999-08-19

PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PCT APPLICATION NUMBER: 01/0000000

;; PRIOR FILING DATE: 1997-12-12  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 21  
;; LENGTH: 591  
;; TYPE: PRF  
;; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 92.5%; Score 2407; DB 4; Length 591;  
Best Local Similarity 82.6%; Pred. No. 3.7e-184;  
Matches 489; Conservative 5; Mismatches 18; Indels 80; Gaps 2;

QY 1 MKKIRIINWSALNMAVAVSELTNRHNTKRASATVTAVALTLLFATVQANATDE----- 54  
DB 1 MKKIRIINWSALNMAVAVSELTNRHNTKRASATVTAVALTLLFATVQASANNEBEEDL 60  
QY 55 ----- 54  
DB 61 YLDPVQRTVAVLIVNSDEKGEKEVEKVEENSDMAVYFNEKGVLTAREITLAKADNLKIKQ 120  
QY 55 -----TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYHLN 101  
DB 121 NGNTNFTYSLKRDLTDLTSVTEKLSFSAANGKRVNITSDTKGLNFAKETAGTNGDTYHLN 180  
QY 102 GIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 161  
DB 181 GIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 240  
QY 162 VRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVIERKDGKLVYTGKGEENGSS 221  
DB 241 VRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVIERKDGKLVYTGKGEENGSS 300  
QY 222 TDEGEGLVTAKEVIDAVNKAQWRMKTITANQOTGQADKEFVYTSQNTVFASGKGTATV 281  
DB 301 TDEGEGLVTAKEVIDAVNKAQWRMKTITANQOTGQADKEFVYTSQNTVFASGKGTATV 360  
QY 282 SKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDETV 341  
DB 361 SKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDETV 420  
QY 342 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDDEGALNVSGSKDANKP 401  
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDG-ALNVSGSKDANKP 479  
QY 402 RITNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPKGS 461  
DB 480 RITNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPKGS 539  
QY 462 MMAIGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 513  
DB 540 MMAIGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 591

RESULT 15  
US-09-377-155-2  
; Sequence 2, Application US/093771155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0.  
; SEQ ID NO 2

;; LENGTH: 592  
;; TYPE: PRF  
;; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 92.3%; Score 2402.5; DB 3; Length 592;  
Best Local Similarity 82.3%; Pred. No. 8.4e-184;  
Matches 488; Conservative 5; Mismatches 19; Indels 81; Gaps 2;

QY 1 MKKIRIINWSALNMAVAVSELTNRHNTKRASATVTAVALTLLFATVQANATDE----- 54  
DB 1 MKKIRIINWSALNMAVAVSELTNRHNTKRASATVTAVALTLLFATVQASANNEPRKDD 60  
QY 55 ----- 54  
DB 61 YLDPVQRTVAVLIVNSDEKGEKEVEKVEENSDMAVYFNEKGVLTAREITLAKADNLKIK 120  
QY 55 -----TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYHL 100  
DB 121 NGNTNFTYSLKRDLTDLTSVTEKLSFSAANGKRVNITSDTKGLNFAKETAGTNGDTYHL 180  
QY 101 NGIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 160  
DB 181 NGIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 240  
QY 161 FVRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVIERKDGKLVYTGKGEENGSS 220  
DB 241 FVRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVIERKDGKLVYTGKGEENGSS 300  
QY 221 STDEGEGLVTAKEVIDAVNKAQWRMKTITANQOTGQADKEFVYTSQNTVFASGKGTATV 280  
DB 301 STDEGEGLVTAKEVIDAVNKAQWRMKTITANQOTGQADKEFVYTSQNTVFASGKGTATV 360  
QY 281 VSKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDET 340  
DB 361 VSKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDET 420  
QY 341 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDDEGALNVSGSKDANKP 400  
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDG-ALNVSGSKDANKP 479  
QY 401 VRTNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPK 460  
DB 480 VRTNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPK 539  
QY 461 SMAAIGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 513  
DB 540 SMAAIGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 592

Search completed: October 6, 2003, 09:35:42  
Job time : 15.7186 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 14.6847 Seconds  
(without alignments)  
3359.577 Million cell updates/sec

Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKIYRIIWSALNMAVAVS.....TASGNSRGHFGASASVGYQW 513

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2407	92.5	591	2 G81133	adhesin NMB0992 [i
2	2351.5	90.4	592	2 A81888	probable surface f
3	526.5	20.2	298	2 I64138	adhesin homolog HI
4	371	14.3	1588	2 A86036	probable adhesin z
5	371	14.3	1588	2 H91188	probable adhesin z
6	365	14.0	1190	2 A82615	surface protein XF
7	361	13.9	1107	2 AC0976	probable autotrans
8	359.5	13.8	2059	2 D82671	surface protein XF
9	333.5	12.8	658	2 AH0110	probable surface p
10	241	9.3	1091	2 G64964	hypothetical prote
11	231.5	8.9	1004	2 C82672	surface-exposed ou
12	231	8.9	1325	2 A64905	yeak protein - Esc
13	222.5	8.6	949	2 D90803	Aida-I adhesin-lik
14	222.5	8.6	1005	2 H85611	probable adhesin z
15	220.5	8.5	1286	2 S28634	adhesin AIDA-I pre
16	211	8.1	1343	2 E90893	hypothetical prote
17	209	8.0	3705	2 AD0123	probable autotrans
18	208	8.0	1343	2 D85724	hypothetical prote
19	207.5	8.0	1018	2 H83135	probable adhesin p
20	206	7.9	1910	2 AF0394	probable adhesin h
21	201	7.7	2249	2 A41477	190K surface antiq
22	198	7.6	5188	2 B85547	probable RTX fami
23	198	7.6	5291	2 F90696	hypothetical prote
24	197.5	7.6	1536	2 A43855	high-molecular-we
25	197.5	7.6	3029	2 S76109	hypothetical prote
26	193	7.4	4919	2 T31105	hypothetical prote
27	192.5	7.4	936	2 I40711	sapB protein - Cam
28	191.5	7.4	1651	2 JC1340	outer membrane pro
29	191	7.3	1477	2 B43855	high-molecular-we

30	189.5	7.3	2468	2 A83412	hypothetical prote
31	188	7.2	2020	2 C48399	ABC-type transport
32	187.5	7.2	365	2 AB3486	cell surface prote
33	187	7.2	961	2 AD0548	putative autotransp
34	187	7.2	3013	2 AB0480	probable invasin x
35	185	7.1	4152	2 T31102	filamentous hemagg
36	184.5	7.1	1417	2 A83080	hypothetical prote
37	184	7.1	2551	2 B98047	hypothetical prote
38	182.5	7.0	1004	2 T00046	surface layer prot
39	182.5	7.0	1109	2 A56143	surface-array prot
40	182	7.0	1655	2 E97835	hypothetical prote
41	181.5	7.0	1275	2 T33369	hypothetical prote
42	181	7.0	1366	2 S57664	IGA-specific metal
43	180.5	6.9	893	2 A37284	surface-array prot
44	180.5	6.9	1268	2 B99789	hemagglutinin/hemo
45	180.5	6.9	1270	2 E85649	hypothetical prote

## ALIGNMENTS

## RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Accession: G81133

R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al., Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzato, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81133

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <RT>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PID:AAF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match	92.5%	Score 2407;	DB 2;	Length 591;
Best Local Similarity	82.6%	Pred. No. 2,7e-118;		
Matches	489;	Conservative	5;	Mismatches 18; Indels 80; Gaps 2;
QY	1	MNKIYRIIWSALNMAVAVSELTRNHTKRASATYKTAVALTLFATYQANATDE-----	54	
DB	1	MNKIYRIIWSALNMAVAVSELTRNHTKRASATYKTAVALTLFATYQANNEDEEDL	60	
QY	55	-----	54	
DB	61	YLDFQRTAVAVLIVNSDKEGTEGEKYEENSDMAVYENKGVLTAREITLAKGDNLIKQ	120	
QY	55	-----	101	
DB	121	NGTFTYSLKKDLTDLISVGEKLSFSANGKAVITSDTKLNFAKETAGNGDTYHIN	180	
QY	102	GIGSTLMDLNTGATTTNVDNTDDEKRRASVSKVDYLANGNIKGKPGPTASDVNF	161	
DB	181	GIGSTLMDLNTGATTTNVDNTDDEKRRASVSKVDYLANGNIKGKPGPTASDVNF	240	
QY	162	VRTDYVEFLSADPKTTTNNVESDNGKTKYKATSVYKEDGKLYGKGGENSS	221	
DB	241	VRTDYVEFLSADPKTTTNNVESDNGKTKYKATSVYKEDGKLYGKGGENSS	300	
QY	222	TDEEGGLVTAKEVDAVNAKAGWRKTTTANGQTQADKFETVSGTGYTFASGNGTATV	281	
DB	301	TDEEGGLVTAKEVDAVNAKAGWRKTTTANGQTQADKFETVSGTGYTFASGNGTATV	360	
QY	282	SKDDGNITVYKVDVNVGDALNVNOLNSGNWLDKRAVAGSSGKVISGNVSPSKMDETV	341	

Dd	361	SKDDQGNRTWYAYDVNWDGALNVNOLQNSGHWLDSKAANAAGSSGKXISGVNPSRSKGMDETV	420
Qy	342	NINAGNNIETTRNGKNIDDIATSMTPQFSSVSLGAGADAPTLVSDEGALNNGSDANKPV	401
Dd	421	NINAGNNIETTRNGKNIDDIATSMTPQFSSVSLGAGADAPTLVSVDG-ALNNGSKSKDKNPV	479
Qy	402	RITVNAPEYKGGDYTTNNAOLKGVQAONLNRIDNTNNGNARAGIAOAIATAGLVQAYLPFGS	461
Dd	480	RITVNAPEYKGGDYTTNNAOLKGVQAONLNRIDNTDNGNARAGIAOAIATAGLVQAYLPFGS	539
Qy	462	MMATGGGYTJGAGATATGYSISISAGGNWIIKGTASGNSRGHFGASASVGYQW	513
Dd	540	MMATGGGYTJGAGATATGYSISISAGGNWIIKGTASGNSRGHFGASASVGYQW	591

## RESULT 2

Probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z2491)  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequenceRevision 05-May-2000 #textChange 02-Feb-2001  
R:Accession: AB1868  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morenson,  
J.; Holtroyd, S.; Jaegels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: AB1775; MUID:20222556; PMID:10761919  
A:Accession: AB1868  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAAB84461.1; PTD:g737986  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match	90.4%	Score 2351.5	DB: 2	Length 592
Best Local Similarity	80.8%	Pred. No. 21e-115		
Matches 480	Conservative	9	Mismatches 22	Indels 83
				Gaps 3
QY	1	MNKIYRIIWNLSALNAAVAVSELTRNHTKRAATYKTAVALATLLEFATVQANATDE-----	54	
Db	1	MNKIYRIIWNLSALNAAVAVSELTRNHTKRAATYKTAVALATLLEFATVQANATDEDEBEL	60	
QY	55	-----	54	
Db	61	ESVORSVVGSIOASMEGSELETISLSMTNDSKBEFVDPYIVVTIKAGNLIKONTNENT	120	
QY	55	-----TGLINVEETEKISFGANGKRVNIISPTKGLNFAKEPAGNGDTYHLN	101	
Db	121	NASSFTYSLKKDGLGLINVEETEKISFGANGKRVNIISPTKGLNFAKEPAGNGDTYHLN	180	
QY	102	GIGSTLDMLNTGATTNVTNDNVTDEKKFAASVKDVLNAGWNIKGVKPGTTA--SDNV	159	
Db	181	GIGSTLDMLNTGATTNVTNDNVTDEKKFAASVKDVLNAGWNIKGVKPGTTA--SDNV	238	
QY	160	DFVFTYDPEVERLSADTKTTTYNVESKONGKTEKIGAKTSVIREKXGKIYTGXGKGNG	219	
Db	239	DFVFTYDPEVERLSADTKTTTYNVESKONGKTEKIGAKTSVIREKXGKIYTGXGKGNG	298	
QY	220	SSTDEGSLYTAKEVIVDAVNRKAGRMKTTTNGOTGQADKEEYTSGTYKVFASANGTTA	279	
Db	299	SSTDEGSLYTAKEVIVDAVNRKAGRMKTTTNGOTGQADKEEYTSGTYKVFASANGTTA	358	
QY	280	TYSKDDOGNTIVKYDVANVGDALNVNOLONGSMNLDSRAVAGSSKRVISGNVSPSKGKME	339	
Db	359	TYSKDDOGNTIVKYDVANVGDALNVNOLONGSMNLDSRAVAGSSKRVISGNVSPSKGKME	418	
QY	340	TVNINAGNIEITKNGKNIDATSMTPPOESSVSLGAGADATLTSLVDEGALNVSSKANK	399	
Db	419	TVNINAGNIEITKNGKNIDATSMTPPOESSVSLGAGADATLTSLVDEGALNVSSKANK	478	
QY	400	PVRTTNVAPGVKEGDVTNVAOLKGAQNILNRRIDNVNGNARAGIAQAATAGLVAQAYLPG	459	

Db 479 PVRITNAPVEVKEGDVTNNAQLKGYAQNINRNIDVNDGNARAGIAQALATATAGLYQVAYLPG 538

Qy 460 KSMALIGCGTTCGACGATGYSISAGCWWIIKGTASGNSGRHFGASASVGYQM 513

Db 539 KSMALIGCGTTCGACGATGYSISAGCWWIIKGTASGNSGRHFGASASVGYQM 592

### RESULT 3

adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence-Revision 18-Aug-1995 #text-Change 24-Oct-1997  
C:Accession: A64138  
R:Flatschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: I64138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U02846; GB:I42023; NID:g15745586; PID:g15745589; TIGR:HI1732

Query Match	20.2%	Score 526.5;	DB 2;	Length 298;
Best Local Similarity	43.1%;	Pred. No. 1.1e-20;		
Matches 129; Conservative	28;	Mismatches 63;	Indels 79;	Gaps 7;

[illegible]

## RESULT 4

C:Probable\_adhesin\_25029 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)  
 C:Species: *Escherichia coli*  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: AB6036  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, M.E.;  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A:Reference\_number: AB5460; MUID:21074935; PMID:11206551  
 A:Accession: AB6036  
 A:Status: preliminary  
 A:Molecule\_type: DNA  
 A:Residues: 1-1588 <SPO>  
 A:Cross\_references: GB:AA005174; NID:g12518349; PIND:AA658749.1; GSDB:GNO0145; UWGP:  
 A:Experimental\_source: Strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: 25029

Query Match	14.3%;	Score 371;	DB 2;	Length 1588;
Best Local Similarity	23.5%;	Pred. No. 1.2e-11;		

[illegible]

Db 976 LLMBETANGAGG-----AYNMSHOCKAIIITNANGSISESDSTDAVNSQULATINNM 1027

QY 54 ---ETGLINV---ETEKISFGANGKKYNIIT-SDFKGLNFAKETAGNCDTTHLNGI--- 103

Db 1028 IEQNQTIIINQAGNTDATTYIOENGAGIIVYRTNDDGLAFNDASAGQVATFIAGYNSVAKG 1087

QY 104 -----GSTLLTMLNTGA-TTNVNTDNY-----TDDEKKRAAS 135

Db 1088 DSSVAIGGGSYSDVDTGIALGSSSVSSRVIAKKGRDSTITENGVAIGYDTTIDGELGLALS 1147

QY 136 VKD-----VYNAGWNIGKVGPGTTASNVDFVRYTDFVEFLSADFTKTTYTNVNESKDNGK 189

Db 1148 IGDGCKYKQIITN-----VADGSEADDAVT-VQOLNAILCAVATTPPKRYHANSTEDSD 1139

QY 190 ---KTEVKIGAKTSVIREK-----DGKLVTKGKGE-----NGSST 222

Db 1200 LAVGTDSLAMCAKTIIVNGDKIGIGIYGAYVDANMLNGIALISGNQVIHVNSIALGNSTT 1259

QY 223 DEGBELVTAKEVIDAVNKKAGNRKMTTTANQO-----TGQADKFEYVTSCTKTFPSGN 275

Db 1260 TRGAGQNTTAYANMDAPONSVEEFSVGSADGQROITNVAAGSADPDADVAVGOLKTYDAQVS 1319

QY 276 GTTATVSGDDQ-----GNITVKYDVNWDAL-----NVNQLONGSNMLDSKAVAG 320

Db 1320 ONTOSTITMLDRNRYTNLDSRVNTNIEGIDJITVTSSTKTFKNTDGVDSASQCKSVLAIGS 1379

QY 321 SSGKVIQSGNVSPSKGKM---DETVINAGNIEITRN---GKNIDIASTMTPOEFSVSLG 374

Db 1380 GSIAADNSVALLGSGSVATEENTISVGSSTNQRRITNVAACKNMTDAVNVNQLKSSSEAG 1439

QY 375 AGADAPLTSVDEGALNVGSKDANKPVARTVVAAPGVKEGDTVNVNQLKVAQO----- 426

Db 1440 VRYPTKADGSDIDYSNITLTGGGNGG--TTRISNVASGVANNDDVNVNVAOLKOSVOETKQYTDQ 1498

QY 427 ---NTNNDIDVNVGNARAGIAQIATATAGLVQAYLPCKSMALIGGTTYLGEAGYALIGSSI 483

Db 1499 RMVEKDNKLSTESTESLGSGLIASAMAMGLPDAITPGASMASIGGTTYNGESAVALGVSMV 1558

QY 484 SAGGNMIIKGTASGNSRGHFGASASVGYOW 513

Db 1559 SANGRMVYKLOGSTNMQEYSNALGAGIGOW 1588

RESULT 6

A82615

surface protein xfi1981 [imported] - xylella fastidiosa (strain 9a5c)

C.Species: xylella fastidiosa

C.Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C.Accession: A82615

R.anonymus, The xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A.Title: The genome sequence of the plant pathogen xylella fastidiosa.

A.Reference number: A82515; MUID:20365717; PMID:10910347

A.Note: for a complete list of authors see reference number A59328 below

A.Accession: A82615

A.Status: Preliminary

A.Molecule type: DNA

A.Residues: 1-1190 <SIM>

A.Cross-references: GB:AE004017; GB:AE003849; NID:9107083; PIDN:AA84783.1; GSPDB:GN

A.Experimental source: strain 9a5c

R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincanli, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.;

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tshunako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A.Reference number: A59328

A:Contents: annotation  
C:Genetics:  
A:Gene: XF1981

Query Match 14.0%; Score 365; DB 2; Length 1190;  
Best Local Similarity 24.8%; Pred. No. 1.7e-11;  
Matches 141; Conservative 83; Mismatches 213; Indels 132; Gaps 20;

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QY 17 VAVSELTRNHTKRASATVKVATLAFATLVQANATDEGLINTEKLSFGAN-----70
DB 682 VTSSSISAGNOKITVAAGTADTDAVNFSQLOAVSTASKGNL-----LASANSNNAP 737
QY 71 GKKNVITSDTGLNFAKETAG-----TNGDTVHLNGIGSTLTMLNT 114
DB 738 GESVDLKTGDNIVISKESGNDVLENTSSSLKLDKLEFGDTVMNTGV-----TVGS 790
QY 115 GATTIVTNDVNTDDEKKRAASKVDLNG-NWIKGVKPGTASD-----157
DB 791 GTTIGSMGLVITDGPSTVSSGI---NAGSOKITVAAGTADTDAVNLSQLTAMAGSGA 846
QY 158 -NVDEVRTYDVEFLSADTKTTTVNESKNGKTEVKIGAKTSYIEKDGKLVTKGKG 216
DB 847 KSVHYSTYD-----GGTGGGNTNGDGTGTRSLAVGGLTASA-----EGATVAGSGGA 896
QY 217 ENG-SSTDEBGLVTAKEYIDAVNKAQWPMKTTTANGOTGQADKETEYVTSKTPASGN 275
DB 897 ASGKSTAIGRNAVASADGSVALGD-GAKDGARGAESTYKYSGLQNNVTGTVSYVDASK 955
QY 276 GTTAVVSADDOGNITVKYDVNVGDALNVNOL-----QNSGMNLSKRAVSSSGKTVSGNS 331
DB 956 GETRTVS-----NVADAKEAT--DAVNLKOLDRAVDADRKYDKNIESISEGOTF-----1003
QY 332 PSKGMDETVNINAGNIEITFRNGKNIDITATSMTPQFSSVSISAGADA-----P 380
DB 1004 -----VKYNSLNN-----SATPIAGVADATATGVCATASGADSIAMGNKA 1043
QY 381 TLSVDEGAL-----NNGSKDANKPVRTTNNAPGYKEGDVTNVAOLKQYAOUL 428
DB 1044 SASADNAVALIGNHSAVDANRANTVSGSAGSER--QVTNNAAAGTADDAVNVSQLNGLTJA 1101
QY 429 NNRIDNVGNAR-----AGTAAIATAGLVQAVLPCKSMKAIIGGTYLGEAGVAIGYSIS 484
DB 1102 KQYTDGVVGSLERRDIDGVAALAIATANLPQATIPGRGMTSVGVSSIRGOSAIATAGVSSVS 1161
QY 485 AGGNMIKGTASGNSRGHFGASASYGYOM 513
DB 1162 ESGRWVFKFSGSANTRSQVIGAGGYOM 1190
```

## RESULT 7

AC0976  
Probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AC0976  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AC0976  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1107 <PAR>  
A:Cross-References: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176  
C:Genetics:  
A:Gene: sapB

Query Match 13.9%; Score 361; DB 2; Length 1107;  
Best Local Similarity 21.7%; Pred. No. 2.5e-11;

Matches 171; Conservative 94; Mismatches 222; Indels 302; Gaps 29;

```
QY 9 WNSALNAN-----VAVSELTRNHTKRASATVKVATLAFATLVQANATDEGLINTEKLSFGAN-----70
DB 337 WNETNSTSASGSSSTTKKITVAAAGELSEEST-----DAVNSQLEFENEKVDONT 388
QY 52 TD-----ETGLINVT-----EKLSCGAN--GKKNVIT 77
DB 389 TDIAANTNITQNSAIEINLNTSVSDIMTSITGLTDMALMDEDEGAFSANGSGSTKIT 448
QY 78 SDTKLNTAKETAGNG-----DTVHLNGIGSTLTMLNTGATNTVNDVNTDDEKKRA 133
DB 449 NVAAAGALSEDSTDAVNSQLEFETNOKVDONTAID--INT-SITNLGTDALSDWDEBA 505
QY 134 ASVKDVLNAGWNIKGVKGTPTASDVDPV---RTYDT-----VEFLSADTKTTTV 180
DB 506 FSASHGTSGTKNTITVAAGELIASDSTDAINSQLEFETNMLISQYNESISQLAGDTSERYI 565
QY 181 N-----VESKNGKTEVKIGAKTSYIEKDGKLVTKGK--KGNGSSTDEG---225
DB 566 TENGTVKRYIRINDGLEGODAYATGNGATAYGDVAVASGAGCLALGONSSSIEGSLAL 625
QY 226 -----EGLY-----TAKEYIDAVNKA-----GWRMKTTPANGGTG 255
DB 626 GSGSTSNRALTITGIRETSATSDGVYIGYNTTDRILLGALISGTDGESTRQITNVADGSEA 685
QY 256 Q-----ADKFEYVTSQTKVTFASGNGTPTATVSKDOGNITVKYDVNV 297
DB 686 QDAVTVROLQNALIGAVTTTPTKYHANSTEDSLAVGNDSLAMGAK-----TIVNADAGI 740
QY 298 GDALVNVNOLN--SGWMLDSKRAVSSSGKTVSGNSP-----332
DB 741 GIGLTLVMAIDAINIAGISNARAHNANSIANGNSQTTGCAQDTYATNMPTPONSVE 800
QY 333 -SKGMD--ETVNNAGN-----NIEITFRNGKNI-----358
DB 801 FSVSGEDGORQITNVAAGSADTDAVNVGOLKATDQVSRNTOITNLTOVSNLDTRYTN 860
QY 359 -----DIATSMTPQF-----SSVSLGAGADAP-----TLSVDE-G 388
DB 861 IENGIGDLYTGSTYFPTNTDGDANAGQASVALIGSSIAAENSVALGTNSVADEAN 920
QY 389 ALNNGSKDANKPVRTTNNAPGYKEGDVTNVAOLK-----422
DB 921 TVSVGSSTQOR--RITNVAAGVNNPDVAVNVOLKASEAGSVREYETNADGSVNSVLANLGD 978
QY 423 -----GVAO-----NLNRIIDNVGNARAGIA 444
DB 979 GSGGTRIGNVSAVNDTDAVNVADLKRSEVEANTTYDQKGEHNSKIKIGIKNKSGLIA 1038
QY 445 QAIATAGLVQAVLPCKSMKAIIGGTYLGEAGVAIGYSISAGGNMIKGTASGNSRGHFG 504
DB 1039 SAMAAAGLPQAVAPGANTSTIGTFNGESAAVAIGVSVSEGGVYKLGQTSNQGDSYS 1098
```

## RESULT 8

DB82671  
Surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: DB82671  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: AB2515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number AS9328 below  
A:Accession: DB82671  
A:Status: preliminary  
A:Molecule type: DNA



A:Residues: 1-2059 <SIM>  
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001  
A:Experimental source: strain gasc  
R:Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Brlones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferrio, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; From  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laiz  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XP1529

Query Match 13.8%; Score 359.5; DB 2; Length 2059;  
Best Local Similarity 24.5%; Pred. No. 6.6e-11;  
Matches 151; Conservative 82; Mismatches 188; Indels 195; Gaps 29;

QY 59 NTEKLSFGANGKV--NIISDTKGLNFAKETAGT-----NGDTTVH--LNGIGSTL 107  
DB 1478 NTLQDK-----DGVKVSNNLDSNELVITSHSTSVKTLANGESVNNRTVYNGGVNI 1532  
QY 108 TDML-----LNTGA--TTNVT-----NDNVTDEKRAASVADVLN 141  
DB 1533 DDVVVVNDLGLSIVGASLTLSCINAGSHKRTNVTAGTEPDVAVNSQLK---SVSEAVD 1589  
QY 142 AGNII-----KGVKPGTASDNDV-----FRTYDTEFLADTK-----TTT 179  
DB 1590 KGTTLTASGANGSKVSGTVDLKNIDGNLAIKSGSDNDVFNLSKDFVDEVTAQNTV 1649  
QY 180 VNESKDNKRETEVIGAKTSVIEKDGKLVTKGNGEN-----GSSTDEEGELVTAK 232  
DB 1650 VNTDGVKVG--SDVSLGAMGLFIANGPSVTASGFNMGDKVISHVAVGMDTAVNVSQK 1707  
QY 233 EVDVAVNKAQMRKKTITANGQT-----QADKEETVTSQTKV-----FAS 273  
DB 1708 QAVQSVTVKATRYSTNDGTOGANYDGGATGSKAIAAGVGTQASGEGAAVAGSMAAS 1767  
QY 274 GNGTY-----ATVSKD-----DQG-----NIPVKYD-----VNVG----- 298  
DB 1768 GKSTALIGRNALISADGSAVALGDGAKDGGKGAESYTGKISGVONNTVGTIVSGDAKGET 1827  
QY 299 -----DALNVQL-----ONSGWNLDS-----KAVAGSSGKYISGN 329  
DB 1828 RSTSNVADAKKAMDVNLRLQDLDAVNAQKSNLQTDMDHETINIEDVFKITFGDSASSVKG- 1886  
QY 330 VSPSKGMDTVINA-----GNIEITRN-----GKNIDATSMTPQFSSVSLGACADAPT 361  
DB 1887 -----MGNVMAAIGTNAVSGTESVALGKNTNVSAD-----NAVALINGSAV-- 1928  
QY 382 LSVDEGALNVGSKDNKPVRTINVAPEGEGDVTVAOLKGYAQNLMNRIDVNGNAR- 440  
DB 1929 -----DRANSVSVSGSGSER--QVTINVAAGTADTDAVNVSQLNOGLITRAKQTTDGMVGLNR 1983  
QY 441 ---AGIAQATATAGVQAVLPGKSMMAIGGTYLGEAGVATIGVSSISAGGNMIIKGTASG 497  
DB 1984 ETSGVYAAATATANLPQAVYQGRGMTSVGVSSYQGGALAVGVSAVSESHWFKRSGSA 2043  
QY 498 NSRGHFGASASVGYQW 513  
DB 2044 NTRSHVGVGAGVGYQW 2059

RESULT 9  
AH0110  
probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain Co92)  
C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Whitt, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G  
ll, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.; Whitehead, S.; Barril  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YP00902

Query Match 12.8%; Score 333.5; DB 2; Length 658;  
Best Local Similarity 23.2%; Pred. No. 3.6e-10;  
Matches 142; Conservative 73; Mismatches 213; Indels 185; Gaps 22;

QY 27 TKRASATVKT-----AVLATILFATVQ-----ANATDEGLINVEREKLSFGANGKRVN 75  
DB 105 TNLAPATISTSTDVAVGSQLVNLVDGTRYFPHANSVNPYDSLASGLETTAVG---PAT 160  
QY 76 IISDTKGL--NFAKETAGTNGDPTVHLNGIGSTLT-----DMLNTG 115  
DB 161 VVSGDNKGVGIGNTALVGAATGGAIT--GFGQVTAAGTATGASNAQAGASLALGAG 217  
QY 116 ATTNTVNDVNTDEKRAASVKDV-----LNAQW-----NIKGVK 150  
DB 218 AVTSQANSIALG-----AASINTVGAQSSYSAVALTPAQASVGLIGTALGNKRIYVA 272  
QY 151 PGTTASDNTVFEV-----TYDTEFLADTKTTV--VNESKNG-----K 189  
DB 273 AGSASSDAVVAQLTAVGDVQONTANTITSLGKVTTLBESMASIANGGVKYPHANSTQ 332  
QY 190 KTEVIGAKTSVI-----REKDGKLVTKGKNGENSGSTD 223  
DB 333 PDSVASSTNSVALIGPASLASGAMNALSAGACAVAIIGDGAASADGSAVALIGGSGDNKGVE 392  
QY 224 EGBGLTAKVDAVNAKQMRKKTITANGOTGQADKEETVTSQTKVTFASGNGTATVSK 283  
DB 393 -----NYIGKYSNANSSGTSVSGVATGGETRVSN 424  
QY 284 DDGDNITVKKYDVAVNGALNVNOLONGSMNLSKRAVAGSSGKYISGNVSPKGMDEVNI 343  
DB 425 VADG-----LDATDVLNLQDLG-----IAATLVVENNVSGLQNGTDMFQV 467  
QY 344 NAGNNI-ETIRNGKNIDI--ATSMTPQFSSVSLGACADAPTL-----VDDEGALN 391  
DB 468 NNSGLAKPATGANSATGAGSAGVSAAGNNTATAGSGAKATRAANSALGANSVADRANSYS 527  
QY 392 VSKDKANKPVRTINVAPEGEGDVTVAOLKGYAQN--LNNRIDVNGNAR----- 440  
DB 528 VGVSGNER--QITNVAPATGTDVAVNPDQKLSISNQTNAATNORYSELKDKLRKONSVL 585  
QY 441 AGIAQATATAGVQAVLPGKSMMAIGGTYLGEAGVATIGVSSISAGGNMIIKGTASG 500  
DB 586 AGIASASMASLTPPTISGSSMTTIGASTRGASLSLGVSSISDSGRWVSKLQASSNTQ 645  
QY 501 GHFGASASVGYQW 513  
DB 646 GDFVIGVGYQW 658

RESULT 10  
G64964  
hypothetical protein b2000 - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: G64964  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of *Escherichia coli* K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: G64964  
A:Status: nucleic acid sequence-not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1091 <BLAT>  
A:Cross-references: GB:AE000291; GB:U00096; NID:91788298; PIDN:MAC75061.1; PID:91788309;  
A:Experimental source: strain K-12, substrain MG1655  
A:Keywords: nucleotide binding; P-loop  
F:683-690/Region: nucleotide-binding motif A (P-loop)

Query Match  
Best Local Similarity 21.5%; Score 241; DB 2; Length 1091;  
Matches 131; Conservative 92; Mismatches 236; Indels 150; Gaps 29;

1 MKKIRIIMNSALNMVAVSELTNRHTRKASATVTAVALTLTLPATVOAN-----ATDE 54  
57 LMTCTRLVNMNMGTGAFVVAASELARARAGKGVAVALSIAVTSPLVLAADIVVHGETVN 116  
55 TGLINVEETKLSFG-ANGKKNVNIISDTKGLNFAKET-----ACTNGDTTTHLNG 102  
117 GGTLANHMDQIVFETNGMTI-----STGLEYGDPNEANTGGQWQDGTANKTTVTSGG 171  
103 I-----GSLIDMLNTGATTNV---TNDVNTDDEK---KRAASYKDYLA-AGNNIKGV 149  
172 LQRVNPGGSVSDTIVISAGGOSLQGRAVNTTNGEOMHNEGALTAGTVINDKGMQV--V 229  
150 KGTGTASDVNDEVR-----YDPEFLSADTKTTTVN-----VESKDNCKRTEV 193  
230 KFGTVAITDV--VNTGABGPDENGDTGQFVRGDAVRTTIKNKGQIYRAEGTANTTVV 287  
194 KIGARTSV-----IKEKDGKLVTKGKGENGSTDEGEL 228  
288 YAGGQGTVGHALDPTTLNGGYQVHNNGTASDTVANSOGWOLVKNQ-GVAGMTVTWQKGR 346  
229 VTAKEDIVAVN--KAGRMKTTTANGOT-----GQADKEFVTVGCTKVTAS 273  
347 LQVDAAGTATNTTLQGGALVTSTATATVGINRLGAFSVVEGKADNV-VLENGGRADVLT 405  
274 GNGTATVATSKDQGNITVYDVNVGDALVNOLONSGMNLDSKAVAGSSGKVIISGVSPS 333  
406 GHTATNT-RVDDGGFLDRA--NGGTATTVS-MGNG-----VLADSGAAVSGTRSDG 454  
334 K-----GKMDETVINAGNNIEITRNKNIDATSTPQSSSVSLGAGADAPLTLSVDEG 388  
455 KAFSIGGGQADALMLEKSSFTLNG---DPAFTVTVNGLEFTRARGTLAATTTLNNGA 510  
389 ALANVSKDANKPVRTTNVAPGVKEGDVTNVADLKGYAQNLRNIDVNGNARAGTAAQIA 448  
511 ILLTSGKTVN-----NDLTITREGD---ALLQGSILNGSVK-SGSGTLTVSNMTL 559  
449 TAGLVQAVLPKGSMAIGGT---YLGEAGYAIGS-----SISAGNNI 490  
560 TOKAVNL---NEGTLTINDSTVTTTVIAQGTALKLKGSTVLNGAIDPTNVTLASGATVN 616  
491 IKGTASGNS 499  
617 IPDNATVOS 625

RESULT 11  
C82672  
surface-exposed outer membrane protein Xf1516 [imported] - *Xylella fastidiosa* (strain 98  
C:Species: *Xylella fastidiosa*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: C82672  
R:Anonymus, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
A:Reference number: AB2515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number AB9328 below  
A:Accession: C82672

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A:Cross-references: GB:AE003981; GB:AE003849; NID:99106543; PIDN:AAF84325.1; GSPDB:GN  
A:Experimental source: strain 985c  
R:Simson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrer, D.M.; Carrer  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincini, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri,  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: AB5328  
A:Contents: annotation  
A:Accession: C82672  
A:Gene: Xf1516

Query Match  
Best Local Similarity 22.1%; Score 231.5; DB 2; Length 1004;  
Matches 154; Conservative 85; Mismatches 250; Indels 207; Gaps 33;

2 NKIYRIIMNSALNMVAVSELTNRHTRKASATVTAVALTLTLPATVOAN-----ATDE 54  
4 NOIYKRFNMLSLGSMVSHMTNDGCSQVNLRHSGVNRSLVLAIGLALTSVTHAOSVK 63  
36 TAVLAT---LLEFATV--QANAT-----DEFGLIN---VEPEKLSFGANGKKNVNIISPT 80  
64 SPAMVTASKVMVAHVDQVNRTRADRIPTGDSGLMTMHMLDMKFFPFNNISIAIGYFSA 123  
81 KGLNF-----AKETAGTGTDTVHLNGISLTLMMLNTGATTVNTN-----DNYTD 127  
124 PAPPNALALGYNSSTVQSANNGVYALGSNSVSGVNSVYALGAGSMASELVNISVGGDGYTG 183  
128 DEKRAASVYKDYLA--NAGNNIKGVKPGTTAS--DNVDEVRVY----- 165  
184 PAVRRIVNVGDIQNNDAVN--KSLDGVYASVNDVAASKTIALTNQVTSVASASGKE 242  
166 -----DYVEF-----LSAOT-----KTTVNVESKD----- 186  
243 STAIGSQAQAVADNTVAFEGRAIANAVGASALGFPSSHAKGISTVYQSVSLGOGVSL 302  
187 -----NGKTEVRIKATSVYIKEDKLVYKGG---KGENSGSTDEGEL--VTAKEV 234  
303 GYNSTVYGBGSFNGLALGNSLVLLQGVDSVALGSGMSASEPVNVYVSGSDGLRGRAVRRI 362  
235 I-----DAVNRKAGWRMKTTTTANGOTGQADKEFV--TSGTVPTEFASGNGTAT--VS 282  
363 VAVGDIQNNDAVNKSLQDGVYASVNDVAASKTIALTNQVTSVASASGKE 242  
283 KDDGNTIYKDVYVNGDALVNOLONSGNLD-----SKVAASSGKVISGNSVPSKG 335  
423 AQADDSSTIA---LGARSANALIGSSALGVGHALGANSTALGOSTAISGCGTSLG-- 476  
336 KMDETVINAGNNIEITRNKNIDATSTPQSSSVSLGAGADAPLTLSVDEGALNVGSK 395  
477 -YNSFVGOSATNGIALGNS-----ALVSVNSVALGAGVASELVN-----ISVGG 522  
396 D-ANKPV--RITNVAPGVKEGDVTNVADLKGYAQNLRNIDVNGNAR--AGIAQA 446  
523 DQVTPAVRRIYVNVGDIQNNDAVNKSLQDGVYASVNDVAASKTIALTNQVTSVASASGKE 242  
447 I---ATAGLVQAVLPKGSMAIG-----GRTYLEGAGTAIGS 481  
583 IGDSTATAGSAAQADDSVVALGTRATANAIGSSVYGVDSRARGINSTALGROSNAIGDG 642  
482 SISAGNNITIK-----GTAAGNSRGHPGA--SASVGY 511  
643 SVSLGFNSFVROSGEHGVALGTDAGVSGKDSIALGT 678

## RESULT 12

A64905 ydek protein - Escherichia coli (strain K-12)

N:Alternate names: protein T

C:Species: Escherichia coli

C&gt;Date: 12-Sep-1997 #sequence, revision 17-Sep-1997 #text\_change 01-Mar-2002

C:Accession: A64905; 152440; S54315

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.: Rose, D.J.; Mau, B.; Shao, Y.

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A64905

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1325 &lt;BLAT&gt;

A:Cross-references: GB:AE000248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PID:g1787788;

A:Experimental source: strain K-12, substrain MG1655

R:Cartwright, P.; Tims, M.; Lithgow, T.; Hoj, P.; Hoogenraad, N.

Biochim. Biophys. Acta 1153, 345-347, 1993

A:Title: An Escherichia coli gene showing a potential ancestral relationship to the gene

A:Reference number: 152440; MUID:94100243; PMID:8274505

A:Accession: 152440

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 &lt;RES&gt;

A:Cross-references: EMBL:X73295; NID:g312392; PIDN:CA51730.1; PID:g312393

A:Note: the difference in length is due to a frameshift error at pos 653

C:Genetics:

A:Gene: ydek

C:Function:

A:Description: probably involved in protein translocation apparatus

C:Keywords: nucleotide binding; P-loop

F:712-719/Region: nucleotide-binding motif A (P-loop)

Query Match 8.9%; Score 231; DB 2; Length 1325;

Best Local Similarity 24.4%; Pred. No. 0.00019;

Matches 146; Conservative 65; Mismatches 245; Indels 142; Gaps 29;

```
QY 1 MNKTYRIIMNSALNAMYAVSELTR-----NHTKRASATVKTAVLATLLEFAVQANAT 52
D 1 MNKTYRIIMNSALNAMYAVSELTR-----NHTKRASATVKTAVLATLLEFAVQANAT 52
QY 53 -----DEGLINVERE-----KLSTGANGKKVNIISDRKGLNFAKETA 90
D 61 GASLEVDNDQITNIDVDVAYDAYLVGWYGTGVNIIAAGNASLTTITTSVIGAN--EDSE 118
QY 91 GTNGDFTVHLNGIGST--LFD-----MLNTG-----ATTNVTNDNVTDDEKKRAASVDK 139
D 119 GT-----VNVIGGTAKRLDSCGNARPLNAGSGSTGLNKKQGHVDG-----GY 162
QY 140 LNAAGNMIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTE----- 192
D 163 LRLGSSSTGY--GTAVNEGEDSVLTLEFELGISTGSLNIT--DKGYVTSVAIILG 216
QY 193 VKIGAKTSYKEDGK-LVYTK-----GKGENGSTDEGBGLVTAKEVIDAVNKAAGW 243
D 217 YQAGSNGQVYVEGGEVLINNDSSLEFQIGNOGTGEATIREGGLVTAENTYIIGGNATG- 275
QY 244 RMTTTPANGQTGADKRETVTSGTKVFASGNGTGTAVSKDDGQNTIVK-YD-VNVDAL 301
D 276 -----IGTLNVO-----DDSVITVRRLYNGYFGNG---TVNISNGLINNKKEVSLVGVDDGS 325
QY 302 N--VNOLQNSGMNL-----DSKAVAGSSGKVIISGNVSPSKGKMDFTVNI 343
D 326 HGVVNVYTDKGMHMFELGTGEAFRTYIGDAGDGLNVSSEKVDGSIITAG---MKER--- 379
QY 344 NAGN-----NIETTRNGKNIDTATSMTPPOFSSVSLGAGADAPPLSYVDEGALNV----- 392
D 380 GTGNITVTKRNSVITNLTGMLGYDGHGEMNINSOGLVNVSGSSLGGETGVGNVSYITTG 439
```

## RESULT 13

Aida-I adhesin-like protein [imported] - Escherichia coli (strain 0157:H7, substrain

C:Species: Escherichia coli

C&gt;Date: 18-Jul-2001 #sequence, revision 18-Jul-2001 #text\_change 18-Jul-2001

C:Accession: D90803

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C

gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and 9

A:Reference number: A96629; MUID:21156231; PMID:11258796

A:Accession: D90803

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-949 &lt;HAY&gt;

A:Cross-references: GB:BA000007; PIDN:BA834819.1; PID:g13360856; GSPDB:GN00154

A:Experimental source: strain 0157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECS1396

Query Match 8.6%; Score 222.5; DB 2; Length 949;

Best Local Similarity 21.7%; Pred. No. 0.00034;

Matches 131; Conservative 80; Mismatches 224; Indels 169; Gaps 28;

```
QY 1 MNKTYRIIMNSALNAMYAVSELTRNHTKRASATVKTAVLATLLEFAVQANATDE 54
D 5 LNTSYRLVNMHITGTLVVASSELARSRGKRAVAVALSLAATSVPALADKVVQAGETVN 64
QY 55 TGLINVTETKLSFG-ANGKKVNIISDRKGLNFAKET-----AGTNGDFTVLLNG 102
D 65 DGTLTNHDNQIVFETANGMTT-----STGELBLGPDSEBNTGGQIOWNGIAGNTTYTNG 119
QY 103 -----IGSTLMDMLNTG-----ATTNVTNDNVTDDEK 130
D 120 ROVLVEGTFASDVIYRBDGGGSLNGLAVNTTNNRGEQWHEGVAATGTTINRBDGYGVK 179
QY 131 KRAASVADVILNAGNINIGVAPGTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKGK 190
D 180 SGLATGTIINTG-----AEGGPDSDN-----SY-TGQKVOGTAESTTIN---KNGRQ 223
QY 191 TEVKIG-AKTSYIKEDGKLVYTKGKG--ENGSTDEGBGLVTAKEVIDAVNKAAGRM- 245
D 224 TILFSLARDTLIYAGDQSYHGRALMTTLNGVQYVHRDGLA-----LNVINSGAQOV 279
QY 246 -----KTTTANGQT-----GQADKFEVTSCTKVFASGNGTGTAVSKDDQ-GNITV 291
D 280 KAGGACNNTTINNGELRVHAGGEATVQWTFGALVT-----STAATVIGTNLNGFTV 334
QY 292 KYDVNVBDALNVNOLQNSGMNLSKAYAGSSGKVI--SGNVSPSKGMDFTVINAGNNI 349
D 335 ENGRADSVVL-----ESGRDLVLESHSAQNTLVLDGGLTAVSAGAKASVTITTSICAL 388
QY 350 EITFRNGKNIDTATSMTPPOF-----SVISGACADAPPLSYVDEGALNV 392
D 389 -IADSGATVE-GTINASKFSTIDTSGASGLLENGGSFTVNAAGQAGNTTVGHRGTLTL 446
QY 393 -----GSKDANKPVRTITVAVGPKEDVYTNVAQLKGVANLNNRIDNVNGNARAGIAQ 445
D 447 AAGSLSGRFQSLSGASGMVNLGVDVSTGDIYNAGEI-----RDN-QTPNMAISR 496
QY 446 AATAG-----LVQAYLPDK-----SMAIIGGTYLCEAGYA---IG 479
D 497 AVAKNSNPVTFHKLTLTTLTGCGGTINMRVRLDGSNASDQVLVINGGQATGKTWLAFTNVG 556
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```

Db      258  VSSGSAISTSYVNSGVTFFAGATVDTFTVNSGNGNINISSGGIVSEETVNVSGTONIY- 316
QY      306  LONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNI--AGNNIETRNKNIDIAF 362
Db      317  -----SGSALSANIKGSOIVNSEGTALNTLVSDGYOHIRNG--GIAS 358
QY      363  -SMTPOFSSVSLGAGADAPTLVYDEGALNVGSKDANKPVRITNVAPGVEGDPVTNVAOL 421
Db      359  GTIVNGSGYVNISSGVAESTIINSGLIRV-----LSDGYARGTILN----- 401
QY      422  KGYAQNLRIDNVNGNARAGIAQAIAIAGLVOAYLPKSMMAIGGTYL--GEAGYAI 478
Db      402  -----NSGRENV--SNGGVSY-----NAMINTGNGNOYIYSDGEATAAI 437
QY      479  ----GYSSISAGS-----NWITKGTASGNSRGHFGASASVG-----YOW 513
Db      438  VNTSGFORINSGGTAPVQNSVVTFTVSSAAKPEDAEVYSGGKQTVYIWM 486

```

Search completed: October 6, 2003, 09:33:17  
 Job time : 18.6847 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 : Search time 7.92203 Seconds

(without alignments)  
3045.266 Million cell updates/sec

Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKIRIRIMNSALNMAVVS.....TASGNSRGHFGASASVGYQW 513

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	241	9.3	1039	1 AG43_ECOLI	P39180 <i>Escherichia</i>
2	231	8.9	1325	1 YDEK_ECOLI	P32051 <i>Escherichia</i>
3	220.5	8.5	1286	1 AIDA_ECOLI	Q03155 <i>Escherichia</i>
4	201	7.7	2249	1 OMPA_RICRI	P15921 <i>ricketsia</i>
5	188	7.2	2003	1 YDBA_ECOLI	P33666 <i>Escherichia</i>
6	182.5	7.0	1656	1 OMPB_RICCA	O06653 <i>r outer mem</i>
7	182	7.0	1655	1 OMPB_RICCN	O09KX3 <i>r outer mem</i>
8	180	6.9	1654	1 OMPB_RICRI	O53047 <i>r outer mem</i>
9	179.5	6.9	737	1 ALYS_ENTFA	P37710 <i>enterococu</i>
10	178.5	6.8	1567	1 ICEN_XANCT	P18127 <i>xanthomonas</i>
11	178	6.8	1953	1 BIGA_SALTY	P25827 <i>salmonella</i>
12	177.5	6.8	2021	1 OMPA_RICCN	O52657 <i>ricketsia</i>
13	176.5	6.8	933	1 SLAP_CAME	P33827 <i>campylobact</i>
14	175	6.7	1025	1 SLAP_CAME	P35828 <i>caulobacter</i>
15	175	6.7	1645	1 OMPB_RICTY	P96989 <i>r outer mem</i>
16	174.5	6.7	1643	1 OMPB_RICPR	O53020 <i>r outer mem</i>
17	173.5	6.7	1300	1 H12K_RICRI	P14914 <i>ricketsia</i>
18	173.5	6.7	1577	1 H1YA_PROMI	P16466 <i>proteus mir</i>
19	170	6.5	1569	1 YPOA_ECOLI	P52143 <i>Escherichia</i>
20	168	6.5	1608	1 H1YA_SERMA	P15320 <i>serratia ma</i>
21	165	6.3	1861	1 APU_THETU	P38536 <i>t amylopul</i>
22	165	6.3	2660	1 YEBJ_ECOS7	O8X8V7 <i>Escherichia</i>
23	162.5	6.2	3591	1 FHAB_BORPE	P12255 <i>bordetella</i>
24	158	6.1	1034	1 ICEN_PANAN	O47879 <i>pantoea ana</i>
25	158	6.1	1258	1 ICEN_ERMHE	P16239 <i>erwinia her</i>
26	158	6.1	1322	1 ICEN_PANAN	P20469 <i>pantoea ana</i>
27	157	6.0	1148	1 ICEN_PSEEX	O30611 <i>pseudomonas</i>
28	156.5	6.0	1007	1 Y741_CHLMO	O9P16 <i>chlamydia m</i>
29	156	6.0	550	1 FLIC_C_SHIRL	O08860 <i>shigella fl</i>
30	155.5	6.0	504	1 FLIC_SALBU	O06869 <i>salmonella</i>
31	155	6.0	948	1 HPII_DEIRA	P56667 <i>deinococcus</i>
32	155	6.0	1210	1 ICEN_PSEFL	P09815 <i>pseudomonas</i>
33	155	6.0	2358	1 YEBJ_ECOLI	P76347 <i>Escherichia</i>

34	154.5	5.9	1005	1 Y456_CHLTR	O84462 <i>chlamydia t</i>
35	152.5	5.9	918	1 Y4JB_CAEEL	P34487 <i>caenorhabd</i>
36	152	5.8	1694	1 IGA2_HAEIN	P44969 <i>haemophilus</i>
37	152	5.8	1702	1 IGA2_HAEIN	P45384 <i>haemophilus</i>
38	150.5	5.8	928	1 PM11_CHLPP	O86164 <i>chlamydia p</i>
39	150.5	5.8	3178	1 YS89_CAEEL	O09624 <i>caenorhabd</i>
40	149.5	5.7	484	1 P60_LISMO	P21171 <i>listeria mo</i>
41	149.5	5.7	1150	1 APMU_PIG	P12021 <i>sus scrofa</i>
42	149	5.7	1196	1 ICEV_PSEEX	O33479 <i>pseudomonas</i>
43	149	5.7	1200	1 ICEN_PSEST	P06620 <i>pseudomonas</i>
44	148	5.7	537	1 TEE6_STRPY	P18481 <i>streptococc</i>
45	148	5.7	1036	1 HPI2_DEIRA	P13126 <i>deinococcus</i>

#### ALIGNMENTS

RESULT 1  
ID AG43\_ECOLI STANDARD: PRT: 1039 AA.  
AC P39180: P75614; P76360; P97241; Q46771;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (AG43) (Fluiffing protein).  
GN FLU OR B2000.  
OS *Escherichia coli*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
OX NCBI\_TaxID=562;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of *Escherichia coli* K-12.";  
RL Science 277:1453-1474(1997).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,  
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,  
RA Yamamoto Y., Horiiuchi T.;  
RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN (3)  
RP SEQUENCE FROM N.A.  
RC STRAIN-ML 308-225;  
RX STRAIN-ML 308-225;  
RA Preliminary sequence of 53-78.  
RN (4)  
RP PRELIMINARY SEQUENCE OF 53-78.  
RX STRAIN-ML 308-225;  
RA MEDLINE=89291704; PubMed=2661530;  
RT Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
*Escherichia coli*.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN (5)  
RP SEQUENCE OF 53-63.  
RC STRAIN-K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RT Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded

Query Match	Best Local Similarity	9.3%	Score 241; DB 1; Length 1039;
Matches	131; Conservative	92; Mismatches	150; Gaps 29;
1	MNKIYRIIWNLSALNMAWVSELTNRNHTKRASATYKTAVALTLPLRATYQAN-----ATDE	54	

Db 5 LMTGCVRLVYNNHNTGAFVVASLARRKRGSGVAVALSILAATVSLPVLADAIIVNPGETVYV 64

QY 55 TGLINVEFEKLSFG-ANGKKVNIISDYKGLNFAKET-----AGNGDTYVHLNG 102

Db 65 GGTLANHDNQIVFETNGMTI-----STGLEYGPDNEANTNGGQVWODGGTANKTTVYVSGG 119

QY 103 I-----GSLTIDMLLNTGATTNV-----TNDVWTDDEK---KRAVSQDVLN-AGMNIKGV 149

Db 120 LQRVNNGGVSPTVTSAGGGSLQGRAVNTLLNGEGQMHEGALATGTATVNDKGMQV--V 177

QY 150 KPGTASDWDVDFVR-----YDVEFLSADFRTKTVYN-----VESKDNGKTEV 193

Db 178 KGGTVAATDV--VNTGABGGPDAENGDTGQFVVRDQAVRTITINKKRGQIVABEGANTTV 235

QY 194 KIGAKTSV-----IKEDKGLVYGGKKGNGSSTDBEGEL 228

Db 236 YAGGDQTVHGHALDITLNGYQYVHANGSTASDPVNSDGMQIVKNG--GVAGNTTVNQGR 294

QY 229 VNAKEVIDAVN---KAGRMKTTTNTNGT-----GQNDKEPTYSGTKYTFAS 273

Db 295 LOVDACGTATVNTLQGGALVSTAATVGTGNRLGANSVYEGKADNV--VLBNKGRDVLVT 353

QY 274 GNGTATVASKDOGNITVKYDVNVGDALNVQNLQSGMNLDSKAVAGSSGKVIISGVNPS 333

Db 354 GHATNT- RYDDGGTLDR--NGGTATTVS-MGNG- ----VLADSGAAYSGTSSDG 402

QY 334 K----GKDEFTVINAGNIEITRNKGNIDATFSMTPOFSSVSLGAGADAPLTVSDDG 388

Db 403 KAFSIGGGADALMLEKGSSFTLNAG---DTAIDTVYNGGLFTARGGTLAGTTLLNCA 458

QY 389 ALNVSGKDANKRVRTITNVA PGKEDDVTNVQNLGVQNMNLRIDNNVGNARAGIAGAL 448

Db 459 IFTLSKTYN-----NLTLTIREG---ALLQGGSLTNGSVK--SGSGTLTVSMTLL 507

QY 449 TAGLVQAVLPGRKSMAIGGGT----YLGEAGVTAIGYS-----SISAGGNWJ 490

Db 508 TQKAVNL---NGGTLELNDSTVTTTQVIAQRTALKLTCISYVLNCAIDPTNTVTLASGATWN 564

QY 491 IKGTASGNS 499

Db 565 IPDNATVQS 573

RESULT 2

YDEK\_ECOLI

ID	YDEK_ECOLI	STANDARD;	PRT;	1325 AA.
AC	P32051; P76140; P77168;			
DT	01-OCT-1993 (Rel. 37, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical lipoprotein ydek precursor (ORF7).			
GN	YDEK OR ORF7 OR B1510.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-K12 / MG1655;			
RC	MEDLINE=9742617; PubMed=9278503;			
RX	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-K12;			
RX	MEDLINE=97251357; PubMed=9097039;			
RA	Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,			
RA	Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,			



RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sampel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
RA Takenoto K., Takeuchi Y., Mada C., Yamamoto Y., Horuchi T.,  
RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome  
RT corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 595-1325 FROM N.A.  
RX MEDLINE=94100243; Pubmed=8274505;  
RA Cartwright P.J., Timms M.W., Litchgow T., Hoef P.B., Hoogenraad N.J.,  
RT "An *Escherichia coli* gene showing a potential ancestral relationship  
RT to the genes for the mitochondrial import site proteins ISP42 and  
RT MOM38.";  
RL Blochim. Biophys. Acta 1153:345-347(1993).  
CC -1 SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
CC (Potential).  
CC -1 SIMILARITY: TO E. COLI YFAL.  
CC -1 SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  
CC ISP42 AND MOM38.  
CC -1 CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
CC FRAMESHIFT IN POSITION 653.  
CC -----  
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CC -----  
DR EMBL: AEO00248; AAC74583.1; -  
DR EMBL: D90793; BAA15190.1; ALT\_INIT.  
DR EMBL: D90794; BAA15197.1; ALT\_INIT.  
DR EMBL: X73295; CAA51730.1; ALT\_FRAME.  
DR PIR: A64905; A64905.  
DR Ecogene: E611780; ydek.  
DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
DR Hypothetical protein; Membrane; Lipoprotein; Signal;  
KW Complete proteome.  
KM SIGNAL 1 18  
FT CHAIN 19 1325 POTENTIAL.  
FT LIPID 19 19 HYPOTHEICAL LIPOPROTEIN YDEK.  
FT CONFLICT 884 884 N->K (IN REF. 3).  
FT CONFLICT 1317 1317 M->S (IN REF. 3).  
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA1AD7D CRC64;

Query Match 8.9%; Score 231; DB 1; Length 1325;  
Best Local Similarity 24.4%; Pred. No. 0.00021;  
Matches 146; Conservative 65; Mismatches 245; Indels 142; Gaps 29;

QY 1 MNKITYITNSALNAVAVASELNR-----NHTKRASTVTVAVLATILFTVQAMT 52  
DB 1 MNRIVYINMCTLOVFQACSELTRRAKSTYVNLKSSGTLTFRSLTGLVLLALSGSAS 60  
QY 53 -----DETGLINVEE-----KLSEFGANGKKVNIISDTKGLNFAKETA 90  
DB 61 GASLEVDNDQITIDPDVAVDAVLGVGNGVNLILAGASALTTITTSVIGAN--EDSE 118  
QY 91 GTNGDPTVHLNGIGST--LTD-----MLNTG---ATTNVTNDVNTDDEKRAASVKDY 139  
DB 119 GT-----VNVIGGTWRLLYDSCGNMARNPLNVGSGTGTLNKKQGHVDG-----GY 162  
QY 140 LNAGMNIGKVPKPTASDNDVFRJTDVTEFLSADTKTTVNVESKDNCKTE----- 192  
DB 163 LRLGSGTGV--GTAVNEGDSVLTLEFLIGSYGSLNLT---DKGIVTSYVAILIG 216  
QY 193 VKIGARTSVYKERDK-LVYTK-----GKGENSGSTDEGGLVTAKEVIDAVKAGW 243  
DB 217 YQAGSGQVYVEKGEMLIKNNDSIEFOJNGQGTGEATIREGIVTAETNIIIGNATG- 275  
QY 244 RMTTANGTGTGADKFEIVTSGTKVTPASGNGTTPVSKDDOGNITVK-YD-VNVGDAL 301

DB 276 -IGTLNVO-----DODSVITVRLLYNGYFGNG---TVNISNNGLLINKKEYSLVGQDGS 325  
QY 302 N--VNQLQNSGNL-----DSKAVAGSSGKTVSGNVSPSKAMDEFTVNI 343  
DB 326 HGAVNTDKGMHFLTGGEAFRTIYIGDAGDELNVSSBEKVSGLITAG---MKET--- 379  
QY 344 NAGN-----NIEITRNGKNIDTATSWTPQSSVSLGAGADAPTLVSDDGALNV----- 392  
DB 380 GTGNTITVKDKNSVITNLGTNLGYDGHGEMNISQGLVNSGSSSLGGETGVGNVSLTTG 439  
QY 393 GSKDANKPVRITVAPGVKGDVTVNVAQLKGVAQNLNRIIDVNVGNARAGIAQALATAGL 452  
DB 440 GMEVKNKNTVTTIGVAGVGLNLISDG--KFVSQNTIFLDKASGIGITLMLMATSSFDRT 497  
QY 453 YQAVLP--GKSMMAIGGGTYLGEAGYAI-----GYSSISAGNMIIKGTASGNSR 500  
DB 498 VGINVGNFSGIIVNNGATLNSTGTGIFGNGASGKGIYVISTDSLMLNLK-TSSTNAQ 554

## RESULT 3

ALDA\_ECOLI STANDARD; PRT; 1286 AA.

AC 003155;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adhesin alda-I precursor.  
GN ALDA-I.  
OS *Escherichia coli*.  
OG Plasmid pIB6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.  
RX STRAIN=0126:H27 / 2787;  
RC MEDLINE=92326638; Pubmed=1625582;  
RA Benz I., Schmidt M.A.;  
RT "Alda-I, the adhesin involved in diffuse adherence of the  
RT diarrhoeagenic *Escherichia coli* strain 2787 (O126:H27), is  
RT synthesized via a precursor molecule.";  
RL Mol. Microbiol. 6:1539-1546(1992).  
CC -1 FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE  
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC *ESCHERICHIA COLI*  
CC TO EPITHELIAL CELLS.  
CC -1 SUBCELLULAR LOCATION: Outer membrane.  
CC -----

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CC -----

DR EMBL: X65022; CAA46156.1; -  
DR PIR: S28634; S28634.  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR InterPro: IPR004899; Perleactin.  
DR Pfam: PF03212; Perleactin; 1.  
DR Pfam: PF03212; Perleactin; 1.  
DR TIGRfams: TIGR01414; autotrans\_bar1; 2.  
KW Cell adhesion; Signal; Outer membrane; Plasmid.  
FT SIGNAL 1 49  
FT CHAIN 50 1286  
FT PROPEP ? 1286  
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 8.5%; Score 220.5; DB 1; Length 1286;  
Best Local Similarity 21.7%; Pred. No. 0.00066;  
Matches 128; Conservative 78; Mismatches 204; Indels 179; Gaps 29;

[illegible]

Query Match	Best Local Similarity	Matches	7.7%, 22.9%, 137;	Score 201; 65;	DB 1; 229;	Length 2249; 168;	Gaps 29;
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CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).							
CC -----							
DR EMBL: M31227; AAA26380.1; -							
DR PIR: A41477; A41477.							
DR InterPro: IPR006315; Autotransporter.							
DR InterPro: IPR005546; Autotransporter.							
DR Pfam: PF03797; Autotransporter; 1.							
DR TIGRfams: TIGR01414; autotrans_bar1; 3.							
DR Antigen: Repeat; Signal; Cell wall; S-layer; Glycoprotein.							
FT SIGNAL 1 28							
FT CHAIN 29 2249							
FT DOMAIN 212 1180							
FT REPEAT 212 286							
FT REPEAT 287 358							
FT REPEAT 359 430							
FT REPEAT 431 505							
FT REPEAT 506 577							
FT REPEAT 578 652							
FT REPEAT 653 724							
FT REPEAT 725 799							
FT REPEAT 800 874							
FT REPEAT 875 949							
FT REPEAT 950 1021							
FT REPEAT 1022 1093							
FT REPEAT 1094 1165							
FT REPEAT 1166 1180							
SO SEQUENCE 2249 AA; 224333 MW; A96646C089DE087 CRC64;							
Query Match	7.7%, 22.9%, 137;	Score 201; 65;	DB 1; 229;	Length 2249; 168;	Gaps 29;		
13 LNMAVAASELNRN--HTKRASATKTVLTLFATFVAQATDEGLINVEFKLSGAN 70	:	:	:	:	:		
787 LNLGASQVGVGDIGNLSLTIISVGAGTALGGAIVKATTKLTINAASVLT---LTNAN 843	:	:	:	:	:		
71 GKRYNIISDTGLNFAKETAGTNGDT--TVHLNGISGSLTDLMLNT----- 114	:	:	:	:	:		
844 AVLIGAVDNT-----TGDDNNGVLLNLNALSGVTEGIDGNTSLATISVGAGTAT 892	:	:	:	:	:		
115 --GATTNVTNDNTVDDEKKRAASAKVDLNAAGWNIKGVKPGTTASDNVDFKTYTVEELS 172	:	:	:	:	:		
893 LGGAVIKATTKTLTN---AASVLTLTNAAVLTGAIDNTGGDNGVLLNLGALSQVT 947	:	:	:	:	:		
173 ADFTK---TVNYESKD--NG--KKEVKIGAKTSVIREKDGKLVTS---KXGEN 218	:	:	:	:	:		
948 GDIGNTSLATISVGAGTALGGAIVKATTKLTLDASAASVAFNPVVVGTGAIDNTGANNN 1007	:	:	:	:	:		
219 GSSTDEGEGLVTAK---EVIDAANKA---GWRKTKTTAN-----GQ 253	:	:	:	:	:		
1008 GIIVFTGISTYTGAVGNTNMLATLVNAGAGLQVGGVKKANTILTLTDNAAAVFTNPVVV 1067	:	:	:	:	:		
254 TGQADKEFTVYSGKRVTFPASFNGSTTAFVSKDDGQNTITVKYDVNVGDL-----N 302	:	:	:	:	:		
1068 TGAIDNTGNANNGI-VFTGNSVTYGVN---GNTNALATVANGAGILQVGGVKKANT 1121	:	:	:	:	:		
303 VN-----QLQNSGWNLDKSAVAGSSGKVISGNSVPSGKMDQETVNNIN 344	:	:	:	:	:		
1122 INLTDNAAVTFNPVVVGTGAIDNTG--NANNGIYTFGNSVTYSDT---GNTALATVN 1176	:	:	:	:	:		
345 AGNNIEITRNG---KNIDATSMTPQFSSVSLGAGADAP-----TSLVDEGALANVSK 395	:	:	:	:	:		
1177 VGAGITTLQAGSSLANANNIDPFARSTLEPNGLDGGKAIPYYPFGKALANGNALNLVNTK 1236	:	:	:	:	:		
396 DANK-----PVRTNVA PG-----VKEDVTNV AOLKGYAQLNNR-----IDNVN 436	:	:	:	:	:		
1237 LLTASHLTLGTVAEINIGAGNLLFTIDASGVDTILN-----AQNINFRARDSVLVLNLT 1291	:	:	:	:	:		
437 GNAARAGLQALATATAGLVQVATPYPGKSMAIIGSGTTLGEGRATVIGSSSISAGNMIKETA 495	:	:	:	:	:		
1292 G---VGVNIIILADLV---APGAD-----GTVVEFGVGNVLNVSNN--VAQTA 1333	:	:	:	:	:		

RESULT 5  
YDBA\_ECOLI  
ID YDBA\_ECOLI STANDARD; PRT: 2003 AA.  
AC P3366; P76087; P76088; P76856; P76857; P76859;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ydba.  
GN YDBA OR B1401/B1405.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_Taxid=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.,  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Salto N.,  
RA Sempel K., Seki Y., Sivasubram S., Tagami Y., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.,  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 464-2003 FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=92190338; PubMed=1665988;  
RA Moszer I., Glaeser P., Danchin A.;  
RT "Multiple insertion sequences near the replication terminus in  
Escherichia coli K-12.";  
RL Biochimie 73:1361-1374(1991).  
CC -1- SIMILARITY: TO S.TYPHIMORIUM ORF NEAR CYSG (AC P25928)  
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR  
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
BETWEEN AMINO ACIDS 839 AND 840.  
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CC -----  
DR EMBL: AE000237; AAC74483.1; ALT\_SEQ.  
DR EMBL: AE000237; AAC74487.1; ALT\_SEQ.  
DR EMBL: D90778; BAA15009.1; ALT\_SEQ.  
DR EMBL: D90778; BAA18880.1; ALT\_SEQ.  
DR EMBL: D90779; BAA18881.1; ALT\_SEQ.  
DR EMBL: X62680; NOT\_ANNOTATED\_CDS.  
DR Ecogene; Egl1307; ydba.  
KM Hypothetical protein; Complete proteome.  
FT CONFLICT 489 489 I -> V (IN REF. 2).  
FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 7.2%; Score 188; DB 1; Length 2003;  
Best Local Similarity 24.9%; Pred. No. 0.045;

Matches 138; Conservative 74; Mismatches 212; Indels 130; Gaps 33;  
QY 46 TVQANATDEGLINV-ETKLSFGANGKKNIIISD-----TKG-----LNFARFCTANG 94  
DB 269 TGDATVNDKGTMTVDPESMGIDGDKAIVNEGSESTTGQTQINGDDATANNNG 328  
QY 95 DTVVHLNGISGTLTDLMLNTGAT-----TNYTNDVTVDEKKRAASVDVL 140  
DB 329 KTVV-DGKSTGEIENGNGKVIQDDDLVSGGGHIDITGDSATVD-NKGITVTVDPE 385  
QY 141 MAGNIRKVRPGTTASDNVDVPTVTVFLSADTKTTVVNESKONGK--TEVKIGA 197  
DB 386 SIGIQVDG-DQAVVNNGESAIITNGGTGTQINGDDATANNNGKTVVQKSTGEI-AGN 443  
QY 198 KTVYRKDKKL-VTGKKG---ENGSTDEGELVAKK-----VIDA---VNRAGW 243  
DB 444 NGKVI-QDDDLVSGGGHIDITGDSATVNDKGTMTVDPESIGIIDDQAIVNEG- 500  
QY 244 RMKTTTANGOTGOADKFEFTVTSCTKYFASGNGTATVSRDD-----QGNITVYDVNVG 298  
DB 501 --ESTITNGGT-----TQINGNDAT-ANNSGKTVVDKGDSTGKTAIGNIGI---VNLD 548  
QY 299 DALNV-----NQLONGNN--LDK-----AVAGSGKVIIGNVSPSKGKDETVINAGN 347  
DB 549 GSLVTVGAGVGENIGNGTNNKGDIVSDTSGIGLINGEGATVVSNTGDIVNS-NEAT 607  
QY 348 NIETTRGNKNDIATSM-TPQFSS-VSLGAGADPPLTVSD-----EGALNVSKDAN 398  
DB 608 GFSITTNISGKVSILAGSQVDFSTGVDLGNNSNVTIAAKDLKVGOKATGINV-SDAN 666  
QY 399 KPVRIIVAVGVEGDTVYNAQL--KGVAQNLNIRIDVNGNARAGI----- 443  
DB 667 -TNYITNGVLYVDKDTADNAAEYFEDPSVGINVYGSNNVTLOGKLVSDSEVTSRQSN 725  
QY 444 ---AQAIATGLVOATLPKSMWAIIGGTYLGE-----AGTAI-----G 479  
DB 726 LFDGSAEKTSGLV-VIGDGMTVMNMGLELIGEKNALDGSQVYSLRTGYSTSVIVVG 784  
QY 480 YSSISAGGNWIKG 493  
DB 785 ESSVYLVNGDTTISG 798

RESULT 6  
OMPB\_RICIA  
ID OMPB\_RICIA STANDARD; PRT: 1656 AA.  
AC O0663;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)  
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
GN OMPB.  
OS Rickettsia japonica.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_Taxid=35790;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-YH;  
RA Uchiyama T.;  
RT "Sequencing of the gene encoding the protein rOmp B of Rickettsia  
japonica.";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
SIMILARITY).  
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-

LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AB003681; BAA20138.1; -  
 CC InterPro: IPR006315; Autotransport.  
 CC InterPro: IPR005546; Autotransporter.  
 CC Pfam: PF03797; Autotransporter; 1.  
 CC TIGRFAMs: TIGR01414; autotrans\_bar1; 2.  
 CC Antigen: S-layer; Cell wall.  
 CC CHAIN 1 1338 120 kDa SURFACE-EXPOSED PROTEIN.  
 CC FT CHAIN 1339 1656 32 kDa BETA PEPTIDE.  
 CC FT DOMAIN 528 533 POLY-GLY.  
 CC SEQUENCE 1656 AA; 168097 MW; 3132A69CD5999F CRC64;  
 Query Match 7.0%; Score 182.5; DB 1; Length 1656;  
 Best Local Similarity 22.7%; Pred. No. 0.068; Mismatches 217; Indels 211; Gaps 32;  
 Matches 144; Conservative 63;  
 37 AVLTLLFAFVQAN-ATDEGLINVEKISFGANG-----KKVNI 76  
 179 AAATSTVFDL--ANPTQKAPLILADNLNLYANGNLNTNGFIQVSDKSFATVKAIN- 235  
 77 ISDTKGLFAKETAGTN-----GDTYHLNGISLTLDMLN-TGATNTVNDNVDDDE 129  
 236 IGDQGGEMFNATNATNALNLQAGTTFNGTGTGRLVLLSKNGATDF--NVYG-- 290  
 130 KKRAASVDVNLNAGMNIKGVKPGTTASDNVDFVETDVEELSDTKTNTN----- 181  
 291 -----SLGCKLKGITELMTVALNGQLINAG-----PANAVIGTNNAGRAAF 334  
 182 VESKDNKRTVEV--KIGAKTSVIRE-----KDGKLVYTGKGG 216  
 335 VVSVDNGKAATIDQVYAKDMVIOASANANGOVNFRHIVDVGIDGTAFKTAASIVATLON 394  
 217 ENGSTDEGEGLYAKEDYDAVNRKAGMKTTTANGGVGADKRETVTSGRKVFASNG 276  
 395 SNFGTTDFG-NLAAQVTVPTM-----TLTGN-FTGDAANN-PGNTAGV-ITFAA-NG 441  
 277 TTATVSKDDGNTVYKVDVNGDALNVLNQLNSGMNLSKAV--AGSSGKYSIGVSPSK 334  
 442 TLASASAD--ANAVTNNITAEASGVGVVQLSGTHRELRLGNAGSVFKLADGIV--IN 497  
 335 GKMDTV----- 341  
 498 GKVQGVTVLVGVLAAAGATTLDGSAITIGDIGNGGGALQSTILANDATKTLTGANII 557  
 342 -----NINA-GNNIETRNKNI-----DATSMTPQFSSVSLGAGADATLSVDD- 387  
 558 SANGTINFGANGGTIKLTSTONNIYVDCDLAIA-TDPTGVVADSLTMAOTLTISGTIG 616  
 388 -----GALNVGSKDA--NRPVRIYNAPGVKEEDV-----TVNAQLKGYAQ 426  
 617 IIGANNITLGGPNISSKTTILNGCNVAINELVIG--NNSGVQFAHNTYILTFTNAAGGK 675  
 427 NLNRRIDVNGNARAGIAQATATAGLVQAYLPGR-----SMAAIGGGTYLGEAGYA--- 477  
 676 IIFPVVNNNTTTLAAGTNLGSAAAPLAIINFGSKGARADYVLNVGEGVNL-----YATNIT 731  
 478 -----IGYSSISAGCNMTIKGTASGNSRHHGASA 507  
 732 TTDAVGSFVFNAGKNIVSGTVGGQGNKKNENTYA 766

OMP, R1CCN STANDARD; PRT: 1655 AA.  
 AC O9KKA3; O9KKA3; O9KKA3; O9KKA3; O9KKA3; O9KKA3; O9KKA3; O9KKA3; O9KKA3; O9KKA3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (RompB)  
 DE (Romp B) (Contains: 120 kDa surface-exposed protein (Surface protein  
 DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).  
 GN OMP OR R1085.  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Malish 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samsom D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
 RL Science 293:2093-2098(2001).  
 RN [2]  
 RP SEQUENCE OF 33-1649 FROM N.A.  
 RC STRAIN=Indian tick typhus, and Malish 7;  
 RX MEDLINE=20393643; PubMed=10939649;  
 RA Roux V., Raoult D.;  
 RT "Phylogenetic analysis of members of the genus Rickettsia using the  
 RT gene coding the outer-membrane protein rompB (ompB)." ;  
 RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).  
 RN [3]  
 RP SEQUENCE OF 353-1655 FROM N.A.  
 RC STRAIN=Malish 7;  
 RA Stenos J., Walker D.;  
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
 RT australis: the most divergent rickettsia of the spotted fever group." ;  
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
 CC SIMILARITY).  
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AE008659; AAL03623.1; -  
 CC EMBL: AF123721; AAF34124.1; -  
 CC EMBL: AF123726; AAF34129.1; -  
 CC EMBL: AF149110; AAD39533.1; -  
 CC PIR: E97835; E97835.  
 DR InterPro: IPR006315; Autotransport.  
 DR InterPro: IPR005546; Autotransporter.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR TIGRFAMs: TIGR01414; autotrans\_bar1; 2.  
 KW Antigen: S-layer; Cell wall; Complete proteome.  
 FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1335 1655 32 kDa BETA PEPTIDE.  
 FT VARIANT 61 61 G -> A (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).

```

FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT CONFLICT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; EA9E19377D5FCE37 CRC64;

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Query Match 7.0%; Score 182; DB 1; Length 1655;

Best Local Similarity 23.8%; Pred. No. 0.072;

Matches 130; Conservative 66; Mismatches 240; Indels 110; Gaps 29;

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QY 25 NHTKRASATKVFVATLLFAVQANADTBETG-LINVEREKLSEFGANGKRVNIISDTKGL 83
DB 308 NGLKRNAGANAFAVIT-----NNGAGRAAGFVVSVD-----NGKATIIDGOVYAK 353
QY 84 NFAKETAGTNGDTTV-HLNGIGSTLIDMLNTGATNTVT-NDNV-TDEKKRAASY---- 136
DB 354 DMVIOANAVGVNFRHIVDGTGTAFKTAASKVAITQNSFGTTDGGNLAQIIVPV 413
QY 137 KQVLNAGNINIKVPEPTASDNVDVRYTD---TYEFLSADTKTTVN---VESKDN- 188
DB 414 TMTLNFTGDSANPNTAG-----VTFDANGTLASASADANVAVTNNITALEASGAGY 468
QY 189 -----KTEVKIGAKTSVYKEKDGKLVYK-----GKGENGSTDEGBLVNAKEY 234
DB 469 VOLSGTHAAELRLGNAGSVFKLADGVINCKVNOTALVGGALAGTITLIDGSATYTG--- 525
QY 235 IDAVNRAGRMKTTTANGOTGADKEFTV-----SGTVFASGNGTATVSKD 285
DB 526 -DIGNAG-----AAALOGITLANDATKTLIGGANIIGANGIINQANGITIKLS--T 578
QY 286 QGNITVYKYD-----NWDALNVQOLNSGNLDSKAVAGSSGVIGSNVSPSKGM- 337
DB 579 QNNIVVDFDLATIDTGTGVADSSLTNAQTLTFINGIGTVGANKTKLGFQNISSKTVLS 638
QY 338 DETVNIN---AGNN--IEITRNKGNIDIAFMTPO---FSSV-----SIGAADAFTLS 383
DB 639 DGDVAINELYIGNAGVQFRAHNTYLLTRTTNAGQKIIIFPVANNNTLATITNIGS-A 697
QY 384 VDDEGALNVGSKDANKPVRTTNVAPGVKEGDTYTNVQOLKGVANLNNRIDNVNG-NARAG 442
DB 698 TNLAEINFGSKCAAVVDYLVNKGYNL-YATNITTTDA---NVGSFIIFNAGCTINIVS 753
QY 443 IAOAINTAGLVQ-----AYLFGKSMALIGGTYLGEAGVYALGYSSISAGMWIITKTA 495
DB 754 -----TVGGQOGNKFENTVALDNGITVKFLGNATFNGNTTIAAN-STLQIGNYTADFVA 806
QY 496 SGNSRG 501
DB 807 SADGTG 812

```

## RESULT 8

OMPB\_RICRI

ID OMPB\_RICRI STANDARD; PRT; 1654 AA.

AC 053047;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein)

DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (rOmpB)

DE (rOmp B) [contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].

GN OMPB.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

OC Rickettsiaceae; Rickettsiidae; Rickettsia.

OX NCBI\_TaxID=783;

RP SEQUENCE FROM N.A.

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RC STRAIN-R;
RX MEDLINE=91267802; PubMed=1724278;
RA Gilmore R.D. Jr., Clephel W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame;
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [1]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN-R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Jostle N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPB/OMPB FAMILY.
CC
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CC
CC EMBL: X16353; CAA34403.1; -.
CC PIR: S18227; S18227.
CC DR InterPro: IPR006315; Autotransport.
CC DR InterPro: IPR005346; Autotransporter.
CC DR Pfam: PF03797; Autotransporter; 1.
CC DR TIGRFAMs: TIGR01414; autotrans_bar1; 2.
CC KW Antigen; s-layer; Cell wall.
CC FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
CC FT DOMAIN 1334 1654 32 KDA BETA PEPTIDE.
CC FT DOMAIN 1181 1188 POLY-TIR.
CC SQ SEQUENCE 1654 AA; 168184 MW; D7AB0FB7087F618 CRC64;

```

Query Match 6.9%; Score 180; DB 1; Length 1654;

Best Local Similarity 23.9%; Pred. No. 0.091;

Matches 123; Conservative 64; Mismatches 203; Indels 124; Gaps 29;

```

QY 70 NGKRVNIISDTKGLNFAKETAGTNGDTTV-HLNGIGSTLIDMLNTGATNTVTND--VT 126
DB 340 NGRVATIDGOVYAKDMVIOGANSATGOVNFHIVDGTGTAFKTAASKVTITQDSNFGM 399
QY 127 DDEKKRAASYK--DVNLAGNINIG--VKPRTASDNVDVRYTD---TYEFLSADTKTT 179
DB 400 TDFGNLAQIKRYNATITLGNFTGDSANPNTAG-----VTFDANGTLESASADANVAV 454
QY 180 VN-----VESKDN-----KTEVKIGAKTSVYKEKDGKLVYK-----GKGENS 220
DB 455 TNNITALEASGAGVQOLSGTHAAELRLGNAGSIFKLADGVINCKVNOTALVGGALAGT 514
QY 515 ITLDGSATITGD--IGNAGGAALQRIITLAN-----DAKTLTLIGGANIIGAGGTTIDL 566
DB 278 -----TATVSKDQGNITVYKYD-----NWDALNVQOLNSGN--LD 314
QY 567 QANGGTIKLTST-----QNNIVVDFDLATIDTGTGVADSSLTNAQTLTNGIKGITGAN 621
DB 315 SKAVA-----GSSGKVIS-GNVSPSKQMDETVINAG-----NNEIETR----- 357
DB 622 NKTGLGPNIGSSKTVLSNNGVA-----INELVINGNCAVQFADDTYLITRTTNAAGCKI 676
QY 358 I--DIATSMTPQFSSVSLGAGADAPTLVSDDDEGALNVGSKDANKPVRTTNVAPGVKEGDV 415
DB 677 IENPVVNGTTLAAGTNIGS-----ATNPILAINEFGSKGVNVD--VLNVGEGYNL--YA 727

```

QY 416 TNVAQLKVAQNLRNLRDNGV-NARAGIAQIATAGLVQ-----AYLPKSMMAIG 467  
DB 728 TINTTTTDA---NWGFEFVFNAGTNIIVSG-----TVGGQGNKRENTALENGTIVKFLGN 778  
QY 468 GTYLGAGYATGYSISAGNMWIKGTASGNSRG 501  
DB 779 ATFNNGTTTAA-NSTLQIGNGYNTADCVASADGTG 811

RESULT 9  
ALYS\_ENTFA STANDARD: PRT: 737 AA.  
AC P37710:  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)  
DE (Beta-glycosidase).  
GN EF0799.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91358349; PubMed=1679432;  
RA Bellevue C., Potvin C., Trudel J., Asselin A., Bellemare G.;  
RT "Cloning, sequencing, and expression in *Escherichia coli* of a  
RT Streptococcus faecalis autolysin";  
RL J. Bacteriol. 173:5619-5623(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=V583 / ATCC 700802;  
RX MEDLINE=22550857; PubMed=12663927;  
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,  
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M., Nelson W.,  
RA Daugherty S., Deboy R.T., Durkin S., Kolonay J., Madupu R.,  
RA Vanthaeven J., Tran B., Upton J., Hansen T., Shetty J., Khouli H.,  
RA Usterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;  
RT "Role of mobile DNA in the evolution of vancomycin-resistant  
RT Enterococcus faecalis";  
RL Science 299:2071-2074(2003).  
CC -!- FUNCTION: Hydrolyzes the cell wall of *E. faecalis* and  
CC M. lysodeikticus. May play an important role in cell wall growth  
CC and cell separation.  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN  
CC BINDING.  
CC -!- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.  
CC -!- SIMILARITY: Contains 6 lysm repeats.  
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CC -----  
DR EMBL: M58002: AAA67325.1: -  
DR EMBL: AE016949: AA080613.1: -  
DR PIR: A38109: A38109.  
DR TIGR: EF0799: -  
DR InterPro: IPR002901: Amidase\_4.  
DR InterPro: IPR002482: LysM.  
DR Pfam: PF01832: Amidase\_4; 1.  
DR Pfam: PF01476: LysM; 5.  
DR SMART: SM00257: LysM; 6.  
DR SMART: SM00047: LY22; 1.  
KW Cell division; Glycosidase; Bacteriolytic enzyme; Cell wall;  
RN Cell division; Septation; Repeat; Signal.  
FT SIGNAL 1 53 POTENTIAL.

FT CHAIN 54 737 AUTOLYSIN.  
FT REPEAT 363 405 LYSM 1.  
FT REPEAT 431 473 LYSM 2.  
FT REPEAT 499 541 LYSM 3.  
FT REPEAT 567 609 LYSM 4.  
FT REPEAT 633 675 LYSM 5.  
FT REPEAT 695 737 LYSM 6.  
FT REPEAT 737 737 LYSM 6.  
FT CONFLICT 85 85 T -> I (IN REF. 1).  
FT CONFLICT 118 118 A -> V (IN REF. 1).  
FT CONFLICT 143 143 A -> T (IN REF. 1).  
FT CONFLICT 417 417 S -> N (IN REF. 1).  
FT CONFLICT 449 449 S -> T (IN REF. 1).  
FT CONFLICT 476 476 A -> T (IN REF. 1).  
FT CONFLICT 484 484 N -> S (IN REF. 1).  
FT CONFLICT 567 632 MISSING (IN REF. 1).  
SQ SEQUENCE 737 AA; 77025 MW; ABB16BD506AC7507 CRC64;

Query Match 6.9%; Score 179.5; DB 1; Length 737;  
Best Local Similarity 23.0%; Pred. No. 0.038;  
Matches 111; Conservative 55; Mismatches 208; Indels 109; Gaps 21;

QY 66 SFGANGKKVNIISDTKGLNFA---KETAGTNGDTTVHLANGISTLPMLNTGATTVT 121  
DB 268 SFQDHAHLKTTSPQAGYIYAAGAKMSNTSSYRDATLVT--GRATDPSTNAKLNNTY 325  
QY 122 NDVYTDDEKKRAASYKDYLANAGWNIG--VKPGTTASNDVDFRTY-----DTVEFLSA 173  
DB 326 AYNLTQ-----YDTPSSGNGTGGTVNPGTGSNNOSGTNTYTVKSGDTLNTKITA 376  
QY 174 DTKTTVAVESKDNKGKTEVKGAKTSVKEKDGKLVYKKGKNGSGSTDE--GEGLVYAK 232  
DB 377 QYGVSAHLRSWNGISGDLIFVQGLIVKKGASGN--TG--DSGSGSNNNSGTTTYTV 433  
QY 233 EVIDAVNKRAGMRKTTTANSGTGQADKEFTVSGTKVTF---ASGN--GTTATVSKDDG 287  
DB 434 KSGDTLNTIAQYGVSAHLRSWNGISGDLIFVQGLIVKKGASGNTGSGNNOS 493  
QY 288 NITVYDYVVGDAAL-----VNQLNSGWNLDKAAVAGSSGKYI-----SGNVSPSK 335  
DB 494 GTNTYTTKSGDTLNTIAQYGVSAHLRSWNGISGDLIFVQGLIVKKGTSNGTSGSS 552  
QY 336 KMDETVNIINAGNIETIRNGKNIDATSMTPQFSSVSLGAGADATLSV--DDEGAL--- 390  
DB 553 -----NGSGN--NNOSGTTTYTTSKSGDTLNTIAQYGVSAHLRSWNGISGDLIF 602  
QY 391 -----NWGSKDAKRPVITNVAPG-----VKEGDVYTNVAQLKVAQNLRNIRD 434  
DB 603 GQKITVKKGANGSGNTNKP--TNNGGATTSTYIKSGDTLN-----K 643  
QY 435 VNGNARAGIAQIATAGLVQAVLPEKSMMAIGGTYLGEAGYATGYSISAGNMWIKGT 494  
DB 644 ISAGFGVSANLRSWNGI-----KGDLI FAGQTIIVKKG-----ASAGNASTNS 689  
QY 495 ASG 497  
DB 690 ASG 692

RESULT 10  
ICEN\_XANCT STANDARD: PRT: 1567 AA.  
AC P18127:  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ice nucleation protein.  
GN IMAX.  
OS Xanthomonas campestris (pv. translucens).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
CC Xanthomonadaceae; Xanthomonas.  
OX NCBI\_TaxID=343;  
RN [1]  
RP SEQUENCE FROM N.A.

CC STRAIN-X56S;  
 RX MEDLINE=9108059; PubMed=2259339;  
 RA Zhao J., Orser C.S.;  
 RT "Conserved repetition in the ice nucleation gene *inx* from  
 RL *Xanthomonas campestris* pv. *translucens*.";  
 CC -1 FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE  
 CC CRYSTALLIZATION IN SUPERCOOLED WATER.  
 CC -1 SUBCELLULAR LOCATION: Outer membrane (By similarity).  
 CC -1 DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS  
 CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A  
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.  
 CC -1 MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE  
 CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.  
 CC -1 SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN  
 CC FAMILY.  
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 CC -----  
 DR EMBL: X52970; CAA37140.1; -;  
 DR HSSP: P06620; IINA;  
 DR InterPro: IPR000258; Ice\_nucleatn.  
 DR Pfam: PF00818; Ice\_nucleation; 81.  
 DR PRINTS: PR00327; ICENDCLENTN.  
 DR PROSITE: PS00314; ICE\_NUCLEATION; 57.  
 KM Ice nucleation; Repeat; Outer membrane.  
 SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

Query Match 6.9%; Score 178.5; DB 1; Length 1567;  
 Best Local Similarity 20.2%; Pred. No. 0.1;  
 Matches 103; Conservative 82; Mismatches 246; Indels 79; Gaps 20;  
 QY 20 SELTRNHTKRASAVKAVLAVLTLFATVQANMDET---GLINTEKLSGANGKRYNI 76  
 DB 808 SDITAGTGTAGADSTLLAG--YGSTQTSGBSSSLTAGYGSTQAR---EGSDV-- 858  
 QY 77 ISDTKGLNFAKETAGTNGDTTVHLNGISLTLDMLNTGATNTNTNNVTDEKKRA5Y 136  
 DB 859 ---TAGY---STGTAGADSTLLSGYGSTQ---AGSSSLTAGYGSTQARKSDV 906  
 QY 137 KDVLNAGMNITKYPGTTASDNDFVRYTDFEFLADTKTTVNVESKDKGKTEYKIG 196  
 DB 907 ---TAGYGSTG---TAGADSTLLAGYGSTQTSGBSSSLTAGYGSTQARKSDMTAG 957  
 QY 197 AKTSVIREKDKGLVTGKGKGENSSSTDEGELVAKEDVAVNKAQRMTKTTANGCTQ 256  
 DB 958 YGSGTGTAGADSTLLAGYGSTQSGS-----BSLTAGYGSTQTAREGSDVT 1003  
 QY 257 ADKEFYVSGTKYTFASNGTTFATVSKDQGNITVKYDVNVGDALNANOLONSGMNDSK 316  
 DB 1004 AGYGSTGTAGADSTLLAGYGSTQTAGSD--SULTAGY---GSTQTAQSGSDVYAGYST 1057  
 QY 317 AVAGSSKVIISGVNPSPKGKMDFTVINAGNINIEITRNKNIDITATSMPTQFSSVSLGAG 376  
 DB 1058 GTAGADSTLLAGYGSTQTAGSDSSLTAGYGST--OTARQGSPI-----TAGYGSTGT-AG 1109  
 QY 377 ADAPTLSVDEGALNVSKDANKPVRTITNAAPGKEDVDYNNVLOLKVAAQLNLRIDNVN 436  
 DB 1110 ADSSLLA--GYGSTQGTGYBSNLTAGYGSTQTAQEDSSLTAGYGSTTAGDSSLLAGYG 1167  
 QY 437 GNARAGIAQAIATP--GLVQAVYLPKSKMAAIGGTYLLEAGY---AIGYSISAGC--NW 489  
 DB 1168 STQTAGVNSLTITGTGSTQTAQESSSLTAGYGST--STAGYDSTLLTAGYGSTQTAQKST 1225  
 QY 490 IIKGTASGNSRGH-----FGASASVGYQ 512  
 DB 1226 LTAGYGSNSTAGHSSSLTAGYGSTQIAGYE 1255

RESULT 11  
 ID BIGA\_SALTY STANDARD: PRT: 1953 AA.  
 AC P25927; P25928; Q9XC03;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative surface-exposed virulence protein biga precursor.  
 GN BIGA OR STM3478.  
 OS *Salmonella typhimurium*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Salmonella*.  
 OX NCBI\_Taxid=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14028;  
 RA Stojilkovic I., Valentine P., Heffron F.;  
 RT "Salmonella typhimurium rhs homolog.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 RN [3]  
 RP SEQUENCE OF 1-765 FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE=91100301; PubMed=1987123;  
 RA Wu J.Y., Siegel L.M., Kredich N.M.;  
 RT "High-level expression of *Escherichia coli* NADPH-sulfite reductase:  
 RT Requirement for a cloned *cysE* plasmid to overcome limiting *str*heme  
 RT cofactor.";  
 RL J. Bacteriol. 173:325-333(1991).  
 CC -1 CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
 CC in positions 414 and 732.  
 CC -----  
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 CC -----  
 DR EMBL: AF133696; AAD39458.1; -;  
 DR EMBL: AE008859; AAL22340.1; -;  
 DR EMBL: M64606; AAA27042.1; ALT\_FRAME.  
 DR EMBL: M64606; AAA27043.1; ALT\_FRAME.  
 KW StyGene; SG10437; Biga.  
 KR Virulence; Repeat; Signal; Complete proteome.  
 RW SIGNAL  
 FT CHAIN 1 27  
 FT 28 1953  
 FT  
 FT DOMAIN 101 252  
 FT REPEAT 101 103 15 X 11 AA TANDEM REPEATS.  
 FT REPEAT 104 113 1 (INCOMPLETE).  
 FT REPEAT 114 122 2 (INCOMPLETE).  
 FT REPEAT 123 133 3 (INCOMPLETE).  
 FT REPEAT 134 144 4.  
 FT REPEAT 145 155 5.  
 FT REPEAT 156 166 6.  
 FT REPEAT 167 177 7.  
 FT REPEAT 178 188 8.  
 FT REPEAT 189 199 9.  
 FT

```

FT REPEAT 200 210 11.
FT REPEAT 211 221 12.
FT REPEAT 222 232 13.
FT REPEAT 233 243 14.
FT REPEAT 244 252 15. (INCOMPLETE)
FT CONFLICT 207 207 D -> DRGDDVTPDD (IN REF. 1).
FT CONFLICT 514 514 A -> R (IN REF. 3).
FT CONFLICT 1698 1698 D -> N (IN REF. 1).
FT CONFLICT 1795 1798 QYLE -> ITLO (IN REF. 1).
FT CONFLICT 1836 1837 SA -> T (IN REF. 1).
SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C95AD91AE CRC64;

```

Query Match 6.8%; Score 178; DB 1; Length 1953;  
 Best Local Similarity 24.7%; Pred. No. 0.14;

Matches 131; Conservative 65; Mismatches 171; Indels 164; Gaps 33;

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QY 84 NFAKETAGTNGDT-----TVHLNGISTLT-----DMILNTG 115
DB 429 NFAGDIAYSGGTATIIIDGNATIKNTGTSISGASGTIVIDGNARVNDGDMITDG 488
QY 116 AT-TVNTDNTVDEKRAASVVDYLNAGWNKIGVPGTTASDNDVFTYDVEFLSAD 174
DB 489 GCGHITGDNVYID-----NAG-----STTVS-----GAD 513
QY 175 TTTTVNVESKDN-----GKTEVKIGAKTIVIEKDK-----LVTKGK-----K 215
DB 514 --ATALYIEG-DNALVINEGNOT-ISGAVGTRIDGDDAHTNTGDIADVAGASAAVILN 569
QY 216 GENGSTDEGEGLVT--AKEVI--DAVNKAGWRMKTATTANGTGQADKEFTVSGTKVTF 271
DB 570 GNGSLITQAGDLVLDGANGITTYGTGNEA-----KNTGNATVVRDADSGFVYVAGKNTF 624
QY 272 -----ASGNGTATVSKDDGNTVKKYVNVGALNVLONSGWNLDSKAVAGSSGK 324
DB 625 KKKGDIDVSLNCTGALVS-GDMSQYTLDDGINV---VSVDSEGVFSATGVSQSDSNA 680
QY 325 V-ISGNVSPS-----KGMDEVTNINAGNNEITNKR-NI---DIANSMPQESS 370
DB 681 YDITGNVNISADYGGODDLAAGAPPLTGAVVNGNGNVTTLGALIDNDLSATGGQYLDV 740
QY 371 VSLGAGADAPLTSLVDEGALNVGSKDANKPVRITNVAPGVKRGDVTNVAQLG---VAON 427
DB 741 VCLSTVGGDNDVEID--GGINT--THSEPLDGT-----ADITGIS-VGSGNSTVILN 788
QY 428 LNNRIDN--VNGN--ARAGIAQAL-----ATAGLVQAYLD-----GKSMAIIGGTY 470
DB 789 GHSITDTMTVGVGHVAVLARNNGSGSLIICDDSVVDVNVASYIPTGYTTYNALIMADGEGTS 848
QY 471 LGEAG-----YAL-----GYSSISAGNMWIKTASGNSRGHFGASASVG 510
DB 849 IENKGDITSHGVYSVIRADNGSEVNSGDILVYATSSNSEDRAAITRASG 899

```

## RESULT 12

OMPA\_RICCN

ID OMPA\_RICCN STANDARD; PRT: 2021 AA.  
 AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;  
 AC Q52670; Q52674;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
 antigen) (rompA) (rOmp A).  
 GN OMPA OR RC1273.  
 OS Rickettsia conorii.  
 OS Rickettsia conorii.  
 OC Bacteria: Proteobacteria: Alphaproteobacteria: Rickettsiales;  
 OC Rickettsiaceae: Rickettsiae; Rickettsia.

NCBI\_TaxId=781;  
 [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-Malish 7;  
 RX MEDLINE=94171067; PubMed=8125327;  
 RA Crocquet-Valdes P.A., Weiss K., Walker D.H.;

```

RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia
RT conorii (Malish 7 strain).";
RL Gene 140:115-119(1994).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN-Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [3].
RP SEQUENCE OF 8-204 FROM N.A.
RC STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;
RX MEDLINE=97015921; PubMed=8682558;
RA Roux V., Fournier P.-E., Raoult D.;
RT "Differentiation of spotted fever group rickettsiae by sequencing and
RT analysis of restriction fragment length polymorphism of PCR-amplified
RT DNA of the gene encoding the protein rompA.";
RL J. Clin. Microbiol. 34:2058-2065(1996).
RN [4].
RP SEQUENCE OF 953-2012 FROM N.A.
RC STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;
RA Raoult D., Fournier P.-E., Roux V.;
RT "Phylogenetic analysis of spotted fever group rickettsiae by study
RT of the outer surface protein rompA.";
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -I- PTM: GLYCOSYLATED (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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DR EMBL: U01028; AAI17405.1; -
DR EMBL: AE008674; AAL03811.1; -
DR EMBL: U43794; AAB49549.1; -
DR EMBL: U43798; AAB49550.1; -
DR EMBL: U43806; AAB49551.1; -
DR EMBL: U45244; AAB49566.1; -
DR EMBL: U46918; AAB49567.1; -
DR EMBL: U63440; AAC35176.1; -
DR EMBL: U63443; AAC35179.1; -
DR EMBL: U83448; AAC35184.1; -
DR EMBL: U83453; AAC35189.1; -
DR InterPro: IPR006315; Autotransport.
DR Pfam: PF03797; Autotransporter_1.
DR TIGRfams: TIGR01414; autotrans_Darf; 1.
KW Antigen; Repeat; Signal; Cell wall; s-layer; Glycoprotein;
KW Complete proteome.
KW
FT SIGNAL 1 38
FT CHAIN 238 946
FT DOMAIN 1424 1528
FT VARIAT 60 60
FT VARIAT 76 76
FT VARIAT 86 137
FT VARIAT 126 133
FT VARIAT 954 954
FT VARIAT 1245 1245
FT VARIAT 1308 1308
FT VARIAT 1877 1877
FT CONFLICT 92 92
FT
FT POTENTIAL.
FT OUTER MEMBRANE PROTEIN A.
FT THR-RICH.
FT THR-RICH.
FT N -> NN (IN STRAIN INDIAN TICK TYPHUS).
FT R -> H (IN STRAIN INDIAN TICK TYPHUS).
FT MISSING (IN STRAIN M1).
FT MISSING (IN STRAIN MORCCAN).
FT VT -> II (IN STRAIN INDIAN TICK TYPHUS).
FT D -> A (IN STRAIN INDIAN TICK TYPHUS, M1
FT AND MORCCAN).
FT N -> H (IN STRAIN MORCCAN).
FT M -> I (IN STRAIN INDIAN TICK TYPHUS).
FT O -> K (IN REF. 1).
FT I -> V (IN REF. 1).

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FT CONFLICT 126 126 V -> I (IN REF. 1).
FT CONFLICT 137 137 T -> N (IN REF. 1).
FT CONFLICT 157 157 G -> D (IN REF. 1).
FT CONFLICT 368 369 IS -> VN (IN REF. 1).
FT CONFLICT 374 388 KATLGAIKATTTK -> LQVGGVKKANTIN (IN
REF. 1).
FT CONFLICT 640 640 N -> D (IN REF. 1).
FT CONFLICT 669 669 V -> I (IN REF. 1).
FT CONFLICT 793 793 N -> D (IN REF. 1).
FT CONFLICT 803 804 VN -> IS (IN REF. 1).
FT CONFLICT 809 823 LRVGGVKKSNNTIN -> KATLGAIKATTTK (IN
REF. 1).
FT CONFLICT 898 898 D -> Y (IN REF. 1).
FT CONFLICT 908 908 P -> N (IN REF. 1).
FT CONFLICT 985 985 N -> K (IN REF. 1).
FT CONFLICT 1009 1009 L -> S (IN REF. 1).
FT CONFLICT 1013 1013 Y -> S (IN REF. 1).
FT CONFLICT 1182 1182 K -> Q (IN REF. 1).
FT CONFLICT 1314 1314 N -> Y (IN REF. 4).
FT CONFLICT 1451 1451 H -> N (IN REF. 1).
FT CONFLICT 1624 1624 G -> D (IN REF. 1).
FT CONFLICT 1628 1628 E -> G (IN REF. 1).
FT CONFLICT 1872 1872 A -> V (IN REF. 1).
FT CONFLICT 1875 1875 T -> P (IN REF. 1).
FT CONFLICT 1878 1879 MS -> LP (IN REF. 1).
FT CONFLICT 1936 1936 E -> A (IN REF. 1).
FT CONFLICT 1965 1970 MTAFLP -> ITPPLS (IN REF. 1).
FT CONFLICT 1997 1997 G -> R (IN REF. 1).
SQ SEQUENCE 2021 AA; 203328 MM; 327FC42D/CB24668 CRC64;
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Query Match Best Local Similarity 6.8%; Score 177.5; DB 1; Length 2021;

Matches 131; Conservative 56; Mismatches 225; Indels 189; Gaps 27;

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QY 19 VSELTNRHTRASTVTAVLALLPFTVQANATDEGLINVEEKLSPGANGKVAIIS 78
DB 670 IKATTTKLTNAASVLTITNVNAVLTGAIDMTTGDVNGVILN-----GALSQVTNIG 723
QY 79 DTGGLNFAKETAG--TNGD-----TVHL--NGISLTLMLTGATTVTNDN----- 124
DB 724 NTNALATISVAGAKATIGAGVAKATTTKLTNDMSAVTFNPVVTGAIDNTGNANNCIAT 783
QY 125 VTDEKKRA---ASVKDLNAGWNINIKVAPGTASDNVDFVRTYDVEFLSADTKTTTV 180
DB 784 FTGDSVTGNIGMTNALATVNVAGGLRVGGVYKSTINMLTQNASAVFTNPVVTGAI 843
QY 181 -NYESKNG-----KTEVKIGAKTSVI 202
DB 844 DNTGNANNGIVTFTGDSVTGNIGNTNALATISVAGAKATLGAIKATTTKLTNDMSAV 903
QY 203 KKKDKRLVTG---KKGKENGSSPDEGEGLVTAKEVIDAVNKKAGWRKTTTANGQCGQAD 258
DB 904 TETNPVVTGAIDNTGNANNGIVTFTGDSVT-----GNIGNTN 942
QY 259 KFTETVTSGRVTEPASGNGTTATVSKDDGNITVKYDVNVGDALNVNQLONGSNV---LD 314
DB 943 ALATVNVAGAVTLQAGSL-----DANNI-----DEGARSTLEFNGLDGGGNAIYYF 991
QY 315 SKAVAGSSGKVISGNV-----PSKGMDETVAINGANNIEITRNCKNIDTATSMTPQF 368
DB 992 KGALANGNNAIILNNTLTALYHLITGTVAE--INIGAGNLFADIASAGVTIILNAODIHF 1050
QY 369 SSVS-----LGAGADAPTLISVD-----DEG-----ALNVGSKDANKPVATIN 405
DB 1051 RAIDSALVLSNLGCVGNNTLILADVLAPGVDEGTVPFDGCVGNLNGS-----N 1100
QY 406 VAPGVKE-GDV-----TNAQLKGVAQN--LNNRIDNVGNARAGIAQA 446
DB 1101 VAGAAARNIGDVGNKFTLLIYNAVTTTDDVNLEGI-QNVLIINNADFTSSTA----- 1152
QY 447 IATAGIVQAVLPKGSMAIGGGTYLGEAGYALIGSSISAG-----NMIIKGTASGNS 499
DB 1153 -FNAGTIO-----INDATYTTIDANN--GNLNIAPGNIKFAHADQILLIONSSGND 1199
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```
QY 500 R 500
DB 1200 R 1200

RESULT 13
SLAP_CAME
ID SLAP_CAME STANDARD; PRF; 933 AA.
AC P35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_Taxid:196;
RN 1
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN-84 -32 / 23D;
RX MEDLINE=9035448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
structure."
RL J. Biol. Chem. 265:14529-14535(1990).
RN 12
RX ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; J05577; AAA23032.1; -.
DR Cell wall; S-layer.
KW SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;
SQ

Query Match Best Local Similarity 6.8%; Score 176.5; DB 1; Length 933;
Matches 128; Conservative 67; Mismatches 231; Indels 165; Gaps 24;
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OY 244 RMKTTTAN-----GQTGQADKF--ETVTSCTKVTAFASGNGTATVSK--DDQGNITVK 292
DB 538 -IDTAFNALQSVSGKGTGGCGKFSVKTGTDGDKIEFV---GTTLEGSVIDAPGNDTFA 593
OY 293 YVNVNGDALNVNQLONGSGMNLDSKAVAG---SSGKVISGNSVPSKGMDETVNINAGNNI 349
DB 594 MKSAALTSTNFMNTMIENINVAISDAVATADLSSAFKNSVITTTTKEAATPTLTINKDOYI 653
OY 350 EITRNGKNIDTATSMTPPOFSSVSLGAGADAPLISVDDEGALNVGSKDANKPRITNVAPG 409
DB 654 -----NFTADAGSVKILITYKLN---DYTALMIVYKVLDAAKD-----TRIALG 696
OY 410 VKEGVTVYVQLKGYAQNINRIDVNGNARAGIQAATAGLVQAVYLPKSMMAIGG-- 467
DB 697 TAAADKALV-----IDTGIETLNTISLVKATSPETTANTVNAKLTDVTIILIDGMQ 747
OY 468 -----GTYLG-----EAGYALIGYSSISAGSNMIIKTCASGNS 499
DB 748 ITLGHAGTAGDTYDYSKVSMDIASALKAGLTEDASAITLGANATIKGSGSGADS 798

RESULT 14
SLAP CAUCR
ID P35828; Q46015; Q9RF12; PRT; 1025 AA.
AC P35828; Q46015; Q9RF12;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (Paracrystalline surface layer protein).
GN RSA OR CCI007.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=93007489; PubMed=1393820;
RA Gilchrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RT crescentus paracrystalline surface layer protein."
RL Can. J. Microbiol. 38:193-202(1992).
RN [2]
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RN Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.R., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouli H., Shetty J., Berry K.,
RA Ullrich T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN [5]
RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=89008089; PubMed=3049545;
RA Fisher J.A., Smit J.K., Agabian N.;
RT "Transcriptional analysis of the major surface array gene of

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RT Caulobacter crescentus."
RL J. Bacteriol. 170:4706-4713(1988).
RN [6]
RP CHARACTERIZATION.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=98292737; PubMed=9620954;
RA Awram P., Smit J.K.;
RT "The Caulobacter crescentus paracrystalline S-layer protein is
RT secreted by an ABC transporter (type I) secretion apparatus."
RL J. Bacteriol. 180:3062-3069(1998).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
CC PHYSICAL BARRIER TO PARASITES AND LYtic ENZYMES.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
CC (TYPE I) SECRETION APPARATUS.
CC -1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
CC -----
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CC -----
DR EMBL: AF062345; AAC38665.2; -.
DR EMBL: AF193063; AAF19365.1; -.
DR EMBL: AE005779; AAK22991.1; ALT_INIT.
DR PIR: A48995; A48995.
DR HSP: P22629; 1SWC.
DR TIGR: CC1007; -.
DR Interpro: IPR001343; Hemlysin_Ca_bind.
DR Pfam: PR00353; hemolysinCabind; 3.
DR PRINTS: PR00313; CABMDCNRP.
RT Cell wall; S-layer; Calcium-binding; Complete proteome.
FT INIT MET 0
SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;

Query Match 6.7%; Score 175; DB 1; Length 1025;
Best Local Similarity 22.1%; Pred. No. 0.093;
Matches 135; Conservative 66; Mismatches 224; Indels 186; Gaps 29;

OY 34 VETAVLATL-----FATVOAN-----ATDEGLINVEKLSFGANGK 73
DB 191 VKAALIGTILNATVSGIGVATATTAAMINDSLDGLSTDMNAGVNLTAVPSSGVSST 250
OY 74 VNIISDTYKGLNFAKETAGTNGDTTV--HLNG-----IGSTL-----TDM 111
DB 251 ISLTGTGDTL-----TGTANNNDTFVAGEVAGATLVGDTLISGAGTIVLMVQAAYTA 305
OY 112 LNTGAT-INVTVNDVTDDEKRAASVKDYLVNAGNMIKGKKPQTSMDVDFPRTDVEF 170
DB 306 LPTGVLTISGIETMNTS-----GAAT--TLNTSSGVGTTLALNTVTSGAATVGTAGACON 358
OY 171 ISADRTTTVNVESSKDNCKTEVKIGATSVIKERDGLVYKKGKENG-----SS 221
DB 359 LRTATTAADANNAVADGGANVTV---ASTGV---ISGTTVYGANNAAGTYSVANSST 412
OY 222 TDESGELVTAKEVIDAVKAKGRMKT-----TANGQT----- 254
DB 413 TTTGAIATVGTGAVVVAQTAGNAVTTLTQADVTVTGNSSTAVVTOATAATAGATVAG 472
OY 255 -----GQADRFETYSG-----KRYVTASGNGTATVSKDDQ 286
DB 473 RVNGAVTTTDSAAASATAGKATATVTLGSPGATTDSSALTTVNL--SGTGSLSLIGR--- 528
OY 287 GNITVYVNVGDALNVNQLONGSGMNLDSKAVAGS-----SGKVISGNSVPSKGMDE 339
DB 529 GALTATPTPANT-LTILNVGLTTTGAIITDSEAAADGFTTINAGSTASTIASLVAADAT 587

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OY 340 TVINAGNIEITRN-----GKNI--DIATSMTPQSSVSLGADAPTL 383  
 DB 588 TLNISGDARVITSTTAALTGITVTSVSGATLGAELTGLV--FTG---GAGADSTLLG 642  
 OY 384 VDDEGALNVGSKDANKPRITNVAPG--VKEGDTVNAQLKGVAONLNRIIDVNGNARA 441  
 DB 643 ATTK-ALVWAGADDTVTYSSATLGAAGSVNGGDDGTDVY-----YANNVSSFS 689  
 OY 442 G-----IAOAITAGLVQAYLPKSMALIGGTYLGEAGYATGYSISA--CGN 488  
 DB 690 ADPAFGFETLVAVGAAAGSHNANGFTALDGLAGATTITTVNAVNVGLTVLAPITGT 749  
 OY 489 WIKGTASGNS 499  
 DB 750 TVFLNATGTS 760  
 RESULT 15  
 OMPB\_RICTY STANDARD: PRF: 1645 AA.  
 ID OMPB\_RICTY  
 AC P96989;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOMPb)  
 DE (rOMP B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).  
 DE OMPB OR SLP.  
 GN Rickettsia typhi.  
 OS Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=785;  
 RN 11  
 RP SEQUENCE FROM N.A..  
 RC STRAIN=Milington;  
 RX MEDLINE=94040787; PubMed=8224886;  
 RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;  
 RT "Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";  
 RL Gene 133:129-133(1993).  
 RN 12  
 RP PARTIAL SEQUENCE.  
 RC STRAIN=Milington;  
 RX MEDLINE=92114896; PubMed=1370573;  
 RA Ching W.M., Carl M., Dasch G.A.;  
 RT "Mapping of monoclonal antibody binding sites on CNBR fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";  
 RT Mol. Immunol. 29:95-105(1992).  
 RN 13  
 RP IDENTIFICATION OF CLEAVAGE SITE.  
 RX MEDLINE=92104668; PubMed=1729180;  
 RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;  
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing.";  
 RT Infect. Immun. 60:159-165(1992).  
 RL -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
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CC -----  
 DR EMBL: L04661; AAB48987.1; -  
 DR PIR: J00896; J00896.  
 DR InterPro: IPR005315; Autotransport.  
 DR InterPro: IPR005346; Autotransporter.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR TIGRFAMs: TIGR01414; autotrans\_bar1; 1.  
 KW Antigen; S-layer; Transmembrane; Cell wall.  
 FT CHAIN 1 1353 120 kDa SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1354 1645 32 kDa BETA PEPTIDE.  
 FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
 FT CONFLICT 657 657 H->N (IN REF. 2).  
 FT CONFLICT 842 842 V->I (IN REF. 2).  
 FT CONFLICT 1071 1071 G->A (IN REF. 2).  
 FT CONFLICT 1306 1306 G->S (IN REF. 2).  
 SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;  
 Query Match 6.7%; Score 175; DB 1; Length 1645;  
 Best Local Similarity 22.3%; Pred. No. 0.16;  
 Matches 145; Conservative 66; Mismatches 230; Indels 208; Gaps 33;  
 OY 11 SALANAVAVSELTNRHTRASATYKTAIVLALILATVQANATDEGLINTEKLSFAN 70  
 DB 156 SKVNAGAIIND--NDLSGVGSIDFTAPSVLEFNLNP--TTQEPAPTLIGDNAVIVGAN 211  
 OY 71 G-----KKVNIISDTKGLNFAKETAGTN-----GDTTVHLNGIGS 105  
 DB 212 GILNTNCFVAVSDFKTFAGITITN--IGNOGILMFRTTDDANALNLOGGATINPENGDS 270  
 OY 106 TLTLMLNTGATTVTNDVNTDDEKRRASVADVNLNAGNITKV-KPGTTA----- 155  
 DB 271 --TKLVIVSKNGNAATEFNTVG-----SLGNGKGVLEFDTTAAAGKLIANG 315  
 OY 156 ---SDN-----VDVFTYDIVERLSADFTTTVNVESKD-----NCKT--- 191  
 DB 316 GAANAIVGTDSGAGRAAEFIVSD--NENAAITISQVYAKDIVIOSANAGGVPEH 370  
 OY 192 --EYKIGAKTVIREKDKLVTKGKGNGS--STDEG-----EGLVTAKEVIDA 237  
 DB 371 LVDVGLGSKTN-FRTADSKVLI---TENAISFGSTDFGNLVAQVIVPNNKILITGNFIDA 425  
 OY 238 VNK---AGRMKTTTANGQ--TGQADKFEVTS-----GKVTFAFG-----NGTT 278  
 DB 426 KNNNGTAG--VITENANGTLVSGNTDPINIVTNIKAIEVEGAGIVOLSGIAGELRLGNA 483  
 OY 279 ATVSKDDGNTTVKTDVAVGALVNVQNSGWNLDRAVAGSSGKTVISGVNSPKGMD 338  
 DB 484 GSIFKLADGTV-INGPVQNPVLVNNNALAAGSIQIDGSAII--TGDI--GNGAVVAALQD 538  
 OY 339 ET-----VINAGNIEITRNGKI-----DIATSMTPQ 367  
 DB 539 ITLANDASKILTLGSAITIGANAGAIHFQANGGITQLSTQNNILVDFDLVTTDQIGV 598  
 OY 368 FSSVSL-----GAGADAPTLVSDEGALNVGSK-----DAN 398  
 DB 599 VDASSILVNQTLTNGISIGTIGANTKL-----GPFNVSSKTLINAGDVAINELVEMND 653  
 OY 399 KPVNIT-NVAPGVEGDTVNAQLKGVAONLNRIIDVNGNARAGIAQAITAGLVQAYL 457  
 DB 654 GSVHLTHNTYVLTITTVINAAOGKIIIVADPIINTPTALADTNGLSAESPLSHIFATKAA 713  
 OY 458 PGKSMMAIGGTYLGEAGYA-----IGYSSISAGANNIIGKTASG 497  
 DB 714 NGDSILHIGKGVNL-----YANNITTTDAVNSGLHFRSGGTSIVSGTVGG 758

Search completed: October 6, 2003, 09:23:58  
 Job time : 10.922 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 37.678 Seconds  
(without alignments)  
3513.485 Million cell updates/sec

Title: US-09-771-382-24  
Perfect score: 2602  
Sequence: 1 MNKIRIIMNSALNMAVAVS.....TASGNSRGHFGASASGYQW 513

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_prodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2552.5	98.1	592	2	0930Y2
2	2514.5	96.6	592	2	09JPS9
3	2476.5	95.2	594	2	09JPI3
4	2472.5	95.0	594	2	09JPS2
5	2472	95.0	599	2	09JPR8
6	2468.5	94.9	590	2	09JPS3
7	2460.5	94.6	598	2	09JPS0
8	2460.5	94.6	598	2	09JPT0
9	2451.5	94.2	598	2	09JPT0
10	2448.5	94.1	594	2	09JPH7
11	2419.5	93.0	600	2	09JPS6
12	2409.5	92.6	594	2	09JPT4
13	2407	92.5	591	16	09JRI8
14	2403	92.4	591	2	09JPS7
15	2402.5	92.3	592	2	09AQF0
16					09aqf0 neisseria m

17	2395	92.0	591	2	0930Y3	093qy3 neisseria m
18	2351.5	90.4	592	16	09JQW4	09jqw4 neisseria m
19	2343.5	90.1	600	2	09JPS5	09jps5 neisseria m
20	2314	88.9	589	2	0930Y1	093qy1 neisseria m
21	2313.5	88.9	598	2	09JPR7	09jpr7 neisseria m
22	2304	88.5	595	2	09JPH0	09jph0 neisseria m
23	2304	88.5	599	2	09JPS8	09jps8 neisseria m
24	2303	88.5	589	2	09JPI0	09jpi0 neisseria m
25	2224.5	85.5	526	2	09JPS4	09jps4 neisseria m
26	2224.5	85.5	530	2	09JPS1	09jps1 neisseria m
27	966.5	37.1	1098	2	048152	048152 haemophilus
28	965.5	37.1	1096	2	08GM79	08gm79 haemophilus
29	939.5	36.1	2353	2	P71401	P71401 haemophilus
30	891.5	34.3	1204	2	08GM76	08gm76 haemophilus
31	873.5	33.6	1210	2	08GM74	08gm74 haemophilus
32	870.5	33.5	1210	2	08GM75	08gm75 haemophilus
33	705.5	27.1	1004	2	08GM77	08gm77 haemophilus
34	687.5	26.4	1002	2	08GM78	08gm78 haemophilus
35	403	15.5	1299	16	09F3X6	09f3x6 pasteurella
36	380	14.6	2314	2	08KOM8	08kom8 moraxella c
37	371	14.3	1588	16	08XDG4	08xdg4 escherichia
38	365	14.0	1190	16	09PC04	09pc04 xyella fas
39	363	14.0	1778	16	08FCB2	08fcb2 escherichia
40	361.5	13.9	1964	2	08KOM9	08kom9 moraxella c
41	361	13.9	1107	16	09F2D8	09f2d8 salmonella
42	360	13.8	1461	16	08ZL64	08z164 salmonella
43	359.5	13.8	2059	16	09PD50	09pd50 xyella fas
44	333.5	12.8	641	16	08CKM1	08ckm1 yersinia pe
45	333.5	12.8	658	16	08ZHU0	08zhu0 yersinia pe

## ALIGNMENTS

RESULT 1  
0930Y2 PRELIMINARY; PRT; 592 AA.  
ID 0930Y2  
AC 0930Y2;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE NHA outer membrane protein.  
GN NHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPRAIN-H41;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157609; AAK68870.1; -;  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
SQ SEQUENCE 592 AA: 61869 MW: F9403A0B4A18EAE7 CRC64;

Query Match 98.1%; Score 2552.5; DB 2; Length 592;  
Best Local Similarity 86.7%; Pred. No. 1.6e-101;  
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLTFATVQANATDE----- 54  
DB 1 MNKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLTFATVQANATDEDEEEL 60  
QY 55 -----TGLINWETKLSFGANGKKNYIISDTKGLNFAKETAGTNGDTTVHLN 101  
DB 61 ESVQRSVGSIQASMEGSVELLETISMTNDSKEFVDPIYVTLKAGDNLIKIKONTNENT 120  
QY 55 -----TGLINWETKLSFGANGKKNYIISDTKGLNFAKETAGTNGDTTVHLN 101

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Db 121 NASSFTYSLKQDLTGLINVEFKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVALN 180
Qy 102 GIGSTLTDLMLNTGATVNTNDNTDDEKKRAASYKVDYLNAGMNIKGVPFGTTASDNDF 161
Db 181 GIGSTLTDLMLNTGATVNTNDNTDDEKKRAASYKVDYLNAGMNIKGVPFGTTASDNDF 240
Qy 162 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVYKIGAKTSVYKEKDKLVTGKGENSS 221
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVYKIGAKTSVYKEKDKLVTGKGENSS 300
Qy 222 TDEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADAFETVTSCTKTFASGNGTATV 281
Db 301 TDEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADAFETVTSCTKTFASGNGTATV 360
Qy 282 SKDDGNTTVKYDVNVGDLNVLNOLNSGMNLSKAVAGSSGKVTISGNVSPSKGMDETV 341
Db 361 SKDDGNTTVKYDVNVGDLNVLNOLNSGMNLSKAVAGSSGKVTISGNVSPSKGMDETV 420
Qy 342 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 401
Db 421 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 480
Qy 402 RTTNAPGVKEDDVYNNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLQVAYLPKGS 461
Db 481 RTTNAPGVKEDDVYNNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLQVAYLPKGS 540
Qy 462 MMAIGGTYLGEAGYAGYSSISAGNNIIKGTASGNSRGHFGASASVGYQM 513
Db 541 MMAIGGTYLGEAGYAGYSSISAGNNIIKGTASGNSRGHFGASASVGYQM 592

RESULT 2
Q9JPS9 PRELIMINARY: PRT: 592 AA.
ID 09JPS9
AC 09JPS9:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226361; AAF42510.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 592 AA: 61917 MW: 4A3471514FD3C879 CRC64;
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Query Match 96.6%; Score 2514.5; DB 2; Length 592;
Best Local Similarity 85.5%; Pred. No. 6.8e-100;
Matches 506; Conservative 2; Mismatches 5; Indels 79; Gaps 1;
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Qy 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFVQANATDE----- 54
Db 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFVQANATDEDEEDEL 60
Qy 55 ----- 54
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Db 61 ESVORSVVGSIQASMEGSGELETTISLMTNDSKEFVDYIVVTLKAGDNLKIKONTNENT 120
Qy 55 -----TGLINVEFKLSFGANGKKVNIISPTKGLNFAKETAGTNGDTTVALN 101
Db 121 NASSFTYSLKQDLTGLINVEFKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVALN 180
Qy 102 GIGSTLTDLMLNTGATVNTNDNTDDEKKRAASYKVDYLNAGMNIKGVPFGTTASDNDF 161
Db 181 GIGSTLTDLMLNTGATVNTNDNTDDEKKRAASYKVDYLNAGMNIKGVPFGTTASDNDF 240
Qy 162 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVYKIGAKTSVYKEKDKLVTGKGENSS 221
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVYKIGAKTSVYKEKDKLVTGKGENSS 300
Qy 222 TDEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADAFETVTSCTKTFASGNGTATV 281
Db 301 TDEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADAFETVTSCTKTFASGNGTATV 360
Qy 282 SKDDGNTTVKYDVNVGDLNVLNOLNSGMNLSKAVAGSSGKVTISGNVSPSKGMDETV 341
Db 361 SKDDGNTTVKYDVNVGDLNVLNOLNSGMNLSKAVAGSSGKVTISGNVSPSKGMDETV 420
Qy 342 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 401
Db 421 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 480
Qy 402 RTTNAPGVKEDDVYNNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLQVAYLPKGS 461
Db 481 RTTNAPGVKEDDVYNNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLQVAYLPKGS 540
Qy 462 MMAIGGTYLGEAGYAGYSSISAGNNIIKGTASGNSRGHFGASASVGYQM 513
Db 541 MMAIGGTYLGEAGYAGYSSISAGNNIIKGTASGNSRGHFGASASVGYQM 592

RESULT 3
Q9JPI3 PRELIMINARY: PRT: 594 AA.
ID 09JPI3
AC 09JPI3:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88; and B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -.
DR EMBL: AF226369; AAF42518.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA: 62086 MW: 1B25E03B90D04B46 CRC64;
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Query Match 95.2%; Score 2476.5; DB 2; Length 594;
Best Local Similarity 84.0%; Pred. No. 2.8e-98;
Matches 499; Conservative 4; Mismatches 10; Indels 81; Gaps 1;
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Qy 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFVQANATDE----- 54
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Db 1 MNKYRIIWSALNAAVAVSELFRNHTKRASATVATVATLTLFATVQASTDDDLXLE 60
QY 55 ----- 54
Db 61 PVQRTAPVLSFHADSECTGEKEVTEEDSNMGVYFDKKVGLAGTTLKAGDNLIKQNTDE 120
QY 55 -----TGLINVEETEKLSPGANGKKVNIISDTKGLNFAKETAAGTNGDTTVH 99
Db 121 NTNASSFTYSLKNDLTDLTSLVEFEKLSFGANGKKVNIISDTKGLNFAKETAAGTNGDTTVH 180
QY 100 LINGSTLTDLMLNTGATTVNTDNTVDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 159
Db 181 LINGSTLTDLTLTNTGATTVNTDNTVDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 240
QY 160 DPAVTYDVEFLSADPTTTTVNVESSKNGKKEVEKIGAKTSVKEKDKLVTGKKGENG 219
Db 241 DPAVTYDVEFLSADPTTTTVNVESSKNGKKEVEKIGAKTSVKEKDKLVTGKKGENG 300
QY 220 SSTDEGGLYTAKEVIDAVNKKAGWRMKTTPANGOTGADKFEYVTSCTKYTFASGNGTTA 279
Db 301 SSTDEGGLYTAKEVIDAVNKKAGWRMKTTPANGOTGADKFEYVTSCTKYTFASGNGTTA 360
QY 280 TVSKDDGNTTVKDYVNVGDLNVLQNSGWNLSKAVAGSSGKVISGVNPSPKGKME 339
Db 361 TVSKDDGNTTVKDYVNVGDLNVLQNSGWNLSKAVAGSSGKVISGVNPSPKGKME 420
QY 340 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDEGALNVSSKANK 399
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDEGALNVSSKANK 480
QY 400 PVRTTNAPGVKEDGYTNVAOLKGVAAQNLNRRIDNVNAGNARAGIAQAIATAGLVQAVLP 459
Db 481 PVRTTNAPGVKEDGYTNVAOLKGVAAQNLNRRIDNVNAGNARAGIAQAIATAGLVQAVLP 540
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 513
Db 541 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 594

RESULT 4
Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92.
GN GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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Best Local Similarity 83.8%; Pred. No. 4,2e-98;
Matches 498; Conservative 4; Mismatches 11; Indels 81; Gaps 1;
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QY 1 MNKYRIIWSALNAAVAVSELFRNHTKRASATVATVATLTLFATVQAAATDE----- 54
Db 1 MNKYRIIWSALNAAVAVSELFRNHTKRASATVATVATLTLFATVQASTDDDLXLE 60
QY 55 ----- 54
Db 61 PVQRTAPVLSFHADSECTGEKEVTEEDSNMGVYFDKKVGLAGTTLKAGDNLIKQNTDE 120
QY 55 -----TGLINVEETEKLSPGANGKKVNIISDTKGLNFAKETAAGTNGDTTVH 99
Db 121 NTNASSFTYSLKNDLTDLTSLVEFEKLSFGANGKKVNIISDTKGLNFAKETAAGTNGDTTVH 180
QY 100 LINGSTLTDLMLNTGATTVNTDNTVDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 159
Db 181 LINGSTLTDLTLTNTGATTVNTDNTVDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 240
QY 160 DPAVTYDVEFLSADPTTTTVNVESSKNGKKEVEKIGAKTSVKEKDKLVTGKKGENG 219
Db 241 DPAVTYDVEFLSADPTTTTVNVESSKNGKKEVEKIGAKTSVKEKDKLVTGKKGENG 300
QY 220 SSTDEGGLYTAKEVIDAVNKKAGWRMKTTPANGOTGADKFEYVTSCTKYTFASGNGTTA 279
Db 301 SSTDEGGLYTAKEVIDAVNKKAGWRMKTTPANGOTGADKFEYVTSCTKYTFASGNGTTA 360
QY 280 TVSKDDGNTTVKDYVNVGDLNVLQNSGWNLSKAVAGSSGKVISGVNPSPKGKME 339
Db 361 TVSKDDGNTTVKDYVNVGDLNVLQNSGWNLSKAVAGSSGKVISGVNPSPKGKME 420
QY 340 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDEGALNVSSKANK 399
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDEGALNVSSKANK 480
QY 400 PVRTTNAPGVKEDGYTNVAOLKGVAAQNLNRRIDNVNAGNARAGIAQAIATAGLVQAVLP 459
Db 481 PVRTTNAPGVKEDGYTNVAOLKGVAAQNLNRRIDNVNAGNARAGIAQAIATAGLVQAVLP 540
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 513
Db 541 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 594

RESULT 5
Q9JPR8 PRELIMINARY; PRT; 599 AA.
AC Q9JPR8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92 (Nhaa outer membrane protein).
GN GNA92 OR NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 599 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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RC STRAIN-H38.
RA Peak 1.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF263883; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match          95.0%; Score 2472; DB 2; Length 599;
Best Local Similarity 83.1%; Pred. No. 4,5e-98;
Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;

QY 1 MNKIRIIMNSALNMVAVSELTRNHTKRASATVTAVALTLFLFTVOANATDE----- 54
DB 1 MNKIRIIMNSALNMVAVSELTRNHTKRASATVTAVALTLFLFTVOANATDEDEEDL 60
QY 55 ----- 54
DB 61 EPPVRSALVLQFMIDKEGNGENESTGNGMSIYDNNHTLHGATVTLKAGDNLKIKONTN 120
QY 55 -----TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAAGTNG 94
DB 121 KNTNENTNDSFTYSLKLDLDTLSVETEKLSFGANGKVNITSDTKGLNFAKETAAGTNG 180
QY 95 DTTVHLANGISTLTMDLINTGATVNTDNDVTDDEKKRAASYKDVNLNAGMNIKGYKPGTT 154
DB 181 DTTVHLANGISTLTMDLINTGATVNTDNDVTDDEKKRAASYKDVNLNAGMNIKGYKPGTT 240
QY 155 ASDNVDVRYTDFEPLSADIKTTTVNVESKDNKGKTEVYKIGAKTSVIEKDKLVTKGK 214
DB 241 ASDNVDVRYTDFEPLSADIKTTTVNVESKDNKGKTEVYKIGAKTSVIEKDKLVTKGK 300
QY 215 KGENSSNDEGEGITAKEVIDAVNKKAGRMKTTTANGOTGOADFEYVTSCTXTYTFASG 274
DB 301 KGENSSNDEGEGITAKEVIDAVNKKAGRMKTTTANGOTGOADFEYVTSCTXTYTFASG 360
QY 275 NGTTAVESKDDOGNTTVKYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSK 334
DB 361 KGTATVSKDDOGNTTVKYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSK 420
QY 335 GKMEFTVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGS 394
DB 421 GKMEFTVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGS 480
QY 395 KDANKPVRTTNVAPGVKGGDTNVNQLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVQ 454
DB 481 KDANKPVRTTNVAPGVKGGDTNVNQLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVQ 540
QY 455 AYLPGKSMALIGGTYLGEAGYAIGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 513
DB 541 AYLPGKSMALIGGTYLGEAGYAIGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 599

RESULT 6
Q9JPS3 PRELIMINARY; PRT: 590 AA.
AC Q9JPS3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA92.
GN GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NGE28;
RX MEDLINE=20175756; PubMed=10710308;

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RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Pettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF26378; AAF4527.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; BAA476AC300D80C8 CRC64;

Query Match          94.9%; Score 2468.5; DB 2; Length 590;
Best Local Similarity 84.4%; Pred. No. 6,2e-98;
Matches 498; Conservative 3; Mismatches 12; Indels 77; Gaps 1;

QY 1 MNKIRIIMNSALNMVAVSELTRNHTKRASATVTAVALTLFLFTVOANATDE----- 54
DB 1 MNKIRIIMNSALNMVAVSELTRNHTKRASATVTAVALTLFLFTVOANATDEDEEDL 60
QY 55 ----- 54
DB 61 DPVQRTAVLVNSDKEGTEGEKEVENSMAVYENEGVLTAGTITLKAGDNLKIKONG 120
QY 55 -----TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAAGTNG 103
DB 121 TMTFTSLKDLDTLSVETEKLSFGANGKVNITSDTKGLNFAKETAAGTNGTTHLNGI 180
QY 104 GSTLTMDLINTGATVNTDNDVTDDEKKRAASVQVNLNAGMNIKGVKPGTTASDNDVFR 163
DB 181 GSTLTMDLINTGATVNTDNDVTDDEKKRAASVQVNLNAGMNIKGVKPGTTASDNDVFR 240
QY 164 TYDVEPLSADIKTTTVNVESKDNKGKTEVYKIGAKTSVIEKDKLVTKGKGGESSSTD 223
DB 241 TYDVEPLSADIKTTTVNVESKDNKGKTEVYKIGAKTSVIEKDKLVTKGKGGESSSTD 300
QY 224 EGEGLVTAKEVIDAVNKKAGRMKTTTANGOTGOADFEYVTSCTXTYTFASGNTATYVSK 283
DB 301 EGEGLVTAKEVIDAVNKKAGRMKTTTANGOTGOADFEYVTSCTXTYTFASGNTATYVSK 360
QY 284 DDQGNITVYKYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGMEFTVNI 343
DB 361 DDQGNITVYKYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGMEFTVNI 420
QY 344 NAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGSKDANKPVRT 403
DB 421 NAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGSKDANKPVRT 480
QY 404 TNVAGVVEGDTNVNQLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVQAYLPGKSM 463
DB 481 TNVAGVVEGDTNVNQLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVQAYLPGKSM 540
QY 464 AIGGTYLGEAGYAIGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 513
DB 541 AIGGTYLGEAGYAIGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 590

RESULT 7
Q9JPS0 PRELIMINARY; PRT: 598 AA.
AC Q9JPS0:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA92 (Nhna outer membrane protein).
GN GNA92 OR NHNA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;

```



[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN-NGH15;  
RC MEDLINE-20175756; PubMed-10710308;  
RA Plazza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-H15;  
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF26381; AAF42530.1; -  
DR EMBL: AF157607; AAK68868.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;  
Query Match 94.6%; Score 2460.5; DB 2; Length 598;  
Best Local Similarity 82.9%; Pred. No. 1,4e-97;  
Matches 496; Conservative 4; Mismatches 13; Indels 85; Gaps 1;  
QY 1 MNKIYRIIMNSALNAMA VSELTRNHRKRSATVATLTLFATVQANATDE----- 54  
DB 1 MNKIYRIIMNSALNAMA VSELTRNHRKRSATVATLTLFATVQANATDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVORTAVVLSFRSDEKTEGEGEDSNNMAVYEDKEKVLKAGATTLKAGDNLIKQNTNE 120  
QY 55 -----TGLINVEETKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 95  
DB 121 NTNENTDSSFTYSLKKDLDTLSVETEKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 180  
QY 96 TTVHLNIGISTLTDLMLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVKPGTTA 155  
DB 181 PTVHLNIGISTLTDLTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVKPGTTA 240  
QY 156 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVYTGK 215  
DB 241 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVYTGK 300  
QY 216 GENGSSSTDEBEGVLTAKVEIDAVNKAAGRKTITANOTGOADKFEVTVSGTKYTFASGN 275  
DB 301 DENGSSSTDEBEGVLTAKVEIDAVNKAAGRKTITANOTGOADKFEVTVSGTKYTFASGN 360  
QY 276 GTTATVSKDQGNITVYKDVNVGDALNVNOLNONGWMLDSKAVAGSSGKYISGNVSPSKG 335  
DB 361 GTTATVSKDQGNITVYKDVNVGDALNVNOLNONGWMLDSKAVAGSSGKYISGNVSPSKG 420  
QY 336 KMETVAINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 395  
DB 421 KMETVAINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 480  
QY 396 DANKPVITNVAPGVKRGDVTNVAQLKGVAQNLNRRIDNNGNARAGIAAIAIATAGLYOA 455  
DB 481 DANKPVITNVAPGVKRGDVTNVAQLKGVAQNLNRRIDNNGNARAGIAAIAIATAGLYOA 540  
QY 456 YLPGRSMMAIGGTYLGEAGYAGYSSISAGGMMIIGTASGNSRGHFGASASVGYOM 513  
DB 541 YLPGRSMMAIGGTYLGEAGYAGYSSISIDTGMNVIKGTASGNSRGHFGASASVGYOM 598  
RESULT 8

Q9JPT0  
ID Q9JPT0 PRELIMINARY; PRT; 598 AA.  
AC Q9JPT0;  
DT 01-OCT-2000 (TReMBLrel. 15 Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA92.  
GN GNA92.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-2996;  
RA MEDLINE-20175756; PubMed-10710308;  
RA Plazza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF26359; AAF42508.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0E2EB3 CRC64;  
Query Match 94.6%; Score 2460.5; DB 2; Length 598;  
Best Local Similarity 82.8%; Pred. No. 1,4e-97;  
Matches 495; Conservative 5; Mismatches 13; Indels 85; Gaps 1;  
QY 1 MNKIYRIIMNSALNAMA VSELTRNHRKRSATVATLTLFATVQANATDE----- 54  
DB 1 MNKIYRIIMNSALNAMA VSELTRNHRKRSATVATLTLFATVQANATDDDDLYLE 60  
QY 55 ----- 54  
DB 61 PVORTAVVLSFRSDEKTEGEGEDSNNMAVYEDKEKVLKAGATTLKAGDNLIKQNTNE 120  
QY 55 -----TGLINVEETKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 95  
DB 121 NTNENTDSSFTYSLKKDLDTLSVETEKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 180  
QY 96 TTVHLNIGISTLTDLMLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVKPGTTA 155  
DB 181 PTVHLNIGISTLTDLTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNIKGVKPGTTA 240  
QY 156 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVYTGK 215  
DB 241 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVYTGK 300  
QY 216 GENGSSSTDEBEGVLTAKVEIDAVNKAAGRKTITANOTGOADKFEVTVSGTKYTFASGN 275  
DB 301 DENGSSSTDEBEGVLTAKVEIDAVNKAAGRKTITANOTGOADKFEVTVSGTKYTFASGN 360  
QY 276 GTTATVSKDQGNITVYKDVNVGDALNVNOLNONGWMLDSKAVAGSSGKYISGNVSPSKG 335  
DB 361 GTTATVSKDQGNITVYKDVNVGDALNVNOLNONGWMLDSKAVAGSSGKYISGNVSPSKG 420  
QY 336 KMETVAINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 395  
DB 421 KMETVAINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 480  
QY 396 DANKPVITNVAPGVKRGDVTNVAQLKGVAQNLNRRIDNNGNARAGIAAIAIATAGLYOA 455  
DB 481 DANKPVITNVAPGVKRGDVTNVAQLKGVAQNLNRRIDNNGNARAGIAAIAIATAGLYOA 540  
QY 456 YLPGRSMMAIGGTYLGEAGYAGYSSISAGGMMIIGTASGNSRGHFGASASVGYOM 513  
DB 541 YLPGRSMMAIGGTYLGEAGYAGYSSISIDTGMNVIKGTASGNSRGHFGASASVGYOM 598  
RESULT 8

Db 541 YLPKSMMAIGGCTYRGAGYAIGYSSISDTGNVWIKKTASGNSRGHFGTSASVGYQW 598

## RESULT 9

0930Y5 PRELIMINARY; PRT; 598 AA.

AC 0930Y5;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Nhma outer membrane protein.

GN Nhma.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-B210;

RA Peak I.R., Strikhantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF157603; AAK68864.1; -.

DR InterPro; IPR005594; Yadaa.

DR Pfam; PF03895; Yadaa; 1.

SO SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 94.2%; Score 2451.5; DB 2; Length 598;

Best Local Similarity 82.6%; Pred. No. 3.3e-97;

Matches 494; Conservative 5; Mismatches 14; Indels 85; Gaps 1;

1 MNKIIRIINSAALNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDE----- 54

1 MNKIIRIINSAALNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60

55 ----- 54

61 PVQRTAVVLSFRSDKEGTEGTEGTEDSNMNAVYFDEKRVLKAGATILKAGDNLKIKONTNE 120

55 -----TGLINVETKLSFGANGKKNIIISDPKGLFAKETAGTND 95

121 NTNEUTNDSSFTYSILKDLTDLTSVETKLSFGANGKNKNIISDTKGLFAKETAGTND 180

96 TTVHNGIGSTLTDMLNTGATTVYNDVYTDDEKKRAASVADVLAGNNIKGVKPTTA 155

181 PTVHNGIGSTLTDLTNTGATTVYNDVYTDDEKKRAASVADVLAGNNIKGVKPTTA 240

156 SUNVDFVRYTYVEFLSADTKTTTVAVESKDKNGKTEVKGAKTSYIKKDKLVYTGK 215

241 SUNVDFVRYTYVEFLSADTKTTTVAVESKDKNGKTEVKGAKTSYIKKDKLVYTGK 300

216 GENGSSTDEGEGLVTAKEVIDAVNKAEMKTTTANGCGOAGDKFETVSGTKVFPASGN 275

301 GENGSSTDEGEGLVTAKEVIDAVNKAEMKTTTANGCGOAGDKFETVSGTKVFPASGN 360

276 GTTATVSKDDQGNITVYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNSPSK 335

361 GTTATVSKDDQGNITVYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNSPSK 420

336 KHEDEVNINAGNNIETTRNGKNIDATSKTPOFSSVSGAGADAPLTVSYDDGALNVGSK 395

421 KHEDEVNINAGNNIETTRNGKNIDATSKTPOFSSVSGAGADAPLTVSYDDGALNVGSK 480

336 DANKVVRITNVAPGKREGDVNTAOLKGAONLNNRIDVNNARAGIAQATATGLVYA 455

481 DANKVVRITNVAPGKREGDVNTAOLKGAONLNNRIDVNNARAGIAQATATGLVYA 540

456 YLPKSMMAIGGCTYRGAGYAIGYSSISAGNNIITKKTASGNSRGHFGTSASVGYQW 513

541 YLPKSMMAIGGCTYRGAGYAIGYSSISDTGNVWIKKTASGNSRGHFGTSASVGYQW 598

## RESULT 10

09JPH7

AC 09JPH7; PRELIMINARY; PRT; 594 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Outer membrane protein GNA992 (Nhma outer membrane protein).

GN GNA992 OR Nhma.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-B2198; and 297-0;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Brooker M., Hündt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-B2198;

RA Peak I.R., Strikhantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF226358; AAF42517.1; -.

DR EMBL; AF226358; AAF42507.1; -.

DR EMBL; AF157604; AAK68865.1; -.

DR InterPro; IPR005594; Yadaa.

DR Pfam; PF03895; Yadaa; 1.

SO SEQUENCE 594 AA; 62361 MW; 436BDEDED6263C5C CRC64;

Query Match 94.1%; Score 2448.5; DB 2; Length 594;

Best Local Similarity 83.2%; Pred. No. 4.4e-97;

Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

1 MNKIIRIINSAALNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDE----- 54

1 MNKIIRIINSAALNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60

55 ----- 54

61 PVQRTAVVLSFRSDKEGTEGTEGTEDSNMNAVYFDEKRVLKAGATILKAGDNLKIKONTNE 120

55 -----TGLINVETKLSFGANGKKNIIISDPKGLFAKETAGTNDPVH 99

121 NTNDSSFTYSILKDLTDLTSVETKLSFGANGKNKNIISDTKGLFAKETAGTNDPVH 180

100 LNGIGSTLTDMLNTGATTVYNDVYTDDEKKRAASVADVLAGNNIKGVKPTTA 159

181 LNGIGSTLTDLTNTGATTVYNDVYTDDEKKRAASVADVLAGNNIKGVKPTTA 240

160 DEVRTYDYVEFLSADTKTTTVAVESKDKNGKTEVKGAKTSYIKKDKLVYTGKKGENG 219

241 DEVRTYDYVEFLSADTKTTTVAVESKDKNGKTEVKGAKTSYIKKDKLVYTGKKGENG 300

220 SSTDEGEGLVTAKEVIDAVNKAEMKTTTANGCGOAGDKFETVSGTKVFPASGN 279

301 SSTDEGEGLVTAKEVIDAVNKAEMKTTTANGCGOAGDKFETVSGTKVFPASGN 360

280 TVSKDDQGNITVYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNSPSK 339

361 TVSKDDQGNITVYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNSPSK 420



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QY 213 KKGNGSSSTDEGEGLVTAKEVIDAVNKAQWIRKTTTANGQTQOQADKFETVTSCTKVTFA 272
    |||||
DB 301 KKGNGSSSTDEGEGLVTAKEVIDAVNKAQWIRKTTTANGQOQADKFETVTSCTKVTFA 360
QY 273 SGNGTATATYKSDQGGITVTKYDVNVGDALNVNOLQSGNWLDSKAAVAGSSGKVTSCNVSP 332
    |||||
DB 361 SGNGTATATYKSDQGGITVTKYDVNVGDALNVNOLQSGNWLDSKAAVAGSSGKVTSCNVSP 420
QY 333 SKGKMDFTVNNAGNNIEITRNGKNIDITATSMTPQPSVSLGAGADAPLTSVDEGALNV 392
    |||||
DB 421 SKGKMDFTVNNAGNNIEITRNGKNIDITATSMTPQPSVSLGAGADAPLTSVDEGALNV 479
QY 393 GSKDANKPVRTINVAAPGVEGDVTNVAOLKGYAQNINRVIDVNGNARAGIAQAIATAGL 452
    |||||
DB 480 GSKDANKPVRTINVAAPGVEGDVTNVAOLKGYAQNINRVIDVNGNARAGIAQAIATAGL 539
QY 453 VQAYLPKSGMMAIGGTTYLGEAGYATGYSSISAGGWIITKGTASGNSRHFPGASASVGYO 512
    |||||
DB 540 VQAYLPKSGMMAIGGTTYLGEAGYATGYSSISAGGWIITKGTASGNSRHFPGASASVGYO 599
QY 513 W 513
    |
DB 600 W 600

```

## RESULT 13

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Q930Y4 PRELIMINARY; PRT; 594 AA.
ID 0930Y4:
AC 0930Y4:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Nhma outer membrane protein.
GN Nhma.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

```

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Query Match 92.6%; Score 2409.5; DB 2; Length 594;
Best Local Similarity 82.0%; Pred. No. 2e-95;
Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

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```

QY 1 MKRIYIINSAALNMAVAVSELTRNTRKASATVKAVALATLLFAVQANADE----- 54
    |||||
DB 1 MKRIYIINSAALNMAVAVSELTRNTRKASATVKAVALATLLFAVQANADE----- 60
QY 55 ----- 54
DB 61 PVQRTAVVLSFRSDKCEKEVEYEDSNMGVYFDKKGVTLACGTTILKADNLKIKONTNE 120
QY 55 -----TGLINVEETKLSFGANGKKNVISDTRKGLNFAKETAGTNGDTYVH 99
    |||||
DB 121 NTNASSFTYSLKLDLTLDTLVSGTEKLSFGANSKNKVNITSDTRKGLNFAKETAGTNGDTYVH 180
QY 100 LNCIGSTLTDLMLNTGATNTVNDNTYDDEKRAASVRYVLNAGNMIKGVKPEBTASDVN 159
    |||||
DB 181 LNCIGSTLTDLMLNTGATNTVNDNTYDDEKRAASVRYVLNAGNMIKGVKPEBTASDVN 240
QY 160 DFVRTVDFVEFLSADTKTTTVANVESKNGKTKTEVKIGATSVYKEKDGKLVGKSGENG 219
    |||||
DB 241 DFVRTVDFVEFLSADTKTTTVANVESKNGKTKTEVKIGATSVYKEKDGKLVGKSGENG 300

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```

QY 220 SSTDEGEGLVTAKEVIDAVNKAQWIRKTTTANGQTQOQADKFETVTSCTKVTFA 279
    |||||
DB 301 SSTDEGEGLVTAKEVIDAVNKAQWIRKTTTANGQTQOQADKFETVTSCTKVTFA 360
QY 280 TVSKDQGNITVTKYDVNVGDALNVNOLQSGNWLDSKAAVAGSSGKVTSCNVSPSKGKMD 339
    |||||
DB 361 TVSKDQGNITVTKYDVNVGDALNVNOLQSGNWLDSKAAVAGSSGKVTSCNVSPSKGKMD 420
QY 340 TVNINAGNNIEITRNGKNIDITATSMTPQPSVSLGAGADAPLTSVDEGALNVGSKDANK 399
    |||||
DB 421 TVNINAGNNIEITRNGKNIDITATSMTPQPSVSLGAGADAPLTSVDEGALNVGSKDANK 480
QY 400 PVRTINVAAPGVEGDVTNVAOLKGYAQNINRVIDVNGNARAGIAQAIATAGLVOAYLPK 459
    |||||
DB 481 PVRTINVAAPGVEGDVTNVAOLKGYAQNINRVIDVNGNARAGIAQAIATAGLVOAYLPK 540
QY 460 KSMMAIGGTTYLGEAGYATGYSSISAGGWIITKGTASGNSRHFPGASASVGYOW 513
    |||||
DB 541 KSMMAIGGTTYLGEAGYATGYSSISAGGWIITKGTASGNSRHFPGASASVGYOW 594

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## RESULT 14

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Q9JR18 PRELIMINARY; PRT; 591 AA.

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ID Q9JR18:
AC Q9JR18:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Adhesin) (Nhma outer membrane
DE protein).
GN GNA992 OR NMB0992 OR Nhma.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487; 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B, B2169, B283, and H44/76;
RX MEDLINE=20175756; PubMed-10710308;
RA Pizze M., Scariato V., Mastignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Stoni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed-10710307;
RA Tettelein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Nelson J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Ciltone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scariato V., Mastignani V., Pizze M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AF226375; AAF42524.1; -  
 DR EMBL; AF002450; AAF41395.1; -  
 DR EMBL; AF226367; AAF42516.1; -  
 DR EMBL; AF226370; AAF42519.1; -  
 DR EMBL; AF226374; AAF42523.1; -  
 DR EMBL; AF157611; AAK6872.1; -  
 DR TIGR; NMB0992; -  
 DR InterPro; IPR005594; Yada.  
 DR Pfam; PF03895; Yada; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 591 AA; 62112 MW; 762233CAE7F73EE6 CRC64;

Query Match 92.5%; Score 2407; DB 16; Length 591;  
 Best Local Similarity 82.6%; Pred. No. 2.6e-95;  
 Matches 489; Conservative 5; Mismatches 18; Indels 80; Gaps 2;

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 QY 55 ----- 54  
 DB 61 YLDPVQRTAVAVLYNSDKEGTEKEKVEENDMAVYENKGVLTAREITTLKAGDNLKTKQ 120  
 QY 55 -----TGLINVETEKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 101  
 DB 121 NGTFEYSLKLDLNLVSQTEKLSFGANGKRVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
 QY 102 GIGSTLMDLNTGATTNVNDNTDDEKRRASVYKVDLNGMNIKGVPCTTASDNDVF 161  
 DB 181 GIGSTLMDLNTGATTNVNDNTDDEKRRASVYKVDLNGMNIKGVPCTTASDNDVF 240  
 QY 162 VRTDYVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVYKEDKGLVYTGKGENGSS 221  
 DB 241 VRTDYVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVYKEDKGLVYTGKGENGSS 300  
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 DB 301 TDEGEGLTAKVEIDAVNKAQWRMKTATTANGOTGOADKFEVTSQTVTFASGNGTTATV 360  
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 DB 361 SKDOGNTTVKYDVNVGDLNVLNOLNSGMNLSKAVAGSSGKYISGVNPSKGMDETV 420  
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 DB 421 NINAGNNEITRNKNIDIASMTPOFSSVSLGAGADPTLSVDEGALNYSKDKANKPV 479  
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 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
 DE Outer membrane protein GMA992.  
 GN GMA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B2147;

RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing";  
 RL Science 287:1816-1820(2000).  
 DR EMBL; AF226366; AAF42515.1; -  
 DR InterPro; IPR005594; Yada.  
 DR Pfam; PF03895; Yada; 1.  
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Query Match 92.4%; Score 2403; DB 2; Length 591;  
 Best Local Similarity 82.4%; Pred. No. 3.8e-95;  
 Matches 488; Conservative 6; Mismatches 18; Indels 80; Gaps 2;

QY 1 MNKTYRIIWSALNAAVAVSELTRNHRKRASATYKTAVALTLFATVOAANTDE----- 54  
 DB 1 MNKTYRIIWSALNAAVAVSELTRNHRKRASATYKTAVALTLFATVOAANBEQEDL 60  
 QY 55 ----- 54  
 DB 61 YLDPVQRTAVAVLYNSDKEGTEKEKVEENDMAVYENKGVLTAREITTLKAGDNLKTKQ 120  
 QY 55 -----TGLINVETEKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 101  
 DB 121 NGTFEYSLKLDLNLVSQTEKLSFGANGKRVNITSDTKGLNFAKETAGTNGDTTVHLN 180  
 QY 102 GIGSTLMDLNTGATTNVNDNTDDEKRRASVYKVDLNGMNIKGVPCTTASDNDVF 161  
 DB 181 GIGSTLMDLNTGATTNVNDNTDDEKRRASVYKVDLNGMNIKGVPCTTASDNDVF 240  
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 QY 222 TDEGEGLTAKVEIDAVNKAQWRMKTATTANGOTGOADKFEVTSQTVTFASGNGTTATV 281  
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 QY 282 SKDOGNTTVKYDVNVGDLNVLNOLNSGMNLSKAVAGSSGKYISGVNPSKGMDETV 341  
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 QY 402 RITNVAPGVKEGDTVNAQLKGVAQNLRIDNVNGNARAGIAOAIATAGLVQAVLPKGS 461  
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 Job time : 40.678 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 : Search time 34.9514 Seconds  
(without alignments)  
1848.325 Million cell updates/sec

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Perfect score: 2063  
Sequence: 1 MNKTYRIINMSALNANWVVS.....TASGNSRGHFGASASVGYQM 407

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2063	100.0	407	22	AAU06184
2	2040	98.9	433	22	AAU06185
3	2005.5	97.2	502	22	AAU06186
4	2000.5	97.0	512	22	AAU06182
5	1961	95.1	591	20	AAV27202
6	1961	95.1	591	20	AAV23746
7	1961	95.1	591	22	AAU06171
8	1956.5	94.8	592	20	AAV23737
9	1954	94.7	591	21	AAV57045

10	1949	94.5	591	20	AAV23741	A surface protein
11	1949	94.5	591	22	AAU06175	N. meningitidis E6
12	1909	92.5	513	22	AAU06183	N. meningitidis H4
13	1893.5	91.8	592	22	AAU06180	N. meningitidis Z2
14	1887.5	91.5	594	20	AAV23740	A surface protein
15	1887.5	91.5	594	21	AAV57044	BASB029 amino acid
16	1887.5	91.5	594	22	AAU06174	N. meningitidis E6
17	1886	91.4	599	20	AAV23743	A surface protein
18	1886	91.4	599	22	AAU06176	N. meningitidis H3
19	1879.5	91.1	594	20	AAV23739	A surface protein
20	1879.5	91.1	594	22	AAU06179	N. meningitidis B2
21	1869.5	90.6	592	20	AAV23744	A surface protein
22	1869.5	90.6	592	22	AAU06172	N. meningitidis H4
23	1864.5	90.4	592	20	AAV27203	Amino acid sequence
24	1864.5	90.4	598	20	AAV23742	A surface protein
25	1864.5	90.4	598	22	AAU06177	N. meningitidis H1
26	1855.5	89.9	598	20	AAV23738	A surface protein
27	1855.5	89.9	598	22	AAU06178	N. meningitidis B2
28	1848	89.6	589	20	AAV23745	A surface protein
29	1848	89.6	589	22	AAU06173	N. meningitidis P2
30	1749.5	84.8	604	22	AAU06181	N. meningitidis su
31	660.5	32.0	1098	17	AAV99392	Haemophilus adhest
32	640	31.0	2411	21	AAV23860	Haemophilus influe
33	638	30.9	2353	17	AAV99393	Haemophilus adhest
34	625.5	30.3	1094	21	AAV23858	Haemophilus influe
35	600	29.1	116	21	AAV37832	Neisserial conserv
36	494	23.9	679	17	AAV99394	Haemophilus adhest
37	494	23.9	679	21	AAV23855	Haemophilus influe
38	402.5	19.5	1004	21	AAV23857	Haemophilus influe
39	391.5	19.0	1002	21	AAV23854	Haemophilus influe
40	366	17.7	72	21	AAV37830	Neisserial conserv
41	341.5	16.6	1104	21	AAV23856	Haemophilus influe
42	341.5	16.6	1104	21	AAV23859	Haemophilus influe
43	331	16.0	1778	22	AAV52677	Escherichia coli p
44	319	15.5	2139	24	ABP12594	M. catarrhalis sur
45	317.5	15.4	2314	22	AAV69136	M. catarrhalis les

## ALIGNMENTS

RESULT 1	
AAU06184	
ID	AAU06184 standard; Protein: 407 AA.
AC	AAU06184;
XX	
XX	24-OCT-2001 (first entry)
DT	
XX	
DE	N. meningitidis PMC21 Nhma deletion mutant #2.
XX	
KW	Surface antigen Nhma; meningococcal disease; meningitis vaccine;
KW	mutant; muteln.
XX	
OS	Neisseria meningitidis strain PMC21.
XX	
FT	Synthetic.
FT	
FT	Key
FT	Peptide
FT	/label= signal_peptide
FT	/label= 52..407
FT	/label= Mature Nhma deletion mutant #2
FT	/note= "predicted mature protein, specifically
FT	claimed in claim 12"
XX	
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XX	WO20015182-A1.
XX	
XX	02-AUG-2001.
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XX	
XX	25-JAN-2001; 2001WO-AU00069.
PF	
XX	
XX	25-JAN-2000; 2000US-0177917.
PR	
XX	

PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 XX Peak IRA, Jennings MP;  
 XX  
 XX WPI: 2001-488774/53.  
 DR N-PSDB: AAS09174.  
 XX  
 PS New NhhA surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 7; 91pp; English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen NhhA  
 CC (AA06182-AA06186). The modified or mutant NhhA polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen NhhA deletion mutant #2.  
 CC  
 XX Sequence 407 AA;  
 XX  
 Query Match 100.0%; Score 2063; DB 22; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 5e-132;  
 Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIRIIMNSALNMVYVSELTRNHTKRASATVKTAVATLLEFATVQASANNVDFVRY 60  
 DB 1 MNKIRIIMNSALNMVYVSELTRNHTKRASATVKTAVATLLEFATVQASANNVDFVRY 60  
 QY 61 DIVEFLSADTKTTTVNVESEKDKGKTEVKIGAKTSYIKEDSKLVYTKDNGSGSTDEG 120  
 DB 61 DIVEFLSADTKTTTVNVESEKDKGKTEVKIGAKTSYIKEDSKLVYTKDNGSGSTDEG 120  
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 DB 121 EGLVTAKEVIDVNVKAGRMKTTTANGOTGQADKEFEYVSGTNVTFASGKTATVSKDD 180  
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 DB 121 EGLVTAKEVIDVNVKAGRMKTTTANGOTGQADKEFEYVSGTNVTFASGKTATVSKDD 180  
 QY 181 OGNTITVMDVNVGDLANVQOLNSGMNLSKAVAGSSGKVISGNSPSKGMDETVNINA 240  
 DB 181 OGNTITVMDVNVGDLANVQOLNSGMNLSKAVAGSSGKVISGNSPSKGMDETVNINA 240  
 QY 241 GNNITITNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKMPVRIITV 300  
 DB 241 GNNITITNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKMPVRIITV 300  
 QY 301 APGVEGDVTNVAQKGVANLNRRIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIG 360  
 DB 301 APGVEGDVTNVAQKGVANLNRRIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIG 360  
 QY 361 GGTYGEAGYALGYSSISDGMIIKGTASGNSRGHFGASASVGYOW 407  
 DB 361 GGTYGEAGYALGYSSISDGMIIKGTASGNSRGHFGASASVGYOW 407

RESULT 2  
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 ID AA06185 standard; Protein; 433 AA.  
 XX  
 AC AA06185;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis PMC21 NhhA deletion mutant #3.  
 XX  
 KM Surface antigen NhhA, meningococcal disease; meningitis vaccine;  
 KM mutant; mutuin.

XX  
 OS Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 XX  
 XX Key  
 FH Peptide  
 FT 1..51  
 FT /label= Signal\_peptide  
 FT 52..433  
 FT /label= Mature\_NhhA\_deletion\_mutant\_#3  
 FT /note= "Predicted mature protein, specifically  
 FT claimed in claim 12"  
 XX  
 XX WO20015182-A1.  
 XX  
 XX 02-AUG-2001.  
 XX  
 PD 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PF 25-JAN-2001; 2000US-0177917.  
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 PR 25-JAN-2001; 2000US-0177917.  
 XX  
 PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI: 2001-488774/53.  
 DR N-PSDB: AAS09175.  
 XX  
 XX New NhhA surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 8; 91pp; English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen NhhA  
 CC (AA06182-AA06186). The modified or mutant NhhA polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen NhhA deletion mutant #3.  
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 XX Sequence 433 AA;  
 XX  
 Query Match 98.9%; Score 2040; DB 22; Length 433;  
 Best Local Similarity 94.0%; Pred. No. 2e-130;  
 Matches 407; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MNKIRIIMNSALNMVYVSELTRNHTKRASATVKTAVATLLEFATVQASAN----- 52  
 DB 1 MNKIRIIMNSALNMVYVSELTRNHTKRASATVKTAVATLLEFATVQASANRAASVDY 60  
 QY 53 -----NVDFVRYDIVEFLSADTKTTTVNVESEKDKGKTEVKIGAKT 94  
 DB 61 LNAGNNIKGVKRPQTASDNDVDFVRYDIVEFLSADTKTTTVNVESEKDKGKTEVKIGAKT 120  
 QY 95 SYIKEDGKLVYTKRKGEGSSTDEGEGLYTAKEVIDVNVKAGRMKTTTANGOTGQADK 154  
 DB 121 SVIKEDGKLVYTKRKGEGSSTDEGEGLYTAKEVIDVNVKAGRMKTTTANGOTGQADK 180  
 QY 155 FETVTSNTVTFASGKTATVSKDDQGNITVMDVNVGDLANVQOLNSGMNLSKAVA 214  
 DB 181 FETVTSNTVTFASGKTATVSKDDQGNITVMDVNVGDLANVQOLNSGMNLSKAVA 240  
 QY 215 GSSGKVISGNSPSKGMDETVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADA 274  
 DB 241 GSSGKVISGNSPSKGMDETVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADA 300  
 QY 275 PTLISVDGALNVGSKDKMPVRIITVNAQKGVANLNRRIDNVGNAR 334



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Db 301 PTLSDVDDALNVGSKDNKPVRTITNVA PGVEGDVTNVAOLKGAQNLNNRIDVQGNAR 360  
QY 335 AGTGAATATAGTGAATGATGPGKSMAGGCTRGEGATGAGTSSISDGGNMIITKGTASGNSR 394  
Db 361 AGTGAATATAGTGAATGATGPGKSMAGGCTRGEGATGAGTSSISDGGNMIITKGTASGNSR 420  
QY 395 GHFGASASVGYQW 407  
Db 421 GHFGASASVGYQW 433  
RESULT 3  
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ID AAU06186 standard; Protein: 502 AA.  
XX AAU06186;  
XX  
XX 24-OCT-2001 (first entry)  
XX  
XX N. meningitidis PMC21 Nhma deletion mutant #4.  
XX  
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine;  
XX mutant; mutlein.  
XX  
XX Neisseria meningitidis strain PMC21.  
OS Synthetic.  
XX  
XX  
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XX claimed in claim 12"  
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XX WO200155182-A1.  
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XX 02-AUG-2001.  
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XX 25-JAN-2001; 2001WO-AU00069.  
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XX 25-JAN-2000; 2000US-0177917.  
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XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
XX  
XX N-PSDB; AAS09176.  
XX  
XX New Nhma surface antigen polypeptides and polynucleotides from  
XX Neisseria meningitidis, useful in producing vaccines for treating or  
XX preventing broad spectrum of Neisseria meningitidis -  
XX  
XX Claim 12; Fig 9; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
XX meningitidis mutant polypeptides of the surface antigen Nhma  
XX (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
XX characterised by deletions of non-conserved amino acids, particularly  
XX the deletion of variable regions. The deletion mutants are useful in  
XX diagnostics, therapeutic and prophylactic vaccines against a broader  
XX spectrum of N. meningitidis, and in designing and/or screening of  
XX medicaments. The mutant proteins when used as a vaccine can effectively  
XX immunise against a broader spectrum of N. meningitidis strains than  
XX would be expected from a corresponding wild-type surface antigen.  
XX The present sequence represents N. meningitidis strain PMC21 surface  
XX antigen Nhma deletion mutant #4.  
XX  
XX Sequence 502 AA;  
Query Match 97.2%, Score 2005.5; DB 22; Length 502;

Best Local Similarity 81.1%; Pred. No. 5.2e-128;  
Matches 407; Conservative 0; Mismatches 0; Indels 95; Gaps 1;  
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QY 53 -----NDVEFRTYDVEFLSADTKTTTVNESKDNKK 85  
Db 121 GIGSTLFDRAASVKNVLAAGNINIKGVKNVDFPRTYDVEFLSADTKTTTVNESKDNKK 180  
QY 86 TEVKIGAKTSYIKKDKGLYTGKRGKENGSTDEGEGLYTAKEVIDAVNKAQMKTKTTTA 145  
Db 181 TEVKIGAKTSYIKKDKGLYTGKRGKENGSTDEGEGLYTAKEVIDAVNKAQMKTKTTTA 240  
QY 146 NGQFGADKFEPTVSGTNVTFASGKGTATVSKDQGNITVYVDVNGDALNVNQLNSG 205  
Db 241 NGQFGADKFEPTVSGTNVTFASGKGTATVSKDQGNITVYVDVNGDALNVNQLNSG 300  
QY 206 WNLDSKAVAGSSGKVISGNVSPSKKMDETVINAGNNIETTRNGKNIDATSMTPQFSS 265  
Db 301 WNLDSKAVAGSSGKVISGNVSPSKKMDETVINAGNNIETTRNGKNIDATSMTPQFSS 360  
QY 266 VSLGAGADAPLTVSDGALNVGSKDNKPVRTITNVA PGVEGDVTNVAOLKGAQNLNNR 325  
Db 361 VSLGAGADAPLTVSDGALNVGSKDNKPVRTITNVA PGVEGDVTNVAOLKGAQNLNNR 420  
QY 326 IDNVDSNARAGIAQIATAGIYQAYLPGKSMAGGCTRGEGATGAGTSSISDGGNMI 385  
Db 421 IDNVDSNARAGIAQIATAGIYQAYLPGKSMAGGCTRGEGATGAGTSSISDGGNMI 480  
QY 386 KGTASGNSRGHFGASASVGYQW 407  
Db 481 KGTASGNSRGHFGASASVGYQW 502  
RESULT 4  
AAU06182  
ID AAU06182 standard; Protein: 512 AA.  
XX  
XX AAU06182;  
XX  
XX 24-OCT-2001 (first entry)  
XX  
XX N. meningitidis PMC21 Nhma deletion mutant #1.  
XX  
XX  
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine;  
XX mutant; mutlein.  
XX  
XX Neisseria meningitidis strain PMC21.  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..51  
XX Protein /label= Signal\_peptide  
XX 52..512  
XX /label= "Mature\_Nhma\_deletion\_mutant\_#1  
XX /note= "Predicted mature protein, specifically  
XX claimed in claim 12"  
XX  
XX WO200155182-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX  
XX (UYQU ) UNIV QUEENSLAND.  
XX

PI	Pink IRA, Jennings MP:
XX	
DR	WPI: 2001.488774/53.
XX	
DR	N-PSDB; AAS09172.
XX	
PT	New Nhba surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 12; Fig 5; 91pp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhba
CC	(AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	would be expected from a corresponding wild-type surface antigen.
CC	The present sequence represents N. meningitidis strain PMC21 surface
CC	antigen Nhba deletion mutant #1.
XX	
SQ	Sequence 512 AA;
Query Match	97.0%; Score 2000.5; DB 22; Length 512;
Best Local Similarity	79.5%; Pred. No. 1.2e-127;
Matches 407; Conservative 0; Mismatches 0; Indels 105; Gaps .1	
QY	1 MNKYYRIIWNLSALNAVVVSELTNRNHRKRASATYKTAVLATLFTFVQASAN----- 52
DB	1 MNKYIRIIWNSALNAVVVSELTRNHKKRASATYKTAVALTLFTFVQASANNETDTSV 60
QY	53 ----- 52
DB	61 GTEKLSESANGKNNTISDTGCLNFAKETAAGTNGDTYHLNGIGSTLTDLLINCATNV 120
QY	53 ----- NVDEVRITDIYEFLSADTKTTTV 75
DB	121 TNDVVDDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVDPVRYDYEPLESLADRKTTTV 180
QY	76 NVESKDNGKKEVYIGAKTSYIKEKDKLVLYGKDKGENGSTDEEGLYTAKEVIDAYNK 135
DB	181 NVESKDNGKKEVYIGAKTSYIKEKDKLVLYGKDKGENSGSTDEEGELYTAKEVIDAYNK 240
QY	136 AGMYKMKTTTAGTGOGADKFETVTSCTNWTFEASGCGTATYSKDDOGNITWYDVNVGDA 195
DB	241 AGMYKMKTTTAGTGOGADKFETVTSCTNWTFEASGCGTATYSKDDOGNITWYDVNVGDA 300
QY	196 LNVNQNLONGMNLDSKAVAGSSGRVYISGVNSPSPSKMDETVINAGNNIEITRNKNIDI 255
DB	301 LNVNQNLONGMNLDSKAVAGSSGRVYISGVNSPSPSKMDETVINAGNNIEITRNKNIDI 360
QY	256 ATSMTPPOFSVSLACGADAPTLVSVDGDLANGSKKDNKPVRTYNVAPCVKBECDVTVAQL 315
DB	361 ATSMTPPOFSVSLACGADAPTLVSVDGDLANGSKKDNKPVRTYNVAPCVKBECDVTVAQL 420
QY	316 KGVNQNLNNRIDNDVGNARAGIAIALTAGIVQAYLPCKSMALGGGYRREGAGCAIGYS 375
DB	421 KGVNQNLNNRIDNDVGNARAGIAIALTAGIVQAYLPCKSMALGGGYRREGAGCAIGYS 480
QY	376 SISDGNMIIKGTASGNSRGHFHFGASASYGYOM 407
DB	481 SISDGNMIIKGTASGNSRGHFHFGASASYGYOM 512
RESULT 5	
ID	AAV27202 standard; Protein: 591 AA.
XX	AAV27202;
CC	

[illegible]

Db 361 SKDOGNITVWYDVNVDALNVNOLNSGWNLDKKAVALGSSGKVIISGNVSPSKGMDETV 420  
 QY 237 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKDKNPKVR 296  
 Db 421 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKDKNPKVR 480  
 QY 297 ITNVAPEGKEDVTNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 356  
 Db 481 ITNVAPEGKEDVTNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 540-  
 QY 357 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGRHGASASVGYOW 407  
 Db 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGRHGASASVGYOW 591

RESULT 6  
 AAY23746  
 ID AAY23746 standard; Protein: 591 AA.

XX AC AAY23746;  
 XX D7 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;  
 XX immunoreactive peptide.

XX OS Neisseria meningitidis.

XX XN WO9931132-A1.

XX PD 24-JUN-1999.

XX PE 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYOU ) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX DR WPI: 1999-418754/35.

XX DR N-PSDB: AAX85798.

XX PT Neisseria meningitidis surface proteins useful for treating N.

XX PT meningitidis infections

XX PS Claim 1; Page 127-128; 132pp; English.

XX CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX S0 Sequence 591 AA;

Query Match 95.1%; Score 1961; DB 20; Length 591;  
 Best Local Similarity 68.9%; Pred. No. 6.6e-125;  
 Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;

QY 1 MNKIYRIWNSALNAWVVSSELTFRNHTKRASATVKTAVLATLFLFATVQASAN----- 52  
 Db 1 MNKIYRIWNSALNAWVVSSELTFRNHTKRASATVKTAVLATLFLFATVQASANNEOEEDL 60  
 QY 53 ----- 52

Db 61 YLDPVORTVAVLIVNSDEKGTGEKEKEVENSMAVYFNEKGVLTAIREITLAKGDNLIKQ 120  
 QY 53 ----- 52  
 Db 121 NGTFYTSLKADLDLISVTEKLSFSAKNGKVNITSOTKGLNFAKETAGTNGOTYVHLN 180  
 QY 53 -----NVD 56  
 Db 181 GIGSTLDTLLNTGATTTVTNDVNTDDEKRRASVKKVDLNGWNIKGVKPGTTASDNVDF 240  
 QY 57 VRTYDVEEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVTKDKGENSS 116  
 Db 241 VRTYDVEEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIERKDGKLVTKDKGENSS 300  
 QY 117 TDEGGLVTAKEVIDAVNKKAGMRKTTTANGOTGADKFEVTYSGTNTVTFASGCTATV 176  
 Db 301 TDEGGLVTAKEVIDAVNKKAGMRKTTTANGOTGADKFEVTYSGTNTVTFASGCTATV 360  
 QY 177 SKDOGNITVWYDVNVDALNVNOLNSGWNLDKKAVALGSSGKVIISGNVSPSKGMDETV 236  
 Db 361 SKDOGNITVWYDVNVDALNVNOLNSGWNLDKKAVALGSSGKVIISGNVSPSKGMDETV 420  
 QY 237 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKDKNPKVR 296  
 Db 421 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKDKNPKVR 480  
 QY 297 ITNVAPEGKEDVTNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 356  
 Db 481 ITNVAPEGKEDVTNVAOLKGAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 540  
 QY 357 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGRHGASASVGYOW 407  
 Db 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGRHGASASVGYOW 591

RESULT 7  
 AAU06171  
 ID AAU06171 standard; Protein: 591 AA.

XX AC AAU06171;

XX DT 24-OCT-2001 (first entry)

XX DE N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.

XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain PMC21.

XX FH Key

XX FT Peptide

XX FT /label= Signal\_peptide

XX FT 1..50

XX FT /label= C1

XX FT /note= "Conserved region 1"

XX FT 51..108

XX FT /label= V1

XX FT /note= "Variable region 1"

XX FT 52..591

XX FT /label= Mature\_NhhA

XX FT /note= "Predicted mature protein, specifically

XX FT claimed in claim 12"

XX FT 109..120

XX FT /label= C2

XX FT /note= "Conserved region 2"

XX FT 121..124

XX FT /label= V2

XX FT /note= "Variable region 2"

XX FT 125..188

XX FT /label= C3

XX FT /note= "Conserved region 3"

XX FT 189..210

XX FT /label= V3

XX FT Region

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FT      /note= "Variable region 3"
FT      Region
FT      211...229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      Region
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237...591
FT      /label= C5
FT      /note= "Conserved region 5"
XX
XX      WO200155182-A1.
XX
XX      02-AUG-2001.
XX
XX      25-JAN-2001; 2001WO-AU00069.
XX
XX      25-JAN-2000; 2000US-0177917.
XX
XX      (UYOU ) UNIV QUEENSLAND.
XX
XX      Peak IRA, Jennings MP;
XX
XX      WPI: 2001-488774/53.
XX      N-PSDB: AAS09161.
XX
XX      New Nhma surface antigen polypeptides and polynucleotides from
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      preventing broad spectrum of Neisseria meningitidis -
XX
XX      Claim 9; Fig 1; 91pp; English.
XX
XX      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Nhma
XX      (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
XX      characterised by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      medicaments. The mutant proteins when used as a vaccine can effectively
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      would be expected from a corresponding wild-type surface antigen.
XX      The present sequence representing the wild type surface antigen Nhma
XX      from N. meningitidis strain PMC21 is 1 of 10 Nhma polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
XX
XX      Sequence 591 AA:
SQ      Query Match      95.1%; Score 1961; DB 22; Length 591;
      Best Local Similarity 68.9%; Pred. No. 6.6e-125;
      Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;
OY      1 MKKIRIIMNSALNMAVVVSELTNRNHTKRASATVTAVALTLLFNTQASAN----- 52
      1 MKKIRIIMNSALNMAVVVSELTNRNHTKRASATVTAVALTLLFNTQASANNEQEDL 60
DB
OY      53 ----- 52
DB
OY      61 YLDPVQRTAVAVLIIVNSDKRGTEKEKEVNEENSDMAYFNEKGVLTAREITLAKADNLKIKO 120
OY      53 ----- 52
DB      121 NGNTFTYSLKLDLFDLSVTEKLSFANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
OY      53 -----NVPF 56
DB      181 GIGSLTLDTLTNGATNTVNDNTDDEKKRAASVKVDVINAGMNKIGVPGTTASDNVDF 240
OY      57 VRTYDVEFLSADFTTTTVNVEKSDGKTEVKGAKTSVIREKDGKLTVTGDKGNGSS 116
      241 VRTYDVEFLSADFTTTTVNVEKSDGKTEVKGAKTSVIREKDGKLTVTGDKGNGSS 300

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OY      117 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGQADKFEFVYTSCTNTVPAQKGTATV 176
DB      301 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGQADKFEFVYTSCTNTVPAQKGTATV 360
OY      177 SKDDGNTITVMYDVVAGLALNVLONSGMNLDSKAVAGSSGKVTSGNVSPSKGMDETV 236
DB      361 SKDDGNTITVMYDVVAGLALNVLONSGMNLDSKAVAGSSGKVTSGNVSPSKGMDETV 420
OY      237 NINAGNNIEITFNGKNIDIASMTPQFSSVSLGAGADAPTLISVDDALNVGSKDKNKPVR 296
DB      421 NINAGNNIEITFNGKNIDIASMTPQFSSVSLGAGADAPTLISVDDALNVGSKDKNKPVR 480
OY      297 ITNVAPEKGEQDVTVAQLKGYAQLNNRIDNVGDNARAQIAQAIATAGLYQATVPGSM 356
DB      481 ITNVAPEKGEQDVTVAQLKGYAQLNNRIDNVGDNARAQIAQAIATAGLYQATVPGSM 540
OY      357 MAIGGGTYRGEAGYVAGYSISDGNWIIKGTASGNSRGRFGASASVGYOW 407
DB      541 MAIGGGTYRGEAGYVAGYSISDGNWIIKGTASGNSRGRFGASASVGYOW 591

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RESULT 8
AAV23737
ID      AAV23737 standard; Protein; 592 AA.
XX
XX      AAV23737;
AC      08-SEP-1999 (first entry)
XX
XX      A surface protein of Neisseria meningitidis.
DE
XX      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
KW
XX      Neisseria meningitidis.
OS
XX      WO931132-A1.
XX      24-JUN-1999.
XX
XX      14-DEC-1998; 98WO-AU01031.
XX
XX      12-DEC-1997; 97GB-0026398.
XX
XX      PA (ISIS-) ISIS INNOVATION LTD.
XX      PA (UYOU ) UNIV QUEENSLAND.
XX
XX      Jennings MP, Moxon ER, Peak IRA;
XX
XX      WPI: 1999-418754/35.
XX      N-PSDB: AAX85788.
XX
XX      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX
XX      Claim 1; Page 86-87; 132pp; English.
XX
XX      The present sequence represents a surface protein of Neisseria
XX      meningitidis which is approximately 62 kDa. The N. meningitidis
XX      surface glycoproteins, nucleic acids, the primers and optionally
XX      a thermostable polymerase, or antibodies are useful in a kit for
XX      the detection of N. meningitidis infection in humans.
XX      The N. meningitidis surface glycoproteins can also be used to
XX      prevent or treat N. meningitidis infection in humans, especially
XX      in the form of vaccines. The proteins and antibodies can also
XX      be used to identify immunoreactive peptides.
XX
XX      Sequence 592 AA:

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```

SQ      Query Match      94.8%; Score 1956.5; DB 20; Length 592;
      Best Local Similarity 68.6%; Pred. No. 1.3e-124;
      Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;

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QY 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLTLLFATVQASAN----- 52
Db 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLTLLFATVQASANNEPRK 60
QY 53 ----- 52
Db 61 LYLDPVQRTAVAVLVNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIK 120
QY 53 ----- 52
Db 121 QNGTNFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNTISDTKGLNFAKETAGTNGDPTVHL 180
QY 53 -----NVD 55
Db 181 NGIGSTLTDLTLNMGATTNTVNDVTDDEKKRAASVYKVDLNAAGNIKGVKPGTTASDNDV 240
QY 56 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTIVYKEKDKLVTGDKDGENGS 115
Db 241 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTIVYKEKDKLVTGDKDGENGS 300
QY 116 STDEGEGLVTAKEVIDAVNKGWPMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTAT 175
Db 301 STDEGEGLVTAKEVIDAVNKGWPMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTAT 360
QY 176 VSKDDGNTVMTDVNVGDALNVNQLONGSMNLDKSAVAGSSGKVISGNTVSPSKKMDET 235
Db 361 VSKDDGNTVMTDVNVGDALNVNQLONGSMNLDKSAVAGSSGKVISGNTVSPSKKMDET 420
QY 236 VNTNAGNNITITRNGKIDTATSWTPPFSSVSLGAGADAPTLYSDGALNVGSKKDKPV 295
Db 421 VNTNAGNNITITRNGKIDTATSWTPPFSSVSLGAGADAPTLYSDGALNVGSKKDKPV 480
QY 296 RITNVAPGVEGDVTNVAQIKGVAQNNRINDVNDGARNAGIAQAITAGIYQAYLPFGKS 355
Db 481 RITNVAPGVEGDVTNVAQIKGVAQNNRINDVNDGARNAGIAQAITAGIYQAYLPFGKS 540
QY 356 MMAIGGTYRGAGAYGALGYSSISDGGMIITKGTASGNSRGHFGASASVGYOW 407
Db 541 MMAIGGTYRGAGAYGALGYSSISDGGMIITKGTASGNSRGHFGASASVGYOW 592

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RESULT 9
AAV57045
ID AAV57045 standard; Protein: 591 AA.
XX
XX AAV57045;
XX
Db 21-FEB-2000 (first entry)
XX
XX BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
XX BASB029: Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KM infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
XX
XX key location/Qualifiers
FH MISC-difference 90
FT MISC-difference 92 /note= "Encoded by AAT"
FT MISC-difference 98 /note= "Encoded by GAT"
FT MISC-difference 98 /note= "Encoded by AAC"
FT MISC-difference 108 /note= "Encoded by AATC"
FT MISC-difference 123 /note= "Encoded by ACA"
FT MISC-difference 269 /note= "Encoded by AAA"
FT MISC-difference 389 /note= "Encoded by CGT"
XX
XX WO9558683-A2.

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XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99MO-EP03255.
PF
XX
XX 13-MAY-1998; 98GB-0010276.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Ruelle J;
PI
XX
XX WPI: 2000-053103/04.
DR
XX N-PSDB: AA239865.
PT
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Nisseria meningitidis BASB029 amino acid sequence from
XX serogroup B strain H44/76. The BASB029 protein is homologous to the
XX Haemophilus influenzae surface fibril (HSF) protein. The invention
XX relates to BASB029 polynucleotide sequences (AA239864-239865) and
XX polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria
XX meningitidis infection in a mammal. Compositions containing BASB029
XX polynucleotides and polypeptides are useful for generating an immune
XX response in an animal. A therapeutic composition comprising an antibody
XX directed against BASB029 is useful in treating humans with Neisseria
XX meningitidis disease. The polynucleotide is useful in the diagnosis of
XX the stage of infection, type of infection, susceptibility to an
XX infection which results from increased or decreased expression of the
XX polynucleotide, and for therapeutic or prophylactic purposes,
XX particularly genetic immunisation. Antibodies against BASB029
XX polynucleotides and polypeptides are also useful for treating infections
XX particularly bacterial infections. The protein is useful in the
XX screening and development of antibacterial drugs. Fused recombinant
XX protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX
XX Sequence 591 AA;
SQ

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Query Match 94.7%; Score 1954; DB 21; Length 591;
Best Local Similarity 68.5%; Pred. No. 2e-124;
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;
QY 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLTLLFATVQASAN----- 52
Db 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLTLLFATVQASANNEDEEDL 60
QY 53 ----- 52
Db 61 YLDPVQRTAVAVLVNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIK 120
QY 53 ----- 52
Db 121 NGSNFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNTISDTKGLNFAKETAGTNGDPTVHL 180
QY 53 -----NVD 56
Db 181 GIGSTLTDLTLNMGATTNTVNDVTDDEKKRAASVYKVDLNAAGNIKGVKPGTTASDNDV 240
QY 57 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTIVYKEKDKLVTGDKDGENGS 116
Db 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTIVYKEKDKLVTGDKDGENGS 300
QY 117 TDEGEGLVTAKEVIDAVNKGWPMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTATV 176
Db 301 TDEGEGLVTAKEVIDAVNKGWPMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTATV 360
QY 177 SKDDGNTVMTDVNVGDALNVNQLONGSMNLDKSAVAGSSGKVISGNTVSPSKKMDETV 236
Db 361 SKDDGNTVMTDVNVGDALNVNQLONGSMNLDKSAVAGSSGKVISGNTVSPSKKMDETV 420

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QY 237 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 296  
DB 421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 480  
QY 297 ITTNAAPGVEGDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLQVAYLPKSKM 356  
DB 481 ITTNAAPGVEGDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLQVAYLPKSKM 540  
QY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGTASGNSGHHFGASASVGYQW 407  
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGTASGNSGHHFGASASVGYQW 591  
RESULT 10  
AAV23741  
ID AAV23741 standard; Protein; 591 AA.  
XX AAV23741;  
XX 08-SEP-1999 (first entry)  
DT A surface protein of Neisseria meningitidis.  
DE A surface protein of Neisseria meningitidis.  
KM Surface protein; surface glycoprotein; infection; vaccine;  
KW Immunoreactive peptide.  
XX Neisseria meningitidis.  
OS Neisseria meningitidis.  
XX W0993132-A1.  
PN 24-JUN-1999.  
PD 14-DEC-1998; 98WO-AU01031.  
XX 12-DEC-1997; 97GB-0026398.  
PR (ISIS-) ISIS INNOVATION LTD.  
XX (UYOU) UNITV QUEENSLAND.  
PA (UYOU) UNITV QUEENSLAND.  
XX Jennings MP, Moxon ER, Peak IRA;  
PI WPI: 1999-418754/35.  
XX DR N-PSDB: AAX85793.  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PT Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX Claim 1; Page 104-106; 132pp; English.  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX SQ Sequence 591 AA.  
Query Match 94.5%; Score 1949; DB 20; Length 591;  
Best Local Similarity 68.5%; Pred. No. 4.3e-124;  
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;

QY 53 ----- 52  
DB 121 NGTNFTYSLKKKDLIDLTVSTGEKLSFSANGKVNITSDTKGLNFAKETAGTNGPTVHLN 180  
QY 53 ----- -ANDF 56  
DB 181 GIGSTLIDLTLNGATTNTNDVNTDDEKKRAASVQDVLNAGMNIKGVPPTTASDNVDF 240  
QY 57 VRTDYVEFLSADRTKTTVNVEESKDNCKTEVKIGAKTSVIREKDGKLVYTGKDKGENGSS 116  
DB 241 VRTDYVEFLSADRTKTTVNVEESKDNCKTEVKIGAKTSVIREKDGKLVYTGKDKGENGSS 300  
QY 117 TDEGEGLVTAKEVIDAVNKAQMRKTTTANGQTOGADKFETVTSGTNTFASGKGTATV 176  
DB 301 TDEGEGLVTAKEVIDAVNKAQMRKTTTANGQTOGADKFETVTSGTNTFASGKGTATV 360  
QY 177 SKDDOGNTTVAVDVAVGALNVNQLONGGWNLDKFAVAGSSGKXVYSGNVSPSKGMDFTV 236  
DB 361 SKDDOGNTTVAVDVAVGALNVNQLONGGWNLDKFAVAGSSGKXVYSGNVSPSKGMDFTV 420  
QY 237 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 296  
DB 421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 480  
QY 297 ITTNAAPGVEGDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLQVAYLPKSKM 356  
DB 481 ITTNAAPGVEGDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLQVAYLPKSKM 540  
QY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGTASGNSGHHFGASASVGYQW 407  
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGTASGNSGHHFGASASVGYQW 591  
RESULT 11  
AAU06175  
ID AAU06175 standard; Protein; 591 AA.  
XX AAU06175;  
XX 24-OCT-2001 (first entry)  
DT N. meningitidis EG329 surface antigen NnhA polypeptide sequence.  
XX N. meningitidis EG329 surface antigen NnhA polypeptide sequence.  
DE Surface antigen NnhA; meningococcal disease; meningitis vaccine.  
XX Surface antigen NnhA; meningococcal disease; meningitis vaccine.  
KW Neisseria meningitidis strain EG329.  
XX Neisseria meningitidis strain EG329.  
OS Neisseria meningitidis strain EG329.  
XX Location/Qualifiers  
FH 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..108  
FT /label= V1  
FT /note= "Variable region 1"  
FT 109..120  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 121..124  
FT /label= V2  
FT /note= "Variable region 2"  
FT 125..188  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 189..210  
FT /label= V3  
FT /note= "Variable region 3"  
FT 211..229  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 230..236  
FT /label= V4  
FT /note= "Variable region 4"

FT Region 237..591  
 FT /label= C5  
 XX /note= "Conserved region 5"  
 PN WO200155182-A1.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-AU00069.  
 XX  
 XX 25-JAN-2000; 2000US-0177917.  
 XX  
 XX (UYOU ) UNIV QUEENSLAND.  
 XX  
 XX Peak IRA, Jennings MP;  
 XX  
 XX WPI; 2001-488774/53.  
 DR N-PSDB; AAS09165.  
 XX  
 XX New Nhma surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 XX Claim 9; Fig 1; 91pp; English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhma  
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhma  
 CC from N. meningitidis strain EG329 is 1 of 10 Nhma polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 CC  
 XX  
 XX Sequence 591 AA;  
 SQ  
 Query Match 94.5%; Score 1949; DB 22; Length 591;  
 Best Local Similarity 68.5%; Pred. No. 4.3e-124;  
 Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;

QY 1 MNKIRIRNSALNAMYVSELTRNHRKASATYKTAVALTLFATYQASAN----- 52  
 DB 1 MNEILRIINSAALNAMYVSELTRNHRKASATYKTAVALTLFATYQASANNEDEEDL 60  
 QY 53 ----- 52  
 DB 61 YLDPVLKTAVALIVNSDEKGEKEKYENSDAVYNEKGVLTAREITLAKAGDNLIKIQ 120  
 QY 53 ----- 52  
 DB 121 NGNFYSLKKDLDTLSTVGTSEKLSFGANGKNVITSDTGLNFAKFTAGNGDTYHLN 180  
 QY 53 -----NVDF 56  
 DB 181 GIGSTLDTLLNGATTNTNDVYDDEKRAASVKDVLNAGWNINIKVRCGTASDVNDF 240  
 QY 57 VRTVDVEFLSADTKTTTANVESKDNKTEVKIGAKTSYIKEDGKLYMGKDGENGSS 116  
 DB 241 VRTVDVEFLSADTKTTTANVESKDNKTEVKIGAKTSYIKEDGKLYMGKDGENGSS 300  
 QY 117 TDEGEGLVATAKEVIDAVNKAQWRMKTJTANGQTGQADKFTVTSGTNVTFASGKTATV 176  
 DB 301 TDEGEGLVATAKEVIDAVNKAQWRMKTJTANGQTGQADKFTVTSGTNVTFASGKTATV 360  
 QY 177 SKDQGNITVYDVNVDALNVNOLNSGNMLDSKAVAGSSGKYSGNVSPSKKMDETV 236  
 DB 361 SKDQGNITVYDVNVDALNVNOLNSGNMLDSKAVAGSSGKYSGNVSPSKKMDETV 420

QY 237 NINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKNKRPV 296  
 DB 421 NINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKNKRPV 480  
 QY 297 ITNVAPGVKGGDYTNVAQLGVAQNLNRRIDNVGNNRAGIAQAIATAGLVQAVLPCKSM 356  
 DB 481 ITNVAPGVKGGDYTNVAQLGVAQNLNRRIDNVGNNRAGIAQAIATAGLVQAVLPCKSM 540  
 QY 357 MAIGGTYRGEAGTAIGSSISDGGNNITIGTAGSNGRCHFGASASGYQM 407  
 DB 541 MAIGGTYRGEAGTAIGSSISDGGNNITIGTAGSNGRCHFGASASGYQM 591

RESULT 12  
 AAU06183  
 ID AAU06183 standard; Protein: 513 AA.  
 XX  
 XX AAU06183;  
 AC  
 XX 24-OCT-2001 (first entry)  
 DT  
 XX N. meningitidis H41 Nhma deletion mutant.  
 DE  
 XX Surface antigen Nhma; meningococcal disease; meningitis vaccine;  
 KW mutant; muten.  
 XX  
 XX Neisseria meningitidis strain H41.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..51  
 FT /label= signal\_peptide  
 FT Protein 52..513  
 FT /label= Mature\_Nhma\_deletion\_mutant  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 XX  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 XX WPI; 2001-488774/53.  
 DR N-PSDB; AAS09173.  
 XX  
 XX New Nhma surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 XX Claim 12; Fig 6; 91pp; English.  
 PS  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhma  
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain H41 surface  
 CC antigen Nhma deletion mutant.  
 CC  
 XX  
 SQ Sequence 513 AA;

```

Query Match      92.5%; Score 1909; DB 22; Length 513;
Best Local Similarity 76.6%; Pred. No. 1.9e-121;
Matches 393; Conservative 4; Mismatches 10; Indels 106; Gaps 2;

OY 1 MKKIRIITNSALNMVYVSELTRNHTKRASATVTAVALTLFFATVQASA----- 51
    |||||||
DB 1 MKKIRIITNSALNMVAVSELTRNHTKRASATVTAVALTLFFATVQANATDEGLNV 60
    |||||||
OY 52 ----- 51
DB 61 ETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTVHNLGSLTMDLNTGATNV 120
    |||||||
OY 52 ----- NNVDFRYDYVEFLSADTKTTTV 75
    |||||||
DB 121 TNDNVTDEKKRAASYKDVNLNAGWNIKGVPKGTASDNDVDFRYDYVEFLSADTKTTTV 180
    |||||||
OY 76 NVESKDNCKTEVKIGAKTSVTKERDKLVTKDKGENSSVDEBGLVTAKEVIDAVNK 135
    |||||||
DB 181 NVESKDNCKTEVKIGAKTSVTKERDKLVTKDKGENSSVDEBGLVTAKEVIDAVNK 240
    |||||||
OY 136 AGMRKTTTANGOTGADKFEETVTSGTNTVTFASGKTATVASKDOGNITVAVDVNGDA 195
    |||||||
DB 241 AGMRKTTTANGOTGADKFEETVTSGTNTVTFASGKTATVASKDOGNITVAVDVNGDA 300
    |||||||
OY 196 LNVNOLQNSGMNLDKRAVAGSSGKVIISGVNSPSKGMDETVINAGNNIEITRNGKNIDI 255
    |||||||
DB 301 LNVNOLQNSGMNLDKRAVAGSSGKVIISGVNSPSKGMDETVINAGNNIEITRNGKNIDI 360
    |||||||
OY 256 ATSMTPORSSVSLGAGADAPTLSDVDCD-ALNYGSKDKNKPVTITVAPVCKGDDVTNVAQ 314
    |||||||
DB 361 ATSMTPORSSVSLGAGADAPTLSDVDCD-ALNYGSKDKNKPVTITVAPVCKGDDVTNVAQ 420
    |||||||
OY 315 LKGVANQNLNRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYREAGYALGY 374
    |||||||
DB 421 LKGVANQNLNRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYREAGYALGY 480
    |||||||
OY 375 SSISDGNWITIKGTASGNSRGHFGASASYGYQM 407
    |||||||
DB 481 SSISAGWNWITIKGTASGNSRGHFGASASYGYQM 513
    |||||||

RESULT 13
AAU06180
ID AAU06180 standard; Protein; 592 AA.
XX
AC AAU06180;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis z2491 surface antigen Nhba polypeptide sequence.
XX
KW Surface antigen Nhba; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain z2491.
XX
FH Key
FT Location/Qualifiers
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..102
FT /label= V1
FT /note= "Variable region 1"
FT 103..114
FT /label= C2
FT /note= "Conserved region 2"
FT 115..124
FT /label= V2
FT /note= "Variable region 2"
FT 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT 189..208
FT Region

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FT /label= V3
FT /note= "Variable region 3"
FT 209..227
FT /label= C4
FT /note= "Conserved region 4"
FT 228..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..592
FT /label= C5
FT /note= "Conserved region 5"
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FT
PN WO20015182-A1.
XX
XX
PD 02-AUG-2001.
XX
XX
PF 25-JAN-2001; 2001WO-AU00069.
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PR 25-JAN-2000; 2000US-0177917.
XX
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
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DR WPI: 2001-488774/53.
XX
DR N-PSDB; AAS09170.
XX
XX
PT New Nhba surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp; English.
XX
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhba
CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhba
CC from N. meningitidis strain z2491 is 1 of 10 Nhba polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 592 AA:
XX
Query Match      91.8%; Score 1893.5; DB 22; Length 592;
Best Local Similarity 66.9%; Pred. No. 2.5e-120;
Matches 396; Conservative 4; Mismatches 7; Indels 185; Gaps 2;

OY 1 MKKIRIITNSALNMVYVSELTRNHTKRASATVTAVALTLFFATVQASA----- 51
    |||||||
DB 1 MKKIRIITNSALNMVAVSELTRNHTKRASATVTAVALTLFFATVQANATDEDEBEL 60
    |||||||
OY 52 ----- 51
DB 61 ESVORSVVGSIOASMEGSELETISLMTNDSKEFVDPIYVTLKAGDNLIKONTNENT 120
    |||||||
OY 52 ----- 51
DB 121 NASSFTYSLKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTVHLN 180
    |||||||
OY 52 ----- NNVDF 56
    |||||||
DB 181 GIGSTLTDTLSSASHVDAGNOSTHYTRAASIKVDNLNAGWNIKGVTGSGTGSSENVDF 240
    |||||||
OY 57 VRTYDVEFLSADTKTTTVNVEKDNCKTEVKIGAKTSVTKERDKLVTKDKGENSS 116
    |||||||
DB 241 VRTYDVEFLSADTKTTTVNVEKDNCKTEVKIGAKTSVTKERDKLVTKDKGENSS 300
    |||||||

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DR WPI: 2000-053103/04.  
DR N-PSDB: AA239864.

CC New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal  
XX  
PS Claim 4; Fig 2; 74pp; English.

XX This is the Neisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain AMCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and  
CC polypeptide sequences (AA157044-157045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes.  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX

Sequence 594 AA:

Query Match 91.5%; Score 1887.5; DB 21; Length 594;  
Best Local Similarity 66.5%; Pred. No. 6.4e-120;  
Matches 395; Conservative 5; Mismatches 7; Indels 187; Gaps 2;

OY 1 MNKIRITWNSALNMAVYVSELTNRNHTKRASATVATATLTLFATVOAS----- 50  
DB 1 MNKIYRIIWSALNMAVAVSELTNRNHTKRASATVATATLTLFATVOASTDDDLYLE 60  
OY 51 ----- 50  
DB 61 PVQRTAVVLSFRSDEKGEKEVTEDSMWGVYFDKKGVLTAGTTILKAGDNLIKQNTNE 120  
OY 51 ----- 50  
DB 121 NTNASSFTYSLKDLTDLTSVTEKLSFSAANSNKVNITSPTKGLNFAKTAETNGDTVH 180  
OY 51 -----ANNV 54  
DB 181 LNGIGSTLTDTLNTGATTNTNDVTDERRAASVADVNLNAGWNKGVKPGTTASDNV 240  
OY 55 DEVRTDYVEFLSADTKTTTVNVEBKDKGKTEYKIGAKTSYIKEDKLVTKGDKGNG 114  
DB 241 DFKRTDYVEFLSADTKTTTVNVEBKDKGKTEYKIGAKTSYIKEDKLVTKGDKGEND 300  
OY 115 SSTDEGELVTAKEVIDAVNRKAGMRKTTTANGQTGAQDKFEYVSGTNVTFASGKGT 174  
DB 301 SSTDKGELVTAKEVIDAVNRKAGMRKTTTANGQTGAQDKFEYVSGTNVTFASGKGT 360  
OY 175 TVSKDDOGNITVMDVNGDALNVNQLNSGMLDSKAVAGSSGKVISGNVSPSKGKMD 234  
DB 361 TVSKDDOGNITVMDVNGDALNVNQLNSGMLDSKAVAGSSGKVISGNVSPSKGKMD 420  
OY 235 TVNINAGNIEITRNGKNIDATSMTPQSSSVISGAGADAPTLISVDG-ALNVGSKKDN 293  
DB 421 TVNINAGNIEITRNGKNIDATSMTPQSSSVISGAGADAPTLISVDGALNVGSKKDN 480  
OY 294 PVRTTNVAPGVKESGDVTNVAQLKGYAQLNNRINDVNGNARAGIAQAATAGLVQAYLPG 353  
DB 481 PVRTTNVAPGVKESGDVTNVAQLKGYAQLNNRINDVNGNARAGIAQAATAGLVQAYLPG 540  
OY 354 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYW 407  
KSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYW 407

DB 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFGASASVGYW 594

Search completed: October 6, 2003, 09:22:30  
Job time : 37.9514 secs



Db 301 TDEBEGLVTAKEVIDAVNKAQWRKMTTANGOTGOADKFEVTVSGTNVTFASGKGTATV 360  
QY 177 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDFTV 236  
Db 361 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDFTV 420  
QY 237 NINAGNNIETRNKGNIDIAITSMTPPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKRPV 296  
Db 421 NINAGNNIETRNKGNIDIAITSMTPPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKRPV 480  
QY 297 ITNAPGVKEGDVTVNAOLKGVNAQNLNRRINDVDSNARAGIAQAATATAGLVAQVYLPGRSM 356  
Db 481 ITNAPGVKEGDVTVNAOLKGVNAQNLNRRINDVDSNARAGIAQAATATAGLVAQVYLPGRSM 540  
QY 357 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 407  
Db 541 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

RESULT 2  
US-09-669-974-21

; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 95.1%; Score 1961; DB 4; Length 591;  
Best Local Similarity 68.9%; Pred. No. 1e-155;  
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;

QY 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52  
Db 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVKTAVLATLLEFATVOASANNEBERDL 60  
QY 53 ----- 52  
Db 61 YLDPVQRTVAVLIVNSDEKTEGKEKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIKQ 120  
QY 53 ----- 52  
Db 121 NGTNFTYSLKKDLTDLTISVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTYVHLN 180  
QY 53 -----NVD 56  
Db 181 GIGSTLDDTLNLTGATTNVNDVNTDDEKKRAASVKKVYLNAGWNKGVKPGTTASDNVDF 240  
QY 57 VRTVDVVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEKDKGLVYTKDKGENSS 116  
Db 241 VRTVDVVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEKDKGLVYTKDKGENSS 300  
QY 117 TDEBEGLVTAKEVIDAVNKAQWRKMTTANGOTGOADKFEVTVSGTNVTFASGKGTATV 176  
Db 301 TDEBEGLVTAKEVIDAVNKAQWRKMTTANGOTGOADKFEVTVSGTNVTFASGKGTATV 360

QY 177 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDFTV 236  
Db 361 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDFTV 420  
QY 237 NINAGNNIETRNKGNIDIAITSMTPPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKRPV 296  
Db 421 NINAGNNIETRNKGNIDIAITSMTPPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKRPV 480  
QY 297 ITNAPGVKEGDVTVNAOLKGVNAQNLNRRINDVDSNARAGIAQAATATAGLVAQVYLPGRSM 356  
Db 481 ITNAPGVKEGDVTVNAOLKGVNAQNLNRRINDVDSNARAGIAQAATATAGLVAQVYLPGRSM 540  
QY 357 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 407  
Db 541 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

RESULT 3  
US-09-377-155-2

; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 94.8%; Score 1956.5; DB 3; Length 592;  
Best Local Similarity 68.6%; Pred. No. 2.4e-155;  
Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;

QY 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52  
Db 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVKTAVLATLLEFATVOASANNEPRKKD 60  
QY 53 ----- 52  
Db 61 YLDPVQRTVAVLIVNSDEKTEGKEKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIK 120  
QY 53 ----- 52  
Db 121 QNGTNFTYSLKKDLTDLTISVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTYVHL 180  
QY 53 -----NVD 55  
Db 181 NGISTLDDTLNLTGATTNVNDVNTDDEKKRAASVKKVYLNAGWNKGVKPGTTASDNVDF 240  
QY 56 FVRTVDVVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEKDKGLVYTKDKGENSS 115  
Db 241 FVRTVDVVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEKDKGLVYTKDKGENSS 300  
QY 116 STDEBEGLVTAKEVIDAVNKAQWRKMTTANGOTGOADKFEVTVSGTNVTFASGKGTATV 175  
Db 301 STDEBEGLVTAKEVIDAVNKAQWRKMTTANGOTGOADKFEVTVSGTNVTFASGKGTATV 360  
QY 176 VSKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDFTV 235  
Db 361 VSKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDFTV 420

QY 236 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNRPV 295  
 DB 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNRPV 480  
 QY 296 RITNVAPEGEGVTVNAOLKGVAQNLNNRIDVNDGNARAGIAOAIATAGLVOAYLPKGS 355  
 DB 481 RITNVAPEGEGVTVNAOLKGVAQNLNNRIDVNDGNARAGIAOAIATAGLVOAYLPKGS 540  
 QY 356 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYQW 407  
 DB 541 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYQW 592

RESULT 4  
 US-09-669-974-2  
 ; Sequence 2, Application US/09669974  
 ; Patent No. 6331173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/669,974  
 ; CURRENT FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US 09/377,155  
 ; PRIOR FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 592  
 ; TYPE: PR  
 ; ORGANISM: Neisseria meningitidis  
 US-09-669-974-2

Query Match 94.88; Score 1956.5; DB 4; Length 592;  
 Best Local Similarity 68.68; Pred. No. 2,4e-155;  
 Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;  
 QY 1 MNKIYRIWNSALNANWVYSELTRNHTKRASATVKTAVLTLLFATVQASAN----- 52  
 DB 1 MNKIYRIWNSALNANWVYSELTRNHTKRASATVKTAVLTLLFATVQASANNEDEEDL 60  
 QY 53 ----- 52  
 DB 61 YLDPYQRTVAVLIVNSDKEGTGEKEKEVEENSDMAVYFNEKGYLTAREITLAKAGDNLIK 120  
 QY 53 ----- 52  
 DB 121 QNGNFTYSLKDLJDLTSVGT EKLFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 180  
 QY 53 ----- 52  
 DB 181 NGIGSTLTDLTLNTGATNTVNDVTDDEKRAASVSKDVLNAGNNIKGVKPGTTASNDV 240  
 QY 56 FVRTYDVEFLSADPTKTTTVNVEESKDKGKTEVYKIGAKTSVYIKEDGKLVTKDKGENGS 115  
 DB 241 FVRTYDVEFLSADPTKTTTVNVEESKDKGKTEVYKIGAKTSVYIKEDGKLVTKDKGENGS 300  
 QY 116 STEGEGLVTAKEVIDAVNKAQWRMKTJTANGOTGAADKFEYVTSQNTVTFASGKTAT 175  
 DB 301 STEGEGLVTAKEVIDAVNKAQWRMKTJTANGOTGAADKFEYVTSQNTVTFASGKTAT 360  
 QY 176 VSKDDGNTITVYDVNVGDALNVQOLNSGNNLDSKAVAGSSGKVISGNSPSKGMDET 235  
 DB 361 VSKDDGNTITVYDVNVGDALNVQOLNSGNNLDSKAVAGSSGKVISGNSPSKGMDET 420  
 QY 236 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNRPV 295

DB 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNRPV 480  
 QY 296 RITNVAPEGEGVTVNAOLKGVAQNLNNRIDVNDGNARAGIAOAIATAGLVOAYLPKGS 355  
 DB 481 RITNVAPEGEGVTVNAOLKGVAQNLNNRIDVNDGNARAGIAOAIATAGLVOAYLPKGS 540  
 QY 356 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYQW 407  
 DB 541 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYQW 592

RESULT 5  
 US-09-377-155-11  
 ; Sequence 11, Application US/09377155  
 ; Patent No. 6197312  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/377,155  
 ; CURRENT FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 591  
 ; TYPE: PR  
 ; ORGANISM: Neisseria meningitidis  
 US-09-377-155-11

Query Match 94.58; Score 1949; DB 3; Length 591;  
 Best Local Similarity 68.58; Pred. No. 1e-154;  
 Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;  
 QY 1 MNKIYRIWNSALNANWVYSELTRNHTKRASATVKTAVLTLLFATVQASAN----- 52  
 DB 1 MNKIYRIWNSALNANWVYSELTRNHTKRASATVKTAVLTLLFATVQASANNEDEEDL 60  
 QY 53 ----- 52  
 DB 61 YLDPYLTVAVLIVNSDKEGTGEKEKEVEENSDMAVYFNEKGYLTAREITLAKAGDNLIK 120  
 QY 53 ----- 52  
 DB 121 NGNFTYSLKDLJDLTSVGT EKLFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 180  
 QY 53 ----- 52  
 DB 181 GIGSTLTDLTLNTGATNTVNDVTDDEKRAASVSKDVLNAGNNIKGVKPGTTASNDV 240  
 QY 57 VRTYDVEFLSADPTKTTTVNVEESKDKGKTEVYKIGAKTSVYIKEDGKLVTKDKGENGS 116  
 DB 241 VRTYDVEFLSADPTKTTTVNVEESKDKGKTEVYKIGAKTSVYIKEDGKLVTKDKGENGS 300  
 QY 117 TDEGEGLVTAKEVIDAVNKAQWRMKTJTANGOTGAADKFEYVTSQNTVTFASGKTAT 176  
 DB 301 TDEGEGLVTAKEVIDAVNKAQWRMKTJTANGOTGAADKFEYVTSQNTVTFASGKTAT 360  
 QY 177 SKDDGNTITVYDVNVGDALNVQOLNSGNNLDSKAVAGSSGKVISGNSPSKGMDET 236  
 DB 361 SKDDGNTITVYDVNVGDALNVQOLNSGNNLDSKAVAGSSGKVISGNSPSKGMDET 420  
 QY 237 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNRPV 296  
 DB 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNRPV 480  
 QY 297 ITNVAPEGEGVTVNAOLKGVAQNLNNRIDVNDGNARAGIAOAIATAGLVOAYLPKGS 356

Db 481 ITNAPGVKESDVTNVAOLKGVANLNNRIDVNGNARAGIAQAIATATAGLVQAYLPGRSM 540  
QY 357 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 407  
|||||  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 6  
US-09-669-974-11  
; Sequence 11, Application US/0966974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 94.5%; Score 1949; DB 4; Length 591;  
Best Local Similarity 68.5%; Pred. No. 1e-154;  
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;  
QY 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVATVATLLEFATVOASAN----- 52  
|||  
Db 1 MNEILRIIWSALNMAVVSSELTNRNHTKRASATVATVATLLEFATVOASANNEBOEDL 60  
QY 53 ----- 52  
Db 61 YLDPLVTFVAVLIVNSKEGTEKEKEVENSMDAVYFNEKGVLTAREITLAKAGDLKIKQ 120  
QY 53 ----- 52  
Db 121 NGINTFYSLKKDLDLTJVSGETEKLFSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
QY 53 -----NVDF 56  
Db 181 GIGSTLTDLLNTGATVNTNDNVTDDEKKRAASVADVLANAGWNIKGVKPGTTASDNDF 240  
QY 57 VRTDVTVEFLSADPTTTVNVESKDKNGKTEVKIGAKTSVKEKCKGLVTGDKGENSS 116  
Db 241 VRTDVTVEFLSADPTTTVNVESKDKNGKTEVKIGAKTSVKEKCKGLVTGDKGENSS 300  
QY 117 TDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADPFETVSGTNTVTFASGKGTATV 176  
Db 301 TDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADPFETVSGTNTVTFASGKGTATV 360  
QY 177 SKDDOGNITVMYDVAVGDLVNLQNSGWNLSKAVAGSSGKVISGVNPSKGMDET 236  
Db 361 SKDDOGNITVMYDVAVGDLVNLQNSGWNLSKAVAGSSGKVISGVNPSKGMDET 420  
QY 237 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDDALNVGSKKNKPYR 296  
Db 421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDDALNVGSKKNKPYR 480  
QY 297 ITNAPGVKESDVTNVAOLKGVANLNNRIDVNGNARAGIAQAIATATAGLVQAYLPGRSM 356  
Db 481 ITNAPGVKESDVTNVAOLKGVANLNNRIDVNGNARAGIAQAIATATAGLVQAYLPGRSM 540

QY 357 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 407  
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 91.5%; Score 1887.5; DB 3; Length 594;  
Best Local Similarity 66.5%; Pred. No. 1.4e-149;  
Matches 395; Conservative 5; Mismatches 7; Indels 187; Gaps 2;  
QY 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVATVATLLEFATVOAS----- 50  
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Db 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVATVATLLEFATVOASTDDDDLYLE 60  
QY 51 ----- 50  
Db 61 PVQRTAVVLSRDSKEGTEKEVEEDSNMGVYFDKGVLTAGTTLAKAGDLKIKONTNE 120  
QY 51 ----- 50  
Db 121 NTMASFTYSLKDLDTLJVSGETEKLFSFANSKNVNTSDTKGLNFAKETAGTNGDTTVH 180  
QY 51 -----ANV 54  
Db 181 LNGISTLTDLLNTGATVNTNDNVTDDEKKRAASVADVLANAGWNIKGVKPGTTASDNV 240  
QY 55 DFVRTYDVEFLSADPTTTVNVESKDKNGKTEVKIGAKTSVKEKCKGLVTGDKGENG 114  
Db 241 DFVRTYDVEFLSADPTTTVNVESKDKNGKTEVKIGAKTSVKEKCKGLVTGDKGENG 300  
QY 115 SSTDGGLVTAKEVIDAVNKAQMRKTTTANGOTGADPFETVSGTNTVTFASGKGT 174  
Db 301 SSTDGGLVTAKEVIDAVNKAQMRKTTTANGOTGADPFETVSGTNTVTFASGKGT 360  
QY 175 TVSKDDOGNITVMYDVAVGDLVNLQNSGWNLSKAVAGSSGKVISGVNPSKGMDE 234  
Db 361 TVSKDDOGNITVMYDVAVGDLVNLQNSGWNLSKAVAGSSGKVISGVNPSKGMDE 420  
QY 235 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDDALNVGSKKNK 293  
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDDALNVGSKKNK 480  
QY 294 FVRTNAPGVKESDVTNVAOLKGVANLNNRIDVNGNARAGIAQAIATATAGLVQAYLP 353  
Db 481 FVRTNAPGVKESDVTNVAOLKGVANLNNRIDVNGNARAGIAQAIATATAGLVQAYLP 540  
QY 354 KSMMAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 407  
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 91.5%; Score 1887.5; DB 4; Length 594;  
Best Local Similarity 66.5%; Pred. No. 1.4e-149;  
Matches 35; Conservative 5; Mismatches 17; Indels 187; Gaps 2;

QY 1 MNRIYRIIMNSALNANWVSELTRNHTKRASATVKTAVLATLTFATVQAAS----- 50  
DB 1 MNRIYRIIMNSALNANWVSELTRNHTKRASATVKTAVLATLTFATVQAASSTDDDLXLE 60  
QY 51 ----- 50  
DB 61 PVORTAVVLSFRSDKEGTEGEVTEDESNMGVYFDKKGVLTAQTTLKAGDNLKIKONTNE 120  
QY 51 ----- 50  
DB 121 NTNASSFTYSLKLDLTLTSVTEKLSFSANSKNVITSDTKGLNFAKKTAEINGDTTVH 180  
QY 51 -----ANNV 54  
DB 181 LNCIGSTLTDTLNTGATTNVTNDNTDDEKKRAASVYKDVLANGMNKGKPGTTASDNV 240  
QY 55 DEVRTYDVEFLSADTKTTTVNVEESKDNKTEVKGAKTSVIREKDGKLVTKGKENG 114  
DB 241 DFRVTYDVEFLSADTKTTTVNVEESKDNKTEVKGAKTSVIREKDGKLVTKGKENG 300  
QY 115 SSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSGTNTFASGKTGA 174  
DB 301 SSTDKGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSGTNTFASGKTGA 360  
QY 175 TVSKDOGNITTVYDVNVDALNVNQLONGSNMNDKSAVAGSSGKVISGNVSPSKGKMD 234  
DB 361 TVSKDOGNITTVYDVNVDALNVNQLONGSNMNDKSAVAGSSGKVISGNVSPSKGKMD 420  
QY 235 TVVINAGNNIETTRNGKNIDIAISMTPOESSVSLGAGADAPTLVSVDG-ALNVGSKDKNK 293  
DB 421 TVVINAGNNIETTRNGKNIDIAISMTPOESSVSLGAGADAPTLVSVDGALNVGSKDKNK 480  
QY 294 PVKITVAVPGKRGDVTNVAQLKGVAONLNRIIDNVGNNARAGIAQAIAATAGIQAATLPG 353  
DB 481 PVKITVAVPGKRGDVTNVAQLKGVAONLNRIIDNVGNNARAGIAQAIAATAGIQAATLPG 540  
QY 354 KSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407  
DB 541 KSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 9

US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 91.4%; Score 1886; DB 3; Length 599;  
Best Local Similarity 66.1%; Pred. No. 2e-149;  
Matches 36; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

QY 1 MNRIYRIIMNSALNANWVSELTRNHTKRASATVKTAVLATLTFATVQAAS----- 51  
DB 1 MNRIYRIIMNSALNANWVSELTRNHTKRASATVKTAVLATLTFATVQAATDEDEEEL 60  
QY 52 ----- 51  
DB 61 EPVYRSALVYQFMIDKNGENENESTGNIGSIYDNNHTLHGATVTLKAGDNLKIKONTN 120  
QY 52 ----- 51  
DB 121 KNTNENTNDSFTYSLKLDLTLTSVTEKLSFGANGKNVITSDTKGLNFAKKTACTNG 180  
QY 52 ----- 51  
DB 181 DTVTHLNGISTLTDTLNTGATTNVTNDNTDDEKKRAASVYKDVLANGMNKGKPGTT 240  
QY 52 --NNVDEVRTYDVEFLSADTKTTTVNVEESKDNKTEVKGAKTSVIREKDGKLVTKGD 109  
DB 241 ASDNVDEVRTYDVEFLSADTKTTTVNVEESKDNKTEVKGAKTSVIREKDGKLVTKGD 300  
QY 110 KGENSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSGTNTFASG 169  
DB 301 KGENSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSGTNTFASG 360  
QY 170 KGTATVYSKDOGNITTVYDVNVDALNVNQLONGSNMNDKSAVAGSSGKVISGNVSPSK 229  
DB 361 KGTATVYSKDOGNITTVYDVNVDALNVNQLONGSNMNDKSAVAGSSGKVISGNVSPSK 420  
QY 230 GKMDVYVINAGNNIETTRNGKNIDIAISMTPOESSVSLGAGADAPTLVSVDG-DALVGS 288  
DB 421 GKMDVYVINAGNNIETTRNGKNIDIAISMTPOESSVSLGAGADAPTLVSVDGKALVGS 480  
QY 289 KDKNKPVRITNVAAGKRGDVTNVAQLKGVAONLNRIIDNVGNNARAGIAQAIAATAGLVQ 348  
DB 481 KDKNKPVRITNVAAGKRGDVTNVAQLKGVAONLNRIIDNVGNNARAGIAQAIAATAGLVQ 540  
QY 349 AYLPGRKSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407  
DB 541 AYLPGRKSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 10  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

1 APPLICANT: PEAK, Ian Richard Anselm  
 2 APPLICANT: JENNINGS, Michael Paul  
 3 APPLICANT: MOXON, E. Richard  
 4 TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 5 FILE REFERENCE: 065064/0128  
 6 CURRENT APPLICATION NUMBER: US/09/669,974  
 7 CURRENT FILING DATE: 2000-09-26  
 8 PRIOR APPLICATION NUMBER: US 09/577,155  
 9 PRIOR FILING DATE: 1999-08-19  
 10 PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 11 PRIOR FILING DATE: 1998-12-14  
 12 PRIOR APPLICATION NUMBER: GB 9726398.2  
 13 PRIOR FILING DATE: 1997-12-12  
 14 NUMBER OF SEQ ID NOS: 33  
 15 SOFTWARE: PatentIn Ver. 2.0  
 16 SEQ ID NO 15  
 17 LENGTH: 599  
 18 TYPE: PRT  
 19 ORGANISM: Neisseria meningitidis  
 20 US-09-669,974-15

Query Match	91.4%	Score 1886;	DB 4;	Length 599;
Best Local Similarity	66.1%;	Pred. No. 2e-149;		
Matches 396;	Conservative 3;	Mismatches 8;	Indels 192;	Gaps 2

Qy	1	MNKIYRIITWNSALNAWVVSSELTNRHTRASTAVTAVALATLIFPTVQSA-----	51
Db	1	MNKIYRIITWNSALNAWVVSSELTNRHTRASTAVTAVALATLIFPTVQSA-----	60
Qy	52	-----	51
Db	61	EPVVSALVLOFMIDKEGNGENESTGICMSIYYDNHNTLHGATVTLKAGDMIKONTN	120
Qy	52	-----	51
Db	121	KNTNENTNDSSFYYSLKCOLJDLFSVETEKLSFGANGKNVITSPTKGLNFAKETAGTNG	180
Qy	52	-----	51
Db	181	DTYHLNGISSTLVDTLTLNLTGATITVTDNDYTDKKKKRAASVKDVLNMGNNIKGVRPGTT	240
Qy	52	--NNVDVRYDYVEELISADRTKTTTVNVESKDNGKKEVYIGAKTSVYKEKDGLVTGMD	109
Db	241	ASDNDVEFHTYDVEELISADRTKTTTVNVESKDNGKKEVYIGAKTSVYKEKDGLVTGKG	300
Qy	110	KGENSSSTDEBEGVLTAKVEIDAVNKKACWRMKTTFANQOTGADAFETVTSSTNTVFAAG	169
Db	301	KGENSSSTDEBEGVLTAKVEIDAVNKKACWRMKTTFANQOTGADAFETVTSSTNTVFAAG	360
Qy	170	KGTATVSKDOGNITVYDVNVGDLNVLNOLONGSMNLDSFAVAGSSGKTVISGNVSPSK	229
Db	361	KGTATVSKDOGNITVYDVNVGDLNVLNOLONGSMNLDSFAVAGSSGKTVISGNVSPSK	420
Qy	230	GKMDETVINAANNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDG-DALNWS	288
Db	421	GKMDETVINAANNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDVDKGLNWS	480
Qy	289	KKDKPVRITVAPGVKEGVDYTNVAOLKGVANOLNNRIDNVGNAAPAGIAQAIATAGLVQ	348
Db	481	KDANKPVRITVAPGVKEGVDYTNVAOLKGVANOLNNRIDNVGNAAPAGIAQAIATAGLVQ	540
Qy	349	AYLNGKSMALIGGGYRGEAGALGYSSISDGGNNITIGTASGNSRGHGASASVGYOM	407
Db	541	AYLNGKSMALIGGGYRGEAGALGYSSISDGGNNITIGTASGNSRGHGASASVGYOM	599

RESULT11  
US-09-377-155-7  
: Sequence 7, Application US/09377155  
: Patent No. 6197312  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul

? APPLICANT: MOXON E. Richard  
 ? TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ? FILE REFERENCE: 065064/0128  
 ? CURRENT APPLICATION NUMBER: US/09/377,155  
 ? CURRENT FILING DATE: 1999-08-19  
 ? PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ? PRIOR FILING DATE: 1998-12-14  
 ? PRIOR APPLICATION NUMBER: GB 9726398.2  
 ? PRIOR FILING DATE: 1997-12-12  
 ? NUMBER OF SEQ ID NOS: 33  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 7  
 ? LENGTH: 594  
 ? TYPE: PRT  
 ? ORGANISM: Neisseria meningitidis  
 ? US-09-377-155-7

Query Match	91.1%;	Score 1879.5;	DB 3;	Length 594;
Best Local Similarity	66.5%;	Pred. No. 6.7e-149;		
Matches 395; Conservative	3;	Mismatches 9;	Indels 187;	Gaps 2;

OY	1	MNKIYRIIWNLSALNAAVVVSELTNRHNTKRASTVTAVALATLEFTVOASA-----	51
Db	1	MNKIYRIIWNLSALNAAVVVSELTNRHNTKRASTVTAVALATLEFTVOANATDDDDLYLE	60
OY	52	-----	51
Db	61	PVQRTAVVLSFRSDEKGTGKEGTFEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE	120
OY	52	-----	51
Db	121	NTNDSFTYSLKKDLTDLTLSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH	180
OY	52	-----NNV	54
Db	181	LNGLGISTLTDTLTLTGATTNTNDNVTDDEKRRASVADVLNAGNINIGVARGTTASDNV	240
OY	55	DEVRTYDVEFLSADTKTTTVNVESKDNKGKTEYKIGAKTSVKEKDKLVTGDKGENG	114
Db	241	DEVRTYDVEFLSADTKTTTVNVESKDNKGKTEYKIGAKTSVKEKDKLVTGDKDENG	300
OY	115	SSTDEGBELVYAKEVYDAVNKAGWGMKTTTNGOGADKPEYVSGNNPFAASCKGTTA	174
Db	301	SSTDEGBELVYAKEVYDAVNKAGWGMKTTTNGOGADKPEYVSGNNPFAASCKGTTA	360
OY	175	TVSKDDQGNITVMYDVNVDALNVQOLNONGMNLDSKAVASSGKVIISGNSPSKGMDE	234
Db	361	TVSKDDQGNITVYKIDVNVGDALNVQOLNONGMNLDSKAVASSGKVIISGNSPSKGMDE	420
OY	235	TVINAGNNIETTRNGKNIDIATSMTPQFSVSYLIGAGADAPTLVSVDG-ALNVGSKDUNK	293
Db	421	TVINAGNNIETTRNGKNIDIATSMAPQFSSVSYLIGAGADAPTLVSVDGALNVGSKDUNK	480
OY	294	PVRITNNAVGYKEGDVTVAOLKGYAQNULNNRIDVNDGNARAGIAQALATAGLVAYLPG	353
Db	481	PVRITNNAVGYKEGDVTVAOLKGYAQNULNNRIDVNDGNARAGIAQALATAGLVAYLPG	540
OY	354	KSMAGIGCGTARGEGVYAGISYSISDGGNMWIIKGTASGNSRGHFASASVGYOM	407
Db	541	KSMAGIGGDTYRGEGVYAGISYSISDGGNMWIIKGTASGNSRGHFASASVGYOM	594

RESULT 12  
 US-09-669-974-7  
 : Sequence 7, Application US/09669974  
 : Patent No. 6333173  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: PEAK Ian Richard Anselm  
 : APPLICANT: JENNINGS, Michael Paul  
 : APPLICANT: MOXON, E. Richard  
 : TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 : FILE REFERENCE: 065064/0128  
 : CURRENT APPLICATION NUMBER: US/09/669, 974/



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: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 594
: TYPE: PRN
: ORGANISM: Neisseria meningitidis
US-09-669-974-7

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Query Match	91.1%	Score 1879.5	DB 4	Length 594
Best Local Similarity	66.5%	Pred. No. 6.7e-149		
Matches 395	Conservative 3	Mismatches 9	Indels 187	Gaps 2
QY	1	MNKIYRIIMNSALNAMYVSELTRNHTKRASATYKATVATLATLLEFATVOASA-----	51	
Db	1	MNKIYRIIMNSALNAMYVSELTRNHTKRASATVATVATLATLLEFATVOANATDDDDLYLE	60	
QY	52	-----	51	
Db	61	PVORTAVVLSFRSDKEGTGEGTEGDEDSMWAYFEDKRVLKAGATTLKAGNLIKIKONTNE	120	
QY	52	-----	51	
Db	121	NTNDSFFYSLKKDLTDLTSYTEKLSFGANGKNYNTISDTIKGLNFAKETAGTNDPPIYH	180	
QY	52	-----NNY	54	
Db	181	LNIGISTLFDLPLNTGATTNVTNDNVTDEKKAASVADVLNAGNNIKGVKPGTASDV	240	
QY	55	DFVFTYDVFELSDTKTTTVNVESKDGKTEYVIGAKTSYIKKKDKLTKGKKGENG	114	
Db	241	DFVFTYDVFELSDTKTTTVNVESKDGKTEYVIGAKTSYIKKKDKLTKGKKGENG	300	
QY	115	SSTDEGELVAKAEVIDAVNKGWMMKTTTANGQGOADKEFTVTSGTNVPFASGKTTA	174	
Db	301	SSTDEGELVAKAEVIDAVNKGWMMKTTTANGQGOADKEFTVTSGTNVPFASGKTTA	360	
QY	175	TYSKDDGCGITVMDVYNGDALNVOLONSGNNLDSKAVAGSSGVYISGNVSPSKGKDE	234	
Db	361	TYSKDDGCGITVMDVYNGDALNVOLONSGNNLDSKAVAGSSGVYISGNVSPSKGKDE	420	
QY	235	TVNINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPLTSDVG-ALNVGSKKDK	293	
Db	421	TVNINAGNNIETTRNGKNIDATISMAFPSSVSLGAGADAPLTSDVDEGALNVGSKDKNK	480	
QY	294	PVRIITNVAPVKEGSDVTVAQLKGVAOMLNRRIDNVNDNARAGIAQAIATATAGLYOAYLPG	353	
Db	481	PVRIITNVAPVKEGSDVTVAQLKGVAOMLNRRIDNVNDNARAGIAQAIATATAGLYOAYLPG	540	
QY	354	KSMALGGGTGREGAGYALIGVSSISDGGNNWIIKGTASGNSRCHFGASASVGYOW	407	
Db	541	KSMALGGGTGREGAGYALIGVSSISDGGNNWIIKGTASGNSRCHFGASASVGYOW	594	

RESULT 13  
US-09-377-155-17  
Sequence 17, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MONON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGENES  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377, 155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031

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: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 17
: LENGTH: 592
: TYPE: prt
: ORGANISM: Neisseria meningitidis
: US-09-377-155-17

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Query Match	90.6%;	Score 1869.5;	DB 3;	Length 592;
Best Local Similarity	66.4%;	Pred. No. 4,6e-148;		
Matches 393;	Conservative 4;	Mismatches 10;	Indels 185;	Gaps 2;
QY	1	MNKIYRIIWNLSALNAWVVSSELTNRNHRKASATYKTAVALLATLLEATVAOASA-----	51	
Db	1	MNKIYRIIWNLSALNAWVVSSELTNRNHRKASATYKTAVALLATLLEATVAOANATDEDEEEL	60	
QY	52	-----	51	
Db	61	ESVORSVVGSIQASMEGSVELETTISLSKTDNSKEFVDPEYIVVTLKAGDNLKIKONTNENT	120	
QY	52	-----	51	
Db	121	NASSFTYSLKRDLDGLINIVETEKLSFGANGKKVNIISDTKGLNFPAKETAGTNGDTYHLN	180	
QY	52	-----	56	
Db	181	GIGSTLTDMLNTGATNTVNDNTYDDEKKRAASVYKDVLMNGMINIKYKPGTTASDNI	240	
QY	57	VRTPDYVEFLSADRTTNTVNVESKONGKKTTEVIGAKTSVYKKEKGKLYTGDKDENSS	116	
Db	241	VRTPDYVEFLSADRTTNTVNVESKONGKKTTEVIGAKTSVYKKEKGKLYTGDKKENSS	300	
QY	117	TDEBEGVLTAKEVIDAANVAKGMRMKTTPANGOTGQADRFETVSGTNTYFASGKCTATY	176	
Db	301	TDEBEGVLTAKEVIDAANVAKGMRMKTTPANGOTGQADRFETVSGTNTYFASGCTATY	360	
QY	177	SKDDOGNTITWADVAVGALVYNQLONSGWNLSAANVAGSSSKVYISGVNPSBKGMDEY	236	
Db	361	SKDDOGNTITWADVAVGALVYNQLONSGWNLSAANVAGSSSKVYISGVNPSBKGMDEY	420	
QY	237	NINAGNNIEITRRNGKNIDIASMTPPOFSSVSLGACADAPTLSDVDG-ALNWSKRDKNPV	295	
Db	421	NINAGNNIEITRRNGKNIDIASMTPPOFSSVSLGACADAPTLSDVDGALNWSKRANKPV	480	
QY	296	RITNVAPGVKEGDYTNVAQLKGVAQNLNRRIDNVGNAFAGIAQAIATAGLVOAYLPGKS	355	
Db	481	RITNVAPGVKEGDYTNVAQLKGVAQNLNRRIDNVGNAFAGIAQAIATAGLVOAYLPGKS	540	
QY	356	MMALGGGTYRREAGYALIGYSSISOGGNNIIGTASGNSRGHGASASVGYOM	407	
Db	541	MMALGGGTYRREAGYALIGYSSISAGGNNIIGTASGNSRGHGASASVGYOM	592	

RESULT 14  
US-09-669-974-17  
Sequence 17, Application US/09669974  
Patent No. 6333173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E, Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669, 974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377, 155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2

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; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17

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Query Match      90.6%; Score 1869.5; DB 4; Length 592;
Best Local Similarity 66.4%; Pred. No. 4.6e-148;
Matches 393; Conservative 4; Mismatches 10; Indels 185; Gaps 2;

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QY 1 MNKIYRIIWSALNAAVVVSELTNRNHTKRASATVAVATLTLFATVOASA----- 51
    |||||||
DB 1 MNKIYRIIWSALNAAVVVSELTNRNHTKRASATVAVATLTLFATVOANATDEDEBEL 60
    |||||||
QY 52 ----- 51
DB 61 ESVQSVVGSIQASMEGSEVELETTLSMTNDSKEFVDPYIVVTLKAGDNLKIKONTNENT 120
    ----- 51
QY 52 ----- 51
DB 121 NASSFTYSLKDDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
    ----- 51
QY 52 ----- 51
DB 181 GIGSTLFDMLNTGATNTVNDNVTDEKKRAASVADVNLNAGWNIKGVKPGTTASDNVDF 240
    ----- 51
QY 57 VRTDVEEFLSADRTTIVNVEESKDNKKTEVKIGAKTSVIREKDKLVTKDKKENGSS 116
    |||||||
DB 241 VRTDVEEFLSADRTTIVNVEESKDNKKTEVKIGAKTSVIREKDKLVTKDKKENGSS 300
    |||||||
QY 117 TDEBGLVTAKEVIDAVNKAQMKRTTANGOTGADAFETVTSNTVTFASGKGTATV 176
    |||||||
DB 301 TDEBGLVTAKEVIDAVNKAQMKRTTANGOTGADAFETVTSNTVTFASGKGTATV 360
    |||||||
QY 177 SKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSKGMDET 236
    |||||||
DB 361 SKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSKGMDET 420
    |||||||
QY 227 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDD -ALNVGSKKDNKP 295
    |||||||
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDD -ALNVGSKKDNKP 480
    |||||||
QY 296 RITNVAPEGKEDVTNVAQLKGAQNLNRRIDNVGNARAGIAQAIAATAGLVOAYLPKGS 355
    |||||||
DB 481 RITNVAPEGKEDVTNVAQLKGAQNLNRRIDNVGNARAGIAQAIAATAGLVOAYLPKGS 540
    |||||||
QY 356 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 407
    |||||||
DB 541 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592
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RESULT 15
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377, 155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13

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; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

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Query Match      90.4%; Score 1864.5; DB 3; Length 598;
Best Local Similarity 65.6%; Pred. No. 1.2e-147;
Matches 392; Conservative 4; Mismatches 11; Indels 191; Gaps 2;

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DB 1 MNKIYRIIWSALNAAVVVSELTNRNHTKRASATVAVATLTLFATVOANATDDDDLYLE 60
    |||||||
QY 52 ----- 51
DB 61 PVORTAVVLSRSDKEGTGEKEGTEDSNMAYVFDEKRVLKAGALTLKAGDNLKIKONTNE 120
    ----- 51
QY 52 ----- 51
DB 121 NTNENTNDSFTYSLKDDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
    ----- 51
QY 52 ----- 51
DB 181 PTVHLNGISLTITDTLNTGATNTVNDNVTDEKKRAASVADVNLNAGWNIKGVKPGTTA 240
    ----- 51
QY 52 -NNVDFVRYDTEFLSADRTTIVNVEESKDNKKTEVKIGAKTSVIREKDKLVTKDKK 110
    |||||||
DB 241 SDNVDFVRYDTEFLSADRTTIVNVEESKDNKKTEVKIGAKTSVIREKDKLVTKDKK 300
    |||||||
QY 111 GENGSSTDEBGLVTAKEVIDAVNKAQMKRTTANGOTGADAFETVTSNTVTFASGK 170
    |||||||
DB 301 DENGSSTDEBGLVTAKEVIDAVNKAQMKRTTANGOTGADAFETVTSNTVTFASGK 360
    |||||||
QY 171 GTTATVSKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSK 230
    |||||||
DB 361 GTTATVSKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSK 420
    |||||||
QY 231 KMDFTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDD -ALNVGSK 289
    |||||||
DB 421 KMDFTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDD -ALNVGSK 480
    |||||||
QY 290 KDNKPVRTITNVAPEGKEDVTNVAQLKGAQNLNRRIDNVGNARAGIAQAIAATAGLVOA 349
    |||||||
DB 481 DANKPVRTITNVAPEGKEDVTNVAQLKGAQNLNRRIDNVGNARAGIAQAIAATAGLVOA 540
    |||||||
QY 350 YLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 407
    |||||||
DB 541 YLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 598
    |||||||

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Search completed: October 6, 2003, 09:35:45
Job time : 13.884 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 11.6505 Seconds  
(without alignments)  
3359.577 Million cell updates/sec

Title: US-09-771-382-25  
Perfect score: 2063  
Sequence: 1 MNKIYRIIINMSALNMAVYVS.....TASGNSRGHFQASASVGYQM 407

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_76:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1961	95.1	591	2	G81133
2	1893.5	91.6	592	2	A81888
3	341	16.5	1190	2	A82615
4	332.5	16.1	2059	2	D82671
5	331	16.0	1588	2	A86036
6	331	16.0	1588	2	H91188
7	320	15.5	1107	2	AC0976
8	307.5	14.9	658	2	AH0110
9	277.5	13.5	288	2	I64138
10	211	10.2	1004	2	C82672
11	188.5	9.1	3705	2	AD0123
12	185	9.0	1286	2	S28634
13	183.5	8.9	365	2	AB3486
14	175.5	8.5	1018	2	H83135
15	175	8.5	1325	2	A64905
16	172	8.3	364	2	A81019
17	172	8.3	585	2	F90961
18	172	8.3	585	2	F85809
19	171.5	8.3	1091	2	G46464
20	170	8.2	1335	2	T17508
21	165	8.0	4919	2	T31105
22	164.5	8.0	1910	2	AF0394
23	162	7.9	584	2	C48658
24	161.5	7.8	936	2	I40711
25	159	7.7	1343	2	E90893
26	159	7.7	1477	2	B43855
27	159	7.7	5188	2	B83547
28	159	7.7	5291	2	F90696
29	158.5	7.7	949	2	D90803

30	158.5	7.7	1005	2	H85611	probable adhesin z
31	156.5	7.6	933	2	S41539	fibrinogen-binding
32	156	7.6	1035	2	AD3303	autotransporter pr
33	156	7.6	1343	2	D85724	hypothetical prote
34	156	7.6	4152	2	T31102	filamentous hemagg
35	155.5	7.5	989	2	D89852	fibrinogen-binding
36	155	7.5	2020	2	C48399	ABC-type transport
37	154	7.5	364	2	AE0169	probable exported
38	154	7.5	920	2	I40614	surface array prot
39	154	7.5	1461	2	E90696	hypothetical prote
40	153.5	7.4	338	2	D90697	adhesin/invasin-11
41	153.5	7.4	338	2	G85547	adhesin/invasin-11
42	151.5	7.3	3013	2	AB0480	probable invasin y
43	151	7.3	595	2	A48658	flagellin - Escher
44	151	7.3	980	2	H90681	probable flagellin
45	151	7.3	980	2	D85532	probable structura

## ALIGNMENTS

RESULT 1									
G81133									
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)									
C:Species: Neisseria meningitidis									
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001									
C/Accession: G81133									
R;Jettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizze, M. Science 287, 1809-1815, 2000									
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MIMD:2015755; PMID:10710307									
A:Accession: G81133									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-591 <TET>									
A:Cross-references: GB:AE002450; GB:AE002098; MID:g7226229; PIDN:AAF1395.1; PID:g722									
A:Experimental source: serogroup B, strain MC58									
C:Genetics:									
A:Gene: NMB0992									
Query Match									
Best Local Similarity 95.1%; Score 1961; DB 2; Length 591;									
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;									
QY	1	MNKIYRIIINMSALNMAVYVSELRNHTKRASATVKTAVLATLFPATVOASAN-----	52						
DB	1	MNKIYRIIINMSALNMAVYVSELRNHTKRASATVKTAVLATLFPATVOASANBQEDL	60						
QY	53	-----	52						
DB	61	YLDPVORTAVLIIVNSDKEGTGEKEVEENSQWAVYFNEKGVLTAREITLKAGDNLIKIKO	120						
QY	53	-----	52						
DB	121	NGTNTYSLKKDLTLTSVCTEKLFSANGKNVITSPTKGLNPAKETAGTNGDTTVHNLN	180						
QY	53	-----	52						
DB	181	GIGSTLDTLTLNGATTTNTNDVTDDEKKRAASVQVDVLAAGNINIGVKRGTTASDQVDF	240						
QY	57	VRTYDVEVERISADFTKTTTAVESKDKNGKTEVIGAKTSYIKKDGKLVTKRGKENGSS	116						
DB	241	VRTYDVEVERISADFTKTTTAVESKDKNGKTEVIGAKTSYIKKDGKLVTKRGKENGSS	300						
QY	117	TDEGEGLVAKVEYIDAVNKGWRRKTTTANGGTGQADKPTVSGTNVFPASGKGTATV	176						
DB	301	TDEGEGLVAKVEYIDAVNKGWRRKTTTANGGTGQADKPTVSGTNVFPASGKGTATV	360						
QY	177	SKDDGNTIVYVNVVNGDALNVQNLDSKAVAGSSGKVISGNNVSPSGKNDDEV	236						

Db 361 SKDDGNTITVAVDVGALNVNOLQNSGWNLDKAVAGSSGKVISGNSVPSKMDFTV 420  
Qy 237 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 296  
Db 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 480  
Qy 297 ITNVAPEKEDVTNVAOLKQVAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLPKSM 356  
Db 481 ITNVAPEKEDVTNVAOLKQVAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLPKSM 540  
Qy 357 MAIGGTYRGEAGYAIIGTSSISDGNWIIKGTASGNSRGRFGASASVGYOM 407  
Db 541 MAIGGTYRGEAGYAIIGTSSISDGNWIIKGTASGNSRGRFGASASVGYOM 591

## RESULT 2

Ab1888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: Ab1888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
N.; Holtroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: Ab1775; MUID:20222556; PMID:10761919  
A:Accession: Ab1888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CA884461.1; PID:9737989  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match 91.8%; Score 1893.5; DB 2; Length 592;  
Best Local Similarity 66.9%; Pred. No. 3,1e-98;  
Matches 396; Conservative 4; Mismatches 7; Indels 185; Gaps 2;  
Qy 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVTAVALTLEFATVOASA----- 51  
Db 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVTAVALTLEFATVOANATDEDEEEL 60  
Qy 52 ----- 51  
Db 61 ESVQSVSVSIQASMEGSELETISLSMTNDSKEFVDPEYIVTAKAGDNLIKONTNENT 120  
Qy 52 ----- 51  
Db 121 NASSETYSLKROLTGLINVEFEKLSFGANGKKVNIISPTKGLNFAKETAGTNGDTTHLN 180  
Qy 52 -----NNYDF 56  
Db 181 GIGSLDTPLTLAGSSASHVDAGNOSTHYTRASIKDVLNAGNNIKVKTGSGTTCSENVDF 240  
Qy 57 VRTDYVEPLSADTKTTTVNVEBKDNKGKTEYKIGAKTSVIEKDKGLVTGKDKGENSS 116  
Db 241 VRTDYVEPLSADTKTTTVNVEBKDNKGKTEYKIGAKTSVIEKDKGLVTGKDKGENSS 300  
Qy 117 TDEGGLVTAKEVIDAVKAKGRMKTTTANGOTGADKEFYVTSNTTTPASGKGTATV 176  
Db 301 TDEGGLVTAKEVIDAVKAKGRMKTTTANGOTGADKEFYVTSNTTTPASGKGTATV 360  
Qy 177 SKDDGNTITVAVDVGALNVNOLQNSGWNLDKAVAGSSGKVISGNSVPSKMDFTV 236  
Db 361 SKDDGNTITVAVDVGALNVNOLQNSGWNLDKAVAGSSGKVISGNSVPSKMDFTV 420  
Qy 237 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 296  
Db 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 480  
Qy 296 RITNVAPEKEDVTNVAOLKQVAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLPKSM 355

Db 481 RITNVAPEKEDVTNVAOLKQVAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLPKSM 540  
Qy 356 MAIGGTYRGEAGYAIIGTSSISDGNWIIKGTASGNSRGRFGASASVGYOM 407  
Db 541 MAIGGTYRGEAGYAIIGTSSISDGNWIIKGTASGNSRGRFGASASVGYOM 592

## RESULT 3

surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)  
A:Accession: Ab2615  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: Ab2615  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: Ab2515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: Ab2615  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1190 <STM>  
A:Cross-references: GB:AE004017; GB:AE003849; NID:99107083; PIDN:AAE84783.1; GSPDB:GN  
A:Experimental source: Strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
B:Rios, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincanli, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Klajim, J.P.; Krieger, J.E.; Kurimae, E.E.; La  
Chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1981

Query Match 16.5%; Score 341; DB 2; Length 1190;  
Best Local Similarity 27.4%; Pred. No. 1.9e-11;  
Matches 121; Conservative 60; Mismatches 161; Indels 100; Gaps 17;  
Qy 8 IMNSALNMAVVSSELTNRNHTKRASATVKT-AV-LATLFAATVOASANNVDFVRYDFE 65  
Db 807 VTSSGINAG-----SKRTVNAAGTADTDVNLSQLTFMAAGSAGKSVHYSTYD----- 856  
Qy 66 LSADTKTTTVNVEBKDNKGKTEYKIGAKTSVIEKDKGLVTGKDKGENG-SSTDEGGLV 124  
Db 857 --GGTGGNNGDGTGTRISAVGVGLTASA-----EGATVAGSGLAAGSAGKSTFAGRAV 910  
Qy 125 TAKEVIDAVNKAQRMKTTTANGOTGADKEFYVTSNTTTPASGKGTATVSDDCNI 184  
Db 911 ASAGSVALGD-GAKDGAEGAESTYKYSGLQNTTVGVSVDASGKSTRTVS-----NV 964  
Qy 185 TWYDVANVGDALNVNOL-----QNSGWNLDKAVAGSSGKVISGNSVPSKMDFTVINA 240  
Db 965 ADAKEAT--DAVNRLQDRAVQADNRRYDNKIEISLSEQGT-----YKNS 1008  
Qy 241 GNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 291  
Db 1009 LNN-----SATP-----IAAGVDATATGATAGTASGADSIAMGNKASASAD 1048  
Qy 292 NKPV-----RITNVAPEKEDVTNVAOLKQVAONLNRRIDNV 329  
Db 1049 NAVAIGHNSVADRANTVSVSGASERQVTNVAAGTADTDVAVNOLNGLITTAQOYTDGV 1108  
Qy 330 DGNAR-----AGIAQAIATAGLVQAVLPKSMMAIGGTYRGEAGYAIIGTSSISDGNWII 385  
Db 1109 VGLRRLQDGGVAAAIATATNLPQATIPGRKHTSVGVSSYRQGSALAVGVSSVSGRNVF 1168

QY 386 KGTASGNSRGHFGASASVGYOM 407  
Db 1169 KFGSGANTRSOVGIGAGVGYOM 1190

## RESULT 4

surface protein XFI529 [imported] - Xylella fastidiosa (strain 9a5c)  
D82671  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: D82671  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2059 <SIM>  
A:Cross-references: GB:AE003982; GB:AE003849; NID:9106554; PIDN:AAF84338.1; GSPDB:GN001  
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H  
as-Neto, E.; Docena, C.; El-Doiry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A:Authors: Ferreira, V.C.A.; Perito, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laigt  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E. de sa, R.G.; Santelli, R.V.; Savasak  
M.; Tshabko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
A:Genetics:  
A:Gene: XFI529

Query Match 16.1%; Score 332.5; DB 2; Length 2059;  
Best Local Similarity 29.3%; Pred. No. 1.1e-10;  
Matches 96; Conservative 53; Mismatches 112; Indels 71; Gaps 12;  
QY 79 SKDNGKTEVKGATKSVIREKDKLVTG--KDKGNGSSTDEGEGLYTAKEVIDAVNKAAG 137  
Db 1792 AKOSGRAESEYTGKYSQVQNNYGVTVSGDAKKEFTSIS--VADAKEMAVN--- 1844  
QY 138 WRKTTTANGOTGADKFEFVTSQNTVTFASGKTATVSKDDGNTTVYDVNVDALN 197  
Db 1845 LRQIDAVAKOSNLOTDM-----RHEININIEDVFRTKGD--S 1880  
QY 198 VNOLONGMNLDSKAVNGSSGKVTSGNVSPSKGMDETVNMGNNNIEITRNKNIDAT 257  
Db 1881 ASSYKMGVNV---AMAIQTNAASGTESVALGK---NTNVASNAVAI--GNG----- 1925  
QY 258 SMTPOFSSVSLGAGADAPTLSSVDGALNVGSKKDKNPVTRTNVAPVKEGDPVTVADLKG 317  
Db 1926 SVADRAANSVSGS-----GSEK-----QYTNVAAGIADIDAVVQSLNQ 1965  
QY 318 VAONLNNRIDNVGNAR---AGIAQAIATPAGLVOAYLPKGSMAIIGGTYRGEAGYAIG 373  
Db 1966 GLITAKQYTDGMVGNLRRRTSGVAAIATNATLQOAVYQGRGMSVGSVSQGSALAVG 2025  
QY 374 YSSISDGCNNITIGTASGNSRGHFGASASVGYOM 407  
Db 2026 VSAVSESGHWFKFGSGSANTRSHVGVAGVGYOM 2059

RESULT 5  
A86036  
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: A86036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86036  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:912518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
A:Genetics:  
A:Gene: Z5029

Query Match 16.0%; Score 331; DB 2; Length 1588;  
Best Local Similarity 26.8%; Pred. No. 9.7e-11;  
Matches 117; Conservative 59; Mismatches 168; Indels 92; Gaps 15;  
QY 46 TYOASANNVDFVRYDVEFLSADTKTNTTVNVEKDKKTEVKGATSVIREK----- 100  
Db 1171 TVROLQAIAGAVATTPKRYHANSTEDSLAVGT-----DSLAMGAKTIVNGDKGIG 1224  
QY 101 -----DGKLVYTKDKGE-----NGSSTDEGEGLYTAKEVIDAVNKAQWRMKT 142  
Db 1225 YGAYVDANALNGIAIGSNAQYIHVNSIAIGNGSTTTRGAQNTYATYNNMDAPQNSVGEFSV 1284  
QY 143 TTANGQ-----TGADKRETVTSQNTVTFASGKTATVSKDDGNTTVY----- 187  
Db 1285 GSADGGQQTITVNAAGSAD---TDAVNV--GQKLVYDAQVSQMTQ--STNLNDRVYTNLD 1336  
QY 188 -----YVNVNGDAL-----NVNOLONGMNLDSKAVNGSSGKVTSGNVSPSKGKM 232  
Db 1337 SRVNIENGIDIVTTSSTKRYFKTNTGCVNDSAGQKRSVAIGSSISIAADNSVALGTSV 1396  
QY 233 ---DETVINAGNNIEITRN--GKN---IDATSMTPQFSSVSLGAGADAPTLSSVDG 282  
Db 1397 ATEENTISVGSSTNQRRITVNAAGKNATDAVNVAQLKSESGVGRYDPAKG---SIDYS 1453  
QY 283 ALNVGSKKDKNPVITVNAAGVYKRGDVTNVAQLKQVQ-----NLNNRIDVNDG 331  
Db 1454 NITLGG--GNGGTRTISNVAGVNNNDVNVNAQLKQVETKQYTDQRMVEKDNLSKTES 1512  
QY 332 NARAGIAQAIATPAGLVOAYLPKGSMAIIGGTYRGEAGYAIGYSSISDGCNNITIGTASG 391  
Db 1513 KLSGCIASAAATGCLPQATYTPGASMASISGGTYNGESAVALGVMSANGRMVYTKLGST 1572  
QY 392 NSRGHFGASASVGYOM 407  
Db 1573 NSQGEYSALGAGIOW 1588

## RESULT 6

H91188  
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain R  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C  
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hatforti, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91188  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA837903.1; PID:913363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
A:Genetics:  
A:Gene: ECs4480

Query Match 16.0%; Score 331; DB 2; Length 1588;

[illegible]

RESULT 7  
 AC0976  
 probable autotransporter sabb [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 A:Note: this species has also been called *Salmonella typhi*  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

Accession: AC0976  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AC0976  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1107 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176  
C:Genetics:  
A:Gene: sapB

Query Match            15.5%     Score 320; DB 2; Length 1107;  
Best Local Similarity 26.7%; Pred. No. 2.6e-10;  
Matches 115; Conservative 59; Mismatches 176; Indels 80; Gaps 15;

OY 46 TVQANSAVVVFRRYYDVEFLSADTK--TTTVVNESKDNCKRTFKV-----IGAKTSVI 97  
|| : | : | : | : | : | : || : | : | : | : | : | : | : | : | : | :  
Db 690 TVRLQLNALGAVTTTTPTPKRYHANSTEEDSLAVGTDSILAMGKATTVNMADAGIGICLNTLLM 749

OY 98 KEKDGLVTGDKGE-----NGSSDTDEG -EGLVTAKEVIDAVNKAGRMKTTHANG 147  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 750 ADAINGCAISGMARHANSIAMGNSQTTRGAOTDYAYMMDPQNCSVG-EFVSGSDDG 808

OY 148 Q-----TGADKFHEIVTSGTNTFASGGCTATTVKDDOQGINTWADV----- 191  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 809 QRQITVAAGSAD---TDAAVN--GQLKVTDQAQSRNFQSITNLNTQVSNLDTRVTNI 861

QY 192 ----VGDALNVNQLONSGMNLD-----SKAVGSSGGKVTSGNVSPSKG---MDETVN 237

Db 862 ENGIGDIDYTTGGSTKFEKFTINDGADANAOGADVASVIAIGSOSIAAENSVALGNVSADEANT 921

QY 238 INAGNNIEITR-----NGKNIDIATSMTPQFSSVSLGACADAPTLVSDGDALNVGS 288

Db 922 VSVSSSTQQRITTVAGAVNNTDAVNAQLKASEAGSVRYETNADG---SVNYSVLNLGD 978

QY 289 KKDKKPVRTINVARGVKEGDPVTNVAOLKGVNQ-----NLNRRIDNVDSNARAGI 337

Db 979 GSGG-TTRIGNVSAAVNDTDAVNAQLKRSVEEANTYTTDDKMGKSNKIKETKMGSGCI 1037

QY 338 AQAIAIATAGLVQAYLPKGSMAAIGGTYRGEAGVAIYSSISDGNMIIKTCTASGNSRGHF 397

Db 1038 ASAAMAMGLPDQAYAPGANMYSIAGCTFENGESAVAIYVMSVSESGGWYKLOGTNSOGDY 1097

QY 398 GASASVGYOW 407

Db 1098 SAAIGAGFQW 1107

```

RESULT 8
AH0110
Probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain CO92),
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence.revision 02-Nov-2001 #text.change 02-Nov-2001
C:Accession: AH0110
P:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Houlden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2000
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB00001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KMP>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:915978974; GSPDB:GN00175
:Genetics:
:Gene: YP00902

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Query Match	14.9%	Score 307.5;	DB: 2;	Length 658;
Best Local Similarity	26.18;	Pred. No. 6.8e-10;		
Matches 115;	Conservative 65;	Mismatches 176;	Indels 85;	Gaps 16;
QY	3	KIVRIINNSALNAAVVVSELTNRHHTKRASATVKTAVL----	ATLFFATVQASAN--	NYDEV 57
		: : : : :    : : : : :	: : : : :	
Db	267	KITCVAAAGSASSDAVNAQVLTAAVGDYQVQONTNANTITSLGRVTTIEGSMASIANGGVYKF		326
QY	58	KTYDT-VEPLADPKTTTVANVESKDNRKTI-----	EYKIGAKTSYKREKDGKLYTRKDK	110
		: : : : :    : : : : :	: : : : :	
Db	327	HANSTOPDVAASGTSNVAIGPASTLASGNAALASGAGAAVIG--	DGAASADGSAVIGQGS	384
QY	111	GENGSTPDEEGELTAKEVIDAVAKAKMRKTTTANQOTQOADKFTETVSTNTVFASGK		170
		: : : : :    : : : : :	: : : : :	
Db	385	GDNRGVEYNTIG-----	KYSNASNSTSSG-----	TVSNGNAT----- 416
QY	171	GTTATYASKDDOGNTITVADYVNGDALVYNOLNSGNMLDSKANAAGSSGKVIYSGNVPSFGK		230
		: : : : :    : : : : :	: : : : :	
Db	417	GETRTVSNVADG-----	LOATDAVNLRLDGG-----	IAASIVVENNVSGLON 459
QY	231	KMETVINAGNNIT-ETTRNGKNIDI--	ATSMTPQFSYSLGAGADAP-----	TL 277
		: : : : :    : : : : :	: : : : :	
Db	460	GTDGMFOYVNSSGLAKPSATGNASATGCAAGSVASGNNSTYFPGSARKATAANSALACANSV		519
QY	278	SYDGDALVSSKKDKNKFPVITTNVAPGVKEGDVTNVAAQLGVAQN----	LNNRIDNVDNA	333
		: : : : :    : : : : :	: : : : :	
Db	520	ADRANSVSYSGVNER--	QITNVAAPATQGTDAVNFQDKFISINQNTAYNTQRYSELKQDL	577
QY	334	R-----	AGTAAIATAGLVQAVLTPKRSMAALIGGCTTYREAGATATGSSISDGGNNITK	386
		: : : : :    : : : : :	: : : : :	
Db	578	RKONSVLASIASMSMASTLPTPTSGSSMTTIGAASTYRQGSALSTLSSVSSITDSGGRNVSK		637



C:Genetics:  
A:Gene: Yaph

Query Match 9.1%; Score 188.5; DB 2; Length 3705;  
Best Local Similarity 23.3%; Pred. No. 0.023;  
Matches 113; Conservative 61; Mismatches 184; Indels 127; Gaps 20;

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OY 1 MNKIRITWNSALANVAVVSELTNRNH--TKRASATVKTAVLATILFATVQASANNVDPVR 58
DB 1 MNITFKVIMNASLANVWVSELAQRIKTKSSRNLSISGVLPKFEQSVSKLFRKNLAL 60
OY 59 TYDVEFLSADTKTTTAVVESKDKGKTEVKIGAKTSVIREKDG---KLVNCKDGENGS 115
DB 61 SLGSLVFLS-----TGFVPAADITVSTQAEISALS-----NGYDKIILIGADITLLGS 109
OY 116 STDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEVTSCTVTFASGKGTAT 175
DB 110 LT---VNMVTSNQVVIDGGKFGFLVNNNTNGL-----VSSG-----SGLTLQON 152
OY 176 VSKDDQGN-----ITVWD-----VNVGDALN-- 197
DB 153 MSKIDSANYYSMVVLNGANTAVNVIYNIDFLGSSQLIYMGAYGATNSIMTFGDLNDV 212
OY 198 -VNOLQNSGMNLDKRAVAG-----SSGKVISGNVSPSKGKDEYVNIAGNNIETTRNGK 251
DB 213 VVNDRAOEIGEVNKLAFGRFHVHTHTGSSVTSFVSTGGANNSTMDFAAGADVKIDRTGS 272
OY 252 NIDATSWTPOF-----SSVSLGAGADAPTLSDGDALNVGSKKDKPVRITVAVGV 304
DB 273 TGDLTSTVNAFATTFADGASFELIANONVSGTITNGLIGISVNS-----IDFGSGV 327
OY 305 K-----EGDVTVAQLKVAQNLNRIIDVNDGNARAGI-AQAIATAGLVQAVLPGKSM 356
DB 328 KIVLOSRSDDGSIIS-----GNGIDNATNTVA-AGINNNASGADANVIYNLCTGSI 375
OY 357 MAIGGTY-----RGEAGYATGYSISDG-GNMIIR--GTASGNSRGHFG 398
DB 376 KATMTGITATKANNANNASDIYIRSGADITAAATGATISATHNGTGVKIKNDGTTTAAIGAI 435
OY 399 ASASY 403
DB 436 SSASI 440
```

#### RESULT 12

S28634  
adhesin AIDA-I precursor - Escherichia coli plasmid pIB6

C:Species: Escherichia coli

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 08-Oct-1999

C:Accession: S28634; S22680; S28881; S72657

R:Benz, I.

submitted to the EMBL Data Library, March 1992

A:Reference number: S28634

A:Molecule type: DNA

A:Residues: 1-1286 <BEN>

A:Cross-references: EMBL:X65022; NID:942254; PIDN:CAA46156.1; PID:942255

R:Benz, I.; Schmidt, M.A.

Mol. Microbiol. 6, 1539-1546, 1992

A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escheri-

A:Reference number: S22680; MUID:92326638; PMID:1625582

A:Accession: S22680

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 839-1286 <BE2>

A:Cross-references: EMBL:X65022

A:Experimental source: strain 2787

A:Accession: S28881

A:Molecule type: protein

A:Residues: 50-56 <BE3>

A:Experimental source: strain 2787

R:Subr, M.; Benz, I.; Schmidt, M.A.

Mol. Microbiol. 22, 31-42, 1996

A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the out

A:Reference number: S72657; MUID:9705419; PMID:8899706

A:Accession: S72657

A:Molecule type: protein

A:Residues: 847-856 <SDH>

A:Experimental source: DABC strain 2787

C:Genetics:

A:Gene: plasmid pIB6

C:Keywords: membrane protein

F:1-49/Domain: signal sequence #status predicted <SIG>

F:50-1286/Product: adhesin AIDA-I #status predicted <MAT>

Query Match 9.0%; Score 185; DB 2; Length 1286;  
Best Local Similarity 25.4%; Pred. No. 0.01;  
Matches 107; Conservative 51; Mismatches 200; Indels 64; Gaps 19;

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OY 1 MNKIRITWNSALANVAVVSELTNRHTRKASATVKTAVLA--TILFATVQASANNVDPVR 58
DB 1 MNKAVSIIMSHSRQAMVAVSELARGH-----GFLAKNTLLVLAIVSTIGNAFAVN 51
OY 59 TYDVEFLSADTKTTTAVVESKDKGKTEVKIGAKTSVIREKDGKLVTKDGENGSTD 118
DB 52 ISGTVSSGCTVSSGETQIVYSGRGSNATVNSGC-TQIV--NNGKTTATVNSSGQNV 108
OY 119 EGEGLVTAKEY---IDAVNKAQWRMKTTTANGQTQADKFEVTSCTVTFASGKGTTA 174
DB 109 GTSATITSTIYNSGIIQVHSSG---VASATNLSGQKQNIYNLGHASNTVIFSG---- 159
OY 175 TVSKDDQGNITVMDVNVGDALNVN---QLONSGMNLDKRAVASSSGKVISGNVSPSKG 231
DB 160 -----GNQIT-FSGGTTDSTNLSGGOQVSSSGVASTNTINS--AQNILSEGA 208
OY 232 MDETVNINAGNNIETTRNGKNIDATSWTPOFSSVSLGAGADAPTLSDGDALNVGSKDK 291
DB 209 I-STHISSGQNOYISA-GANATEIYNSGSGFORVNSGAVATGVLSGCTQNVSSGSAI 265
OY 292 NKPVRTVNAFAGVKEGDTVNAQLKVAQNLNRIIDVNDGNARAGIAO--AIATAGLVQA 349
DB 266 STSVYNSGVQVFAFATVTDVTVNSGQNMNTSS-----GGIYSETTVVNSGTONI 315
OY 350 YLPGRSMMA-IGGCTYRGEAGYATGYSISDPGNNIIR--GTASG---NSRGRFGASASY 403
DB 316 YSGSALSANIKGQIYNSGTAIIN-TLVSDGGIQLHNGIAGSGTIYNSGIVNIS-SG 373
OY 404 GY 405
DB 374 GY 375
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#### RESULT 13

AB3486  
cell surface protein [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C:Accession: AB3486

R:DelVecchio, V.G.; Kaparatl, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanov

; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A:Reference number: AD3252; PMID:11756688

A:Accession: AB3486

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <KUR>

A:Cross-references: GB:AE008917; PIDN:ALU53053.1; PID:917983913; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME1872

A:Map position: 1

Query Match 8.9%; Score 183.5; DB 2; Length 365;  
Best Local Similarity 23.1%; Pred. No. 0.0027;  
Matches 77; Conservative 38; Mismatches 82; Indels 137; Gaps 11;







GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 6.28512 Seconds  
(without alignments)  
3045.266 Million cell updates/sec

Title: US-09-771-382-25  
Perfect score: 2063  
Sequence: 1 MNKIYRIIWSALNMAVYVS.....TASGNSRGHFGASASYGYQM 407

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	9.0	1286	1 AIDA_ECOLI	003155 escherichia
2	175	8.5	1325	1 YDEK_ECOLI	P32051 escherichia
3	171.5	8.3	1039	1 AG43_ECOLI	P39180 escherichia
4	155	7.5	2003	1 YDBA_ECOLI	P33666 escherichia
5	149.5	7.2	930	1 PMP8_CHLPN	092393 chlamydia p
6	145.5	7.1	1300	1 120K_RICRI	P14914 rickettsia
7	145.5	7.1	1654	1 OMPB_RICRI	053047 r outer mem
8	145	7.0	1953	1 BIGA_SALTY	P25927 salmonella
9	143	6.9	933	1 SLAP_CAME	P35827 campylobact
10	142.5	6.9	550	1 FLIC_SHIFL	008860 shigella fl
11	141	6.8	1025	1 SLAP_CANCR	P35828 cauliobacter
12	141	6.8	1645	1 OMPB_RICRY	P96989 r outer mem
13	141	6.8	1655	1 OMPB_RICCN	09KX83 r outer mem
14	140.5	6.8	1608	1 HLYA_SERMA	P15330 serratia ma
15	139.5	6.8	1861	1 APU_THERU	P18536 t amylopull
16	139.5	6.8	3178	1 YS89_CAEEL	009646 caenorhabdi
17	138.5	6.7	1567	1 ICEN_XANCT	P18127 xanthomonas
18	138	6.7	2660	1 YEEB_ECO57	08X877 escherichia
19	137.5	6.7	1569	1 YFJA_ECOLI	P52143 escherichia
20	136	6.6	497	1 FLIC_ECOLI	P52143 escherichia
21	136	6.6	2249	1 OMPA_RICRI	P04949 escherichia
22	135	6.5	455	1 YADA_YEREN	P15921 rickettsia
23	135	6.5	1592	1 GTF2_STPDD	P14499 yersinia en
24	135	6.5	1656	1 OMPB_RICJA	P27470 streptococc
25	134	6.5	1928	1 HXA2_HAEIN	006653 r outer mem
26	133	6.4	2021	1 OMPA_RICCN	P45354 haemophilus
27	131	6.3	434	1 YADA_YERPS	052657 rickettsia
28	131	6.3	928	1 PM10_CHLPN	P10858 chlamydia p
29	131	6.3	1398	1 TOP2_PLAFL	P41001 plasmodium
30	130.5	6.3	523	1 P60_LISSE	001839 listeria se
31	130.5	6.3	1210	1 ICEN_PSEFL	P09815 pseudomonas
32	130.5	6.3	1577	1 HLYA_PROMI	P16466 proteus mir
33	129.5	6.3	575	1 FLA2_CAMJE	P22251 campylobact

34	129.5	6.3	716	1 CX80_EUPOC	09n9x3 euptotes oc
35	127.5	6.2	367	1 FLIC2_PROMI	P42273 proteus mir
36	127.5	6.2	445	1 G6PI_BACTN	08a5w2 bacteroides
37	127.5	6.2	880	1 LYTD_BACSU	P39848 bacillus su
38	127.5	6.2	1148	1 ICERK_PSEEX	030611 pseudomonas
39	127.5	6.2	1153	1 PVDB_PLAKN	P50453 plasmodium
40	127	6.2	366	1 PGLB_ASPFL	P41750 aspergillus
41	127	6.2	461	1 US45_LACTIC	P22865 lactococcus
42	127	6.2	524	1 P60_LISME	001839 listeria we
43	127	6.2	2358	1 YEEB_ECOLI	P76347 escherichia
44	126.5	6.1	1007	1 Y741_CHLMU	09pj16 chlamydia m
45	126	6.1	1076	1 NUP1_YEAST	P20676 saccharomyc

## ALIGNMENTS

```

RESULT 1
AIDA_ECOLI
ID AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC 003155;
DF 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adhesin aida-I precursor.
GN AIDA-I.
OS Escherichia coli.
OC Plasmid PIB6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 50-56.
RC STRAIN=0126:H27 / 2787;
RX MEDLINE=9232636; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -1- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC -1- ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC -----
CC EMBL; X65022; CAA46156.1; -.
CC PIR; S28634; S28634.
CC InterPro: IPR006315; Autotransport.
CC InterPro: IPR005546; Autotransporter.
CC InterPro: IPR004899; Peractin.
CC Pfam: PF03797; Autotransporter; 1.
CC DR Pfam: PF03212; Peractin; 1.
CC DR TIGRFAMs: TIGR01414; autotrans_parl; 2.
CC KW Cell adhesion; Signal; Outer membrane; Plasmid.
CC FT SIGNAL 1 49
CC CHAIN 50 ? ADHESIN AIDA-I.
CC PROPEP ? 1286
CC SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
Query Match 9.0%; Score 185; DB 1; Length 1286;
Best Local Similarity 25.4%; Pred. No. 0.0048;
Matches 107; Conservative 51; Mismatches 200; Indels 64; Gaps 19;
OY 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVKTAVLA--TLLEFTVQASANNDEVR 58
||| | ||| : ||:| ||| | ||| ||| | : : |

```

```
DB 1 MNKAYSIWHSRQAMVIYASLARGH-----GEVLAKTLLVLAVSTIGNAPAVN 51
QY 59 TYDVEFLADTKTTTNNVESKDKGKTEVIGAKTSVYKEKGLVTKDKGENSSSTD 118
DB 52 ISGTVSSGCTVSSGCTQLVYSGRNSNATVNSGC-TQLV--NNGKTTATVYNSGSGOV 108
QY 119 EGEGLVTAKEY-----IDAVNKAGMRKTTTANGTGQADKFTVTSNTVTFASCKGTTA 174
DB 109 GTSGLTISTIVNSGCIQHVSSGC-----VASATNLSGGAQNIYINLHASVTYFSG----- 159
QY 175 TVSKDQDNITVYMDVNVGDLNLNV--OLONSGMNLDSKAVAGSSGIVSGVSPSKG 231
DB 160 -----GNQTI-FSGGITDSTINISSGQQRVSSGCVASNTTINSSG--FQNLISEBA 208
QY 232 MDETVINAGNNEIETRNKKNIDATSMTPQPSVSLGAGADAPPLSYDGDALVNSKRD 291
DB 209 I--STHISSGNOYISA-GANATERIVNSGFGQVRVNSGVAAGVLTGSGTQVSSGSAI 265
QY 292 NKPVATITVAPGVKRGSDVTYNAQLKGVANLNLRIDNDGNARAGIAQ--AIATGLVOA 349
DB 266 STSVYNSGVQVVFAGATVTDPTVNSGQNISS-----GGIVSETTVNVSGTONI 315
QY 350 YLPGRKMAA-IGGGTYRGEAGYAGYSSISDGMNIIK--GTPASG--NSRGHFAGASAV 403
DB 316 YSGGSAISANIKGSOIVNSEGTAIN-TLYSDGCTYHNRGCTIAGSTIYNSGTYNIS-SG 373
QY 404 GY 405
DB 374 GY 375

RESULT 2
YDEK_ECOLI STANDARD; PRT; 1325 AA.
ID YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051: P76140: P77168:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipid protein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617: PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Klapatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357: PubMed=9097039;
RA Alida H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizubuchi K., Mori H., Mori T., Motomura K.,
RA Nakabe S., Nakamura Y., Nishimoto H., Nishio Y., Oshida T., Saito N.,
RA Sampaio G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243: PubMed=8274505;
RA Carwright P.J., Timms M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
```

```
RT MOM38."; Biochem. Acta 1153:345-347(1993).
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: TO E. COLI YEAL.
CC -1- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC -----
DR EMBL: AE000248; AAC74583.1; -.
DR EMBL: D90793; BAA15190.1; ALT_INIT.
DR EMBL: D90794; BAA15197.1; ALT_INIT.
DR EMBL: X73295; CAA51730.1; ALT_FRAME.
DR PIR: A64905; A64905.
DR Ecocyc: B31780; ydek.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLUCERIDE (POTENTIAL).
FT CONFLICT 884 884 N->K (IN REF. 3).
FT CONFLICT 1317 1317 M->S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A06FA19AD7D CRC64;

Query Match 8.5%; Score 175; DB 1; Length 1325;
Best Local Similarity 21.5%; Pred. No. 0.018;
Matches 122; Conservative 58; Mismatches 200; Indels 188; Gaps 23;

QY 1 MNKIRIITNSALNMAVYSELTR-----NHTKRASATVKTAVLATLLPATVOASAN 52
DB 1 MNRIYRVLINCTQLQVFOACSELTRRAGTSYVNLKSSGLTKFRLFLGVLALSGSAS 60
QY 53 -----NDVFRITD-----YEFLSADPKTT-T 74
DB 61 GASLEVDNDQITNIDTDVADYALVGYGTGLNLIAAGNASLTTITTSVIGANDSSET 120
QY 75 VNV-----ESKNGKRTVEY-KIGAKTSVYKEK-----DGKLVGKDKGENSSDGE 121
DB 121 VAVLGCTRKRLDSDGNMARNPLVNGSGTGLTNIKQGHVDGGLRLGSGTGGVGTVNSGE 180
QY 122 GLVTAKEYID-----AVNKAG-WRMKTTTA 145
DB 181 DSVLTTELFEIGSYSGTSLNITDKGYVTSIYVALIGYQAGSNGVYVEKGEMLIKNDS 240
QY 146 -----NGQCGAOKFEYVTSCTVTF-----ASGKTATVAVSDQDNITVMD- 189
DB 241 SIEFOIGNQGTGEA-----TIREGGLVTAENTIIIGNNAGTIGLVNVDSDVTVRLYNG 296
QY 190 -----VNVGDALN--VNOLONSGMNL-----D 209
DB 297 YPGNQTIVINSNGLINKKEYSLVGVQDSHGAVNTYDKGHNHFLGTGEAFRIYITGDAGD 356
QY 210 SKAVAGSSGKVISGNVSPSKGMDT-----VINAGNNEIETRNKKNIDAT 257
DB 357 GELNVSSGKVDSGITIGT-----MKETGCGNITVKKDKNSYITMLGTNLGVDGHEMISNQ 413
QY 258 SMTPOFSSVSLGAGDAPPLSYDGDALVNSKRD-NKPVRTITVAPGVKRGSDVTYNAQLK 316
DB 414 GLVNSNGSSSLGYG-----ETGVGNYSITTGGMMEVKNKYTTIGVAGGNLINSOGG--K 467
QY 317 GVAONLNNRIDVNDNARAGIAQATAGLVQAYLP--GKSMATIGGGTYRGEAGYAI-- 372
DB 468 FVSQNTITFLGDKASGIGTLNIMDATISSPDYGVINAGVNSGATVNSGATLNSGTGFLG 527
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QY 373 -----GYSSISDGMNIIINGTAGSNR 394  
DB 528 GNASGKGIWNISITSLMNLK-TSSTNMQ 554

RESULT 3  
AG43\_ECOLI  
ID AG43\_ECOLI STANDARD; PRT; 1039 AA.  
AC P39180; P75614; P76360; P97241; Q46771;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (AG43) (Fluffing protein).  
GN FLU OR B2000.  
OS Escherichia coli.  
OC Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251538; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
RA Nishimoto K., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,  
RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,  
RA Yamamoto Y., Horiiuchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 4.0-1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML 308-225;  
RA Henderson I.R., Owen P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP PRELIMINARY SEQUENCE OF 53-78.  
RC STRAIN=ML 308-225;  
RX MEDLINE=99291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN [5]  
RP SEQUENCE OF 53-63.  
RC STRAIN=K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded  
in the genome of Escherichia coli K-12.";  
RL Electrophoresis 18:1259-1313(1997).  
RN [6]  
RP GENE NAME.  
RX MEDLINE=97257509; PubMed=9103983;  
RA Henderson I.R., Meehan M., Owen P.;  
RT "Antigen 43, a phase-variable bipartite outer membrane protein,  
determines colony morphology and autoaggregation in Escherichia coli  
K-12.";  
RL FEMS Microbiol. Lett. 149:115-120(1997).  
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY

CC FUNCTION AS AN ADHESIN.  
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA  
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA  
CC CHAIN).  
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.  
CC -1- SIMILARITY: TO ADHESIN AID-1 AND TO BORDETELLA PERTACTIN.  
CC -----  
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CC -----  
CC EMBL; AE000291; AAC75061.1; ALT\_INIT.  
CC EMBL; D90838; BAI15825.1; ALT\_INIT.  
CC EMBL; D90839; BAI15832.1; ALT\_INIT.  
CC EMBL; U24429; AAB47869.1; -.  
CC HSSP; P07505; 1SRD.  
CC Ecogene; EGI2686; flu.  
CC InterPro; IPR006315; Autotransport.  
CC InterPro; IPR005546; Autotransporter.  
CC InterPro; IPR004899; Pertactin.  
CC Pfam; PF03797; Autotransporter; 1.  
CC Pfam; PF03212; Pertactin; 1.  
CC TIGRfams; TIGR01414; autotrans barl; 1.  
CC Outer membrane; Signal; Complete proteome.  
CC SIGNAL  
CC 1 32  
CC CHAIN  
CC 53 551  
CC FT 552 1039  
CC FT VARIANT 2  
CC FT VARIANT 41 42  
CC FT VARIANT 46 46  
CC FT VARIANT 157 157  
CC FT VARIANT 188 188  
CC FT VARIANT 303 305  
CC FT VARIANT 320 320  
CC FT VARIANT 372 372  
CC FT VARIANT 493 493  
CC FT VARIANT 497 497  
CC FT VARIANT 585 585  
CC FT VARIANT 709 709  
CC FT VARIANT 721 721  
CC FT VARIANT 751 753  
CC FT VARIANT 803 803  
CC FT VARIANT 815 815  
CC FT VARIANT 824 824  
CC FT VARIANT 829 835  
CC FT VARIANT 845 847  
CC FT VARIANT 855 855  
CC FT VARIANT 888 888  
CC FT VARIANT 1025 1025  
CC FT CONFLICT 61 63  
CC FT SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;  
CC -----  
CC Query Match 8.3%; Score 171.5; DB 1; Length 1039;  
CC Best Local Similarity 20.3%; Pred. No. 0.021;  
CC Matches 102; Conservative 57; Mismatches 195; Indels 149; Gaps 18;  
QY 1 MNKIRIIMNSALNAVVSSELTNRNHRKASATYKTAFLATLAFVQA-----SAN 52  
DB 5 LNTCYRLVNMNMTCAPFVYASSLAARGRGVAVALSIAVTSPLVLAADLVIRPGETVN 64  
QY 53 NVDFVRIVYVEFLISADTKTTTVAE-SKDN-----GKTEYKIG----- 91  
DB 65 GGTLANHDNQLVEFTNGMTSTGLEYGPDNEANTGQWQDGGTANKTFTVSGLORVN 124  
QY 92 -----AKTSVIREKRGKXIVTQK--DKGENGSTDEGELVYAKVYIDAVNNKAGMR----- 139  
DB 125 PGGSVDTIVISAGGGSLOGRNAVFTTLNGEGQNMHEGAIATGTIV---NDKGWQVVKPCT 181

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QY 140 MKTTTA-----NGTGADKFEV-----TSGINVTASGK 171
DB 182 VATTVVVWGAEGGPDANGDGTGVRGAVRTTINKNGRQIVRAEGTANTVYVAGGQ 241
QY 172 TTAATVSKDDGNTVWYVNVGDALNVQNLQNSGANTL-DSKAVNASSGCVISGNSPSG 230
DB 242 TVHGALDTTLTGCGYQYVHNGSTASD-TVVNSDGMQIYKNGVAGCNTVYNOKGRLOVDAG 300
QY 231 KMDETVINAG-----NNIEITRGNKNIDTSMTPQF 263
DB 301 GTAFTVTLKGGALVSTAATVGTINRLGAFSVEGKADNV-VLENGRGLDVLTCHTATN 359
QY 264 SSVSLGA-----GADAPTLV-----DGDALNVGSKKNKRVRTITNAPVKEGDV 309
DB 360 TRVDDGGTLVDNRNGTATTVSMGNGVLLADSGAAVSGTRSDGK-----AFSIGGQGA 412
QY 310 TVNAOLKGVAAQNLNRINDNVGDNARAGIAQATATAGLVQAVYPRKSMALGGGTGREG 369
DB 413 DALMEKSSFTLN-----AGDTATDTT-----VNGGLFTTARGG 446
QY 370 YAGYSISIDGGMWIKGTASGN 392
DB 447 TLGGTTTLNNGAILTLGSKTVNN 469

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RESULT 4
YDBA_ECOLI
ID YDBA_ECOLI STANDARD; PRT; 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RT Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitakawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubaram S., Tagami H., Takeuchi T.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RT DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -1- SIMILARITY: TO S.TYPHIMORIUM ORF NEAR CYSG (AC P25928).
CC CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.

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CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR Ecocycle; EG11307; ydba.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 I -> V (IN REF. 2).
FT CONFLICT 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220DE CRC64;

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Query Match 7.5%; Score 159; DB 1; Length 2003;  
 Best Local Similarity 23.1%; Pred. No. 0.36;  
 Matches 107; Conservative 59; Mismatches 164; Indels 134; Gaps 25;

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QY 26 HTKRASATV---KTAVALTLLPATVQASANNVDFRYDVEILSADTKT----- 72
DB 164 YTENADGTISLDSNGRKATINLMQIDEANNV-----ALEGSADGATKWOYNHNGE 216
QY 73 ---TVNVESKNGKTEKIGAKTSV---IKEDGKIYTGDKENG-----SS 116
DB 217 LVITGDNKTAVNNNGKTT---VDGKSTGEIINGNKKYIODGDLVSGGHCIDITGDSA 273
QY 117 TDEGGLVYAKE-----VIDA---VKNAGRMKTTTANGTGQADKFEVTVT----- 159
DB 274 TVDNKNGTMTVYDPESMGIIODGKAIVNNEG---ESTITNGGTGQINGDATTANNNGKT 330
QY 160 -----SGTNVTFASGK-----GTTATVSKDDGNTITVMDVAVG 193
DB 331 TVDGKDSGTGEIINGNKKYIODGDLVSGGHCIDITGDSATV---DNKGTMTVTDPESIG 388
QY 194 DALANNQ---LQNSGNNLDSKAAVAGSSGKVISGN---VSPSKG-----MDETININAGNN- 243
DB 389 IOVDDQAVVAVNNEG---ESAITNGGTGQIINGDATTANNNGKTTVYDGKDSGTETETAGNNG 445
QY 244 -----IEITRGNKNIDI-ATSMTPQFSVSLGAGADAPTLTVSDGDLNVGSKKDNRPV 295
DB 446 KVIQDGDLDVSGGHCIDITGDSATVVDNKNCTMTVTDPESIGIQIDGDAIVNNEGES--- 502
QY 236 RITTNVAPGVKEGDVTNVAOLKGVAAQNLNNR-IDNVGNNARAGIAQATATAGLVQAVYLRGK 354
DB 503 TITNGGTG-----TQINGNDATTANNNGKTTVYDGKDSGTG-TRTAGNIGIVN--LDG- 549
QY 355 SMMAIAGGTYRGEAGYVAGYSISIDGGMWIKGTASGNSRGHFG 398
DB 550 SLTVTGG-----AHGVENIINGNVNKKGDIYVSDTSGIG 584

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RESULT 5
PMP8_CHLPN
ID PMP8_CHLPN STANDARD; PRT; 930 AA.
AC Q92393; Q9RB66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
DE protein 8) (Outer membrane protein 11).
GN PMP8 OR OMP11 OR CPN0446 OR CP0307.
OS Chlamydia pneumoniae (Chlamydiaceae; Chlamydiales; Chlamydiales; Chlamydiales).
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_Taxid=83558;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-VR1310;  
RX MEDLINE=20007584; PubMed=10539856;  
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,  
RA Madsen A.S., Knudsen K., Falk E., Birke Lund S.;  
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their  
RT role in immunopathogenicity.";  
RN Am. Heart J. 138:S491-S495(1999).  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN-CWL029;  
RX MEDLINE=99206606; PubMed=10192388;  
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
RA Ollinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
RN Nat. Genet. 21:385-389(1999).  
[3]  
RN SEQUENCE FROM N.A.  
RC STRAIN-AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Reed T.D., Bunham R.C., Shen C., Gail S.R., Heidelberg J.F., Bass S.,  
RA White O., Hickey E.K., Peterson J., Utherback T., Berry K., Bass S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Gyalini M., Nelson C.W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser S.M.;  
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia  
RT pneumoniae AR39.";  
RN Nucleic Acids Res. 28:1397-1406(2000).  
[4]  
RN SEQUENCE FROM N.A.  
RP STRAIN-J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RT from Japan and CWL029 from USA.";  
RN Nucleic Acids Res. 28:2311-2314(2000).  
-1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)  
(POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.  
CC  
CC  
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CC  
CC  
CC EMBL: AJ133034; CAB37068.1; -  
DR EMBL: AE001627; AAD18590.1; -  
DR EMBL: AE002193; AAF38164.1; -  
DR EMBL: AF002546; BAA98654.1; -  
DR PIR: A81591; A81591.  
DR PIR: D72078; D72078.  
DR PHCI-2DPAGE; Q92393; -  
DR TIGR: CP0307; -  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR InterPro: IPR003368; Chlamydia\_PMP.  
DR Pfam: PF03797; Autotransporter; 1.  
DR Pfam: PF02415; DUF145; 2.  
DR TIGRFAMS: TIGR01414; autotrans\_bar1; 1.  
DR TIGRFAMS: TIGR01376; POMP\_repeat; 6.  
KW Outer membrane; Signal; Multigene family; Complete proteome.  
FT SIGNAL 1 26 POTENTIAL.  
FT CHAIN 27 930 PROBABLE OUTER MEMBRANE PROTEIN PMP8.  
FT CONFLICT 177 177 T->A (IN REF. 3 AND 4).  
SQ SEQUENCE 930 AA; 97669 MW; 46A9B5E3BB913C4C CRC64;

OY		26	HTKRSASATVKAVALATLLEFAIVQASANNVDPRVIYDVEFLSADTKTITYNVEKDNGK	85
OY		27	:	:
Dd		6	HKLIISSLTPLPILIIISLATYAGDASLSPTD-----SEFGAGSGTFTEPKSTLDANG--	55
OY		86	TEVMIGAKTSYIKREKDKLVYGXOKGE-NGSSSTDGEGGLVYAKEVITAVNKAGRMKTYY	144
Dd		56	TNYVLSCNVYIINDAKGTALTCCEFFETTGDLITFTGGKYSFSEFWTVDGSNAGAASTT-	114
OY		145	ANGOTGADKEEYVTSGTNVYFASGKGTTATVSKD-----DOGNITWAYDVNV-	192
Dd		115	-----ADKALLTFTGSNSLFIAPGTYVASGKSTLISAGALMLDTJONG--TIIFSQNV	165
OY		193	-----GDALVNNOLONSGMNLDSKAAVASSGKVIGSVNPSFKMDPEVINAGNNIEI	246
Dd		166	NEANNNGGAITTKTLTSLG-NTSSITFEFTSNACKILGAIYSSAA---ASISGNTGOLVFM	221
OY		247	TRNRCK-----NIIDATSMTPQFSVY-----SIGAG-----AAPTLSYVGDA	283
Dd		222	NNKETGGGALGFPASSSIT-QNSSLFPSCNTATADAGKGAICYCKETGETPYLLTISG--	278
OY		284	LNVSKSKDNKPVRITTNVAPGVKEGDV-TNVVOLKGVAQNLT--NNRIDNVGDNAHAGIAQA	340
Dd		279	-----NKLTLTAENSSVYGGACALCAHGDLISAAGPTLFSNNRC-----GNTAAGGGA	326
OY		341	IATAGLYOAYLPGRKSMAIIGGGYRGEAGYAIGYSSIDSGNWIIKCTASGNSRG--HFQ	398
Dd		327	IAlAD-----SGSLTSLANOGDIYFILGNTLTSTSPASTRNAYILG	367
OY		399	ASASY 403	
Dd		368	SSAKI 372	

RESULT 6  
120K\_RICRI STANDARD: PRT; 1300 AA.  
AC PI4914;  
DT 01-APR-1996 (Rel. 14, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 120 kDa surface-exposed protein.  
GN P120.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_Taxid=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90136087; PubMed=2515418;  
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
RT RT Cloning, expression and sequence analysis of the gene encoding the  
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
RL Mol. Microbiol. 3:1579-1586(1989).  
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS  
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPTOPES  
CC CONFERRING ANTIGENICITY TO THE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.

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EMBL; X16353; CAAB34402.1; -.  
PIR; S07575; S07575.  
DR InterPro; IPR006315; Autotransport

InterPro: IPR005546; Autotransporter.  
DR Pfam: PF03797; Autotransporter; 1.  
DR TIGRfams: TIGR01414; autotrans\_bar1; 2.  
KW Antigen; Glycoprotein; Cell wall; S-layer.  
FT CAROXYD 66 66 N-LINKED (POTENTIAL).  
FT CAROXYD 86 86 N-LINKED (POTENTIAL).  
FT CAROXYD 103 103 N-LINKED (POTENTIAL).  
FT CAROXYD 147 147 N-LINKED (POTENTIAL).  
FT CAROXYD 268 268 N-LINKED (POTENTIAL).  
FT CAROXYD 330 330 N-LINKED (POTENTIAL).  
FT CAROXYD 375 375 N-LINKED (POTENTIAL).  
FT CAROXYD 415 415 N-LINKED (POTENTIAL).  
FT CAROXYD 424 424 N-LINKED (POTENTIAL).  
FT CAROXYD 430 430 N-LINKED (POTENTIAL).  
FT CAROXYD 436 436 N-LINKED (POTENTIAL).  
FT CAROXYD 444 444 N-LINKED (POTENTIAL).  
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FT CAROXYD 547 547 N-LINKED (POTENTIAL).  
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FT CAROXYD 655 655 N-LINKED (POTENTIAL).  
FT CAROXYD 698 698 N-LINKED (POTENTIAL).  
FT CAROXYD 710 710 N-LINKED (POTENTIAL).  
FT CAROXYD 799 799 N-LINKED (POTENTIAL).  
FT CAROXYD 800 800 N-LINKED (POTENTIAL).  
FT CAROXYD 826 826 N-LINKED (POTENTIAL).  
FT CAROXYD 844 844 N-LINKED (POTENTIAL).  
FT CAROXYD 861 861 N-LINKED (POTENTIAL).  
FT CAROXYD 879 879 N-LINKED (POTENTIAL).  
FT CAROXYD 920 920 N-LINKED (POTENTIAL).  
FT CAROXYD 926 926 N-LINKED (POTENTIAL).  
FT CAROXYD 1116 1116 N-LINKED (POTENTIAL).  
FT CAROXYD 1128 1128 N-LINKED (POTENTIAL).  
FT CAROXYD 1140 1140 N-LINKED (POTENTIAL).  
FT CAROXYD 1146 1146 N-LINKED (POTENTIAL).  
FT CAROXYD 1211 1211 N-LINKED (POTENTIAL).  
SQ SEQUENCE 1300 AA; 132801 MW; E09F52C3F67243D CRC64;

Query Match 7.1%; Score 145.5; DB 1; Length 1300;  
Best Local Similarity 22.5%; Pred. No. 0.74;  
Matches 100; Conservative 50; Mismatches 177; Indels 117; Gaps 19;

30 ASATPKTAVLTLEFAVQASANNVDFRYD---TVFELSDRTTIVN---VESKDN 82  
53 AOKIPNAILTLTGNTGASNPGNAGYTFEDANGTLESASADANVAVTNITALEASGA 112  
83 G-----KTEVKIGAKTSVKEKDKLVTKDK-----GENGSTDEGGLVTAKEV 129  
113 GVVQLSGTHAEELRLGNAGSIFKLADGVINKVQTRALVYGALAAGTITLDGSAITITGD 172  
130 IDAVNKAGWRMKTATTANGOTGOADKFTVT--SGTNVTRASG-----KGTAVSKDDQ 181  
173 IGNAGGAALORITLAN-----DAKKTLLTGAGANIIGAGGTTDLQANGTIRKL--STQ 225  
182 GNITVYVYV-----NYGDALNVQLONSGMN-----LDSKAVA-----GSSKAVIS- 222  
226 NNIVVDFDLATATDOTGVVDASSLTNAQTITLNGKIGTIGANNKTLGOFNIGSSSTVLSN 285  
223 GNV-----SPSKMDETVINAGNNIETIRNKNIDI 255  
286 GNVAINELVINGDGAVOFAHDTYLTITRTTNAAGCKIIFNRYVNNGTITLAA---GTNIGS 342  
256 ATSMTPQFSSVSLGAGADAPTLVYDGAALNVGSKKDNKPRVT---NVAPQVKEGDYTN 311  
343 ATNPLAEINFGSKGVNVDT-----VLNVEGAVLNATNTTITTDANVGSVFVNAAGTN 394  
312 VAQLKGVANLNRRNDNDGNARAGIAQAIATAGLVQAVLPKSSMAIGGGTYREAGYA 371  
395 IVS-GTVGGGQGNKFNVT-----ALENGTIVKFLGNATFNCGNTTIA 434  
372 IGYSSISDGNMIIGKTASGNSRG 395  
435 AN-STLQIGKNYTDCAVASADGTG 457

RESULT 7  
OMP\_RICRI STANDARD; PRT; 1654 AA.  
AC 053047;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)  
DE (rOmp.B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide).  
GN OMPB.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiasee; Rickettsia.  
OX NCBI\_TaxId=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=92167802; PubMed=1724278;  
RA Gilmore R.D., Jr., Cleplak W., Jr., Pollicastro P.F., Hackstadt T.;  
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame:  
RT evidence for protein processing from a large precursor.";  
RT Mol. Microbiol. 5:2361-2370(1991).  
RL [2]  
RP SEQUENCE OF 279-1654 FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90136087; PubMed=2515418;  
RA Gilmore R.D., Jr., Joste N., McDonald G.A.;  
RT "Cloning, expression and sequence analysis of the gene encoding the  
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
RL Mol. Microbiol. 3:1579-1586(1989).  
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERION IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMP/OMP-B FAMILY.  
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CC -----  
DR EMBL: X16353; CAA34403.1; -.  
DR PIR: S18227; S18227.  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR Pfam: PF03797; Autotransporter; 1.  
DR TIGRfams: TIGR01414; autotrans\_bar1; 2.  
KW Antigen; S-layer; Cell wall.  
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.  
FT DOMAIN 1181 1188 POLY-THR.  
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 7.1%; Score 145.5; DB 1; Length 1654;  
Best Local Similarity 22.5%; Pred. No. 0.98;  
Matches 100; Conservative 50; Mismatches 177; Indels 117; Gaps 19;

30 ASATPKTAVLTLEFAVQASANNVDFRYD---TVFELSDRTTIVN---VESKDN 82  
407 AOKIPNAILTLTGNTGASNPGNAGYTFEDANGTLESASADANVAVTNITALEASGA 466  
83 G-----KTEVKIGAKTSVKEKDKLVTKDK-----GENGSTDEGGLVTAKEV 129  
467 GVVQLSGTHAEELRLGNAGSIFKLADGVINKVQTRALVYGALAAGTITLDGSAITITGD 526



QY 130 IDAVNAGRMKTTTANGOTGQADKFEVY-SEGTNTFASG-----KGTATVSKDQ 181  
 Db 527 IGVAGAAALQRTTLAN-----DAKTLILIGANIGAGGCTIDQANGCTIKL-SYQ 579  
 QY 182 GNTTWYDV-----NGDALNVNOLNSGWN-----LDSKAVA---GSSGKVIS- 222  
 Db 580 NNIVVDFDLATADQGVVDASSLTNAQCLTTLNGKIGTIGANKTTLGQFVIGSSKTYLVS 639  
 QY 223 GNV-----SPKSGKMEDEVINNAQNNIEITFNCKNIDI 255  
 Db 640 GNVAINELVIGNDGAVQAHDTYLLTRTTNAGQKXITPNPVVNGTTLAA---GTLGSG 696  
 QY 256 ATSMPTQFSSVSIGAGADAPTLSVDDGALNVGSKKNKPVRIT---NVAPGVKEGDVTN 311  
 Db 697 ATNPPLAEINFGSGVAVDT-----VLNFGSVLXKXNTITTTAANGSEFVFNAGCTN 748  
 QY 312 VAOGLKVAONLNRRIDNVQGNARAGIAQALATAGLVQAVLPGKSMALIGGTYRGEAGYA 371  
 Db 749 IYS-GTVGGQCGKKEFTV-----ALENGTTFELGNATFNGWTTTIA 788  
 QY 372 IGVSSISDGGNMTIKGTASGNSRG 395  
 Db 789 AN-STLQIGSNYADCVASADGTG 811

RESULT 8  
 BIGA\_SALTY STANDARD; PRT; 1953 AA.  
 AC P25927; P25928; Q9XC03;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Putative surface-exposed virulence protein biga precursor.  
 GN BIGA OR STM478.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_Taxid=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14028;  
 RA Stojiljkovic I., Valentine P., Heffron F.;  
 RT "Salmonella typhimurium rhs homolog.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SCS1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 LT2.";  
 RL Nature 413:852-856(2001).  
 RN [3]  
 RP SEQUENCE OF 1-765 FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE=91100301; PubMed=1987123;  
 RA Wu J.Y., Siegel L.M., Kredich N.M.;  
 RT "High-level expression of Escherichia coli NADPH-sulfite reductase:  
 RT requirement for a cloned cysC plasmid to overcome limiting streptame  
 cofactor.";  
 RL J. Bacteriol. 173:325-333(1991).  
 CC - CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
 CC in positions 414 and 732.  
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 CC -----  
 CC EMBL: AF133696; AAD39458.1; -  
 CC DR EMBL: AE008859; AAL22340.1; -  
 CC DR EMBL: M64606; AAA27042.1; ALT\_FRAME.  
 CC DR EMBL: M64606; AAA27043.1; ALT\_FRAME.  
 CC DR StryGene: SGI0437; biga.  
 CC KX Virulence; Repeat; Signal: Complete proteome.  
 CC FT SIGNAL 1 27  
 CC FT CHAIN 28 1953  
 CC FT  
 CC FT DOMAIN 101 252  
 CC FT REPEAT 101 103  
 CC FT REPEAT 104 113  
 CC FT REPEAT 114 122  
 CC FT REPEAT 123 133  
 CC FT REPEAT 134 144  
 CC FT REPEAT 145 155  
 CC FT REPEAT 156 166  
 CC FT REPEAT 167 177  
 CC FT REPEAT 178 188  
 CC FT REPEAT 189 199  
 CC FT REPEAT 200 210  
 CC FT REPEAT 211 221  
 CC FT REPEAT 222 232  
 CC FT REPEAT 233 243  
 CC FT REPEAT 244 252  
 CC FT REPEAT 207 207  
 CC FT CONFLICT 514 514  
 CC FT CONFLICT 1698 1698  
 CC FT CONFLICT 1795 1798  
 CC FT CONFLICT 1836 1837  
 CC SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;  
 CC  
 CC Query Match 7.0%; Score 145; DB 1; Length 1953;  
 CC Best Local Similarity 23.2%; Pred. No. 1.3;  
 CC Matches 97; Conservative 54; Mismatches 158; Indels 110; Gaps 22;

QY 8 IYNSAL--NANVYVSELTNRHTRASATYKTVATLTLFTVQASANNDFRTYTVR 65  
 Db 286 VMVYSEDDNOM---QLTTADGKTLNVTGMDVTDANA--AVIGTQENGLYWK-YDSRGY 338  
 QY 66 L-SADRTTIVANESKONCKTEVKIGAKSVIKKDGKIVTKDGEN-----GSSTDE 119  
 Db 339 LITADNTTVISGDDOHNSDRGMDISG---QDKTVIISG-DRTVNTLTGDDSVYTDG 392  
 QY 120 GEGLYTAKEVYIDAVNAGRMKTTTANGOTGQADKFEVYSGTNVTFASGCTTAVYSKD 179  
 Db 393 ATGMV-----ISGCGTTNTISGSHSTVDNATG-ALISGNTTTNAGD 433  
 QY 180 ----DQNTIVYVNVNGDALNVNOLNSGWNLDSKAVAGSSGKVISGNVSPSGKMDTEV 236  
 Db 434 IAVSGGCTAIIIDGNATIKNTGTSIDSG-----AGSTGVYIGGNARVANNDDGMTI 485  
 QY 237 NINAGNNIETRNKNDIDATISMTPOFSSVSLGAGADAPTLSDG---ALNVGSKDKN 293  
 Db 486 T-DGGTGGHTTGNVVIDNAGSTTV-----SGADATVLYEGDALVINEGNO--- 532  
 QY 294 PVRTIVYAPGVK-EGDVTNVAQLKGVANLNRRIDNVQGNARAGIAQALATAGLVQAVYLP 352  
 Db 533 --TISGAVGTRIDGDAAHTTNGDIA-----VDGAGSAAVIINGNGSLTQA--- 578  
 QY 353 GKSMALIGGTYRGEAGYAIGYSSISDGGWIK-GTASGNSGHHGASA-----SYGY 405  
 Db 579 -----GDLVLTVDGAMGITTYGT--GNEAKNKGATVADPADSVGF 615

RESULT 9  
 SLAP\_CAME STANDARD; PRT; 933 AA.  
 AC P35827;

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE S-layer protein (Surface array protein) (SAP).  
 GN SAP.  
 OS Campylobacter fetus.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=196;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
 RC STRAIN=84-32 / 23D;  
 RX MEDLINE=90354448; PubMed=2387868;  
 RA Blaser M.J., Gotschlich E.C.;  
 RT "Surface array protein of Campylobacter fetus. Cloning and gene  
 structure."  
 RT J. Biol. Chem. 265:14529-14535(1990).  
 RN [2]  
 RP ERRATUM.  
 RX MEDLINE=91035477; PubMed=2229082;  
 RA Blaser M.J., Gotschlich E.C.;  
 RL J. Biol. Chem. 265:19372-19372(1990).  
 CC -I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
 CC CRITICAL FOR VIRULENCE.  
 CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -----  
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 CC -----  
 DR EMBL: J05577; AAA3032.1; -  
 DR Cell wall; S-layer.  
 KW SEQUENCE 933 AA; 96757 MW; F88C729B4B5B1E9 CRC64;  
 SQ  
 Query Match 6.9%; Score 143; DB 1; Length 933;  
 Best Local Similarity 24.7%; Pred. No. 0.7;  
 Matches 100; Conservative 50; Mismatches 151; Indels 104; Gaps 20;  
 QY 28 KRASATV-  
 DB 475 KRAAKVLTNTAATDQTFTLKANA-----TNSLEFDSATFTKTSVTASG-----520  
 QY 87 EVKIGAKTSVKEKDKLVTKGDKENGSSSTDESGLVTAKEVIDAVKAKGRMKTTAN 146  
 DB 521 -----SGKLVTKGAEVETLVNID-----TTAFNALQSV-----SF 551  
 QY 147 GGTGADKFEVTSCTNTVTFASGKTATVSK--DDOGNITVYVYVNGDALNVQLONS 204  
 DB 552 GKTGGGKGF-SVKTGTGDKIEFVGTTLTBSVIDADPNDRITAMKSAJLTANFMINI 610  
 QY 205 GWNLDKRVAG-----SSGKVIAGNVSPSKGKMDVYNINAGNIEITRNGK-----252  
 DB 611 ENVALISDAVATADSSSAFKNSVITTEKADDTTLTKDKDVIYNITADAGSVKLITVKL 670  
 QY 253 -----IDIAVSMTPQFSSVSGAGADAPTLSVDG--DALNVS-KKDKKPRITNV 300  
 DB 671 NDVYALMIVYKIVLDAAKKDTINIALGTRAADKALVIDIGIEITLNTSLVKATSPETTANT 730  
 QY 301 APGVKEDPTNV-----AQL-----KGAQNLNRRIDNVGNA-RAGI-----AQAATAGLVQ 348  
 DB 731 V-NMKLDTVTSIIIDGMQITLGHAGTAGTDSKYVSMIDASALKAGLTFDASAI-TLG-----785  
 QY 349 AYLPEKSMALGGTGTGREGAGTAIGYSIS--DGNMIIKGTASGN 392  
 DB 786 -----ANATIKGGS-----GADSIYVKGNIIVDLVAGCD 815

RESULT 10  
 ID FLIC\_SHIFL STANDARD; PRT; 550 AA.  
 AC 008860;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Flagellin.  
 GN FLIC OR SF1966.  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 OX NCBI\_TaxID=623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IID642;  
 RX MEDLINE=94335647; PubMed=8057852;  
 RA Tomlinaga A., Mahmoud M.A.-H., Mukaihara T., Enomoto M.;  
 RT "Molecular characterization of intact, but cryptic, flagellin genes  
 in the genus Shigella."  
 RT Mol. Microbiol. 12:277-285(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=301 / Serotype 2a;  
 RX MEDLINE=22272406; PubMed=12384590;  
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
 RA Yu J.;  
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity  
 RT through comparison with genomes of Escherichia coli K12 and O157."  
 RL Nucleic Acids Res. 30:4432-4441(2002).  
 CC -I- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO  
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.  
 CC -----  
 CC -I- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D16819; BAA04093.1; -  
 DR EMBL: AE015215; AAN43516.1; -  
 DR PIR: S44980; S44980.  
 DR InterPro: IPR001029; Flagellin\_C.  
 DR InterPro: IPR001492; Flagellin\_N.  
 DR Pfam: PF00700; Flagellin\_C; 1.  
 DR Pfam: PF00669; Flagellin\_N; 1.  
 DR PRINTS: PR00207; FLAGELLIN.  
 KW Flagella.  
 SQ SEQUENCE 550 AA; 56636 MW; CC921C9ABEF200B6 CRC64;  
 Query Match 6.9%; Score 142.5; DB 1; Length 550;  
 Best Local Similarity 21.9%; Pred. No. 0.4;  
 Matches 79; Conservative 55; Mismatches 165; Indels 61; Gaps 15;  
 QY 46 TVOASA-----NNVDFV-----TYDVEFLSADTKTTTVNVESSDKKTEVKGATGS 95  
 DB 96 TVOASTGNSDSDLSIDIDEIKSRIDETDRVSGQTFENGAVNLADGSMK--TGVGANDG 153  
 QY 96 VIKEDKGLVTKGDKENGSSSTDEGEGL-----VTAKEVIDAVNKAQWRKKTITANGQTS-- 150  
 DB 154 QTITIDLKIDSDITGLANGFNWNGGAVANAAASADLVANATVYVGGKTYVSAGYDAK 213  
 QY 151 QADKFEVTSCTNV--TFASGKTATVS--KDOGNTVYVYVNGDALNVQLONS 206  
 DB 214 ASDLAGVSDGDTVOATINNGFTPAASATNYKYSASKSYSFDTTASAADVQKILTPG- 272  
 QY 207 NLDSKAVAGSSGK-----VLSGNVSPSKGKMDVYNINAGNNI-----ETTRNGKNIDLAT 257

Db 273 -----VGDYAGTITIDSDADVOYISSDGKITASGDKLYIDTGRITKNGS---GA 321  
 Qy 258 SMTPOFSVSLGAGADAPTLVSDGDLNVGSKDKNRPVRTTNVAPGVKEDDVNNVQLKG 317  
 Db 322 SLIEBASITLAANNKATTTIDIGTSTISF-TGNSITPDTITVYTGAK---VQOAFDKA 377  
 Qy 318 VAONLNN-----RIDNVGNARAGI-----AQAIAPAGLVQAVLPKSKMAIGGG 362  
 Db 378 VSTRSGNNVDEFTTAGYVNGTGAVTKGVDVYDNNNEALTTSDPTVDPIYDIDDDGSYVNGSG 437

RESULT 11  
 ID SLAP\_CAUCR STANDARD: PRT; 1025 AA.  
 AC P35828: 046015: 09REF12;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE S-layer protein (Paracrystalline surface layer protein).  
 GN R5AA OR CCI007.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.  
 RC STRAIN-ATCC 19089 / CB15;  
 RA MEDLINE=93007489; PubMed=1393820;  
 RA Gilchrist A., Fisher J.A., Smit J.K.;  
 RT "Nucleotide sequence analysis of the gene encoding the Caulobacter  
 RL Can. J. Microbiol. 38:193-202(1992).  
 RN [2]  
 RP REVISIONS TO 376; 636 AND 842-843.  
 RA Avram P.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Bingle W.H., Avram P.A., Nornellini J.F., Smit J.K.;  
 RT "The secretion signal of C. crescentus S-layer protein is located in  
 RL the C-terminal 82 amino acids of the molecule."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 19089 / CB15;  
 RA MEDLINE=21173698; PubMed=11259647;  
 RA Nielsen W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Oteback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 RN [5]  
 RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.  
 RC STRAIN-ATCC 19089 / CB15;  
 RA MEDLINE=89008089; PubMed=3049545;  
 RA Fisher J.A., Smit J.K., Agabian N.;  
 RT "Transcriptional analysis of the major surface array gene of  
 RL Caulobacter crescentus."  
 RL J. Bacteriol. 170:4706-4713(1988).  
 RN [6]  
 RP CHARACTERIZATION.  
 RC STRAIN-ATCC 19089 / CB15;  
 RA MEDLINE=98292737; PubMed=9620954;  
 RA Avram P., Smit J.K.;  
 RT "The Caulobacter crescentus paracrystalline S-layer protein is  
 RL secreted by an ABC transporter (type I) secretion apparatus.";  
 RL J. Bacteriol. 180:3062-3069(1998).

CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A  
 CC PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER  
 CC (TYPE I) SECRETION APPARATUS.  
 CC -1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE  
 CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A  
 CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.  
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 CC -----  
 DR EMBL: AF062345; AAC38665.2; -  
 DR EMBL: AF193063; AAF19365.1; -  
 DR EMBL: AE005779; AAK22991.1; ALT\_INIT.  
 DR PIR: A48995; A48995.  
 DR HSSP: P22629; ISWC.  
 DR TIGR: CCI007; -  
 DR InterPro: IPR001343; Hemlysn\_Ca\_bind.  
 DR Pfam: PF00353; hemolysincbind; 3.  
 DR PRINTS: PR00313; CABNDNGRPT.  
 KM Cell wall; S-layer; Calcium-binding; Complete proteome.  
 FT INT\_MET 0  
 FT SEQUENCE 1025 AA; 98001 MW; AD7A326E1363DBAC CRC64;  
 SQ

Query Match 6.8%; Score 141; DB 1; Length 1025;  
 Best Local Similarity 23.5%; Pred. No. 1;  
 Matches 114; Conservative 46; Mismatches 180; Indels 146; Gaps 22;

Qy 11 SALNMYVSEL-TRNHTKRASATVKTAVLATLIFA-----TVQASANNVDFVT 59  
 Db 304 TALPTGVITISGIETMNTSGAAITLNTSSGVTGLTALNTVSGAAQVTFAGAG----- 356  
 Qy 60 YDIVEFLSADTKTTTVVEKDKCKTEVIGAKTSYIKKDKGLVYKXKGENG----- 114  
 Db 357 -----QNTLTATTAQAANNVAVDGGANYV---ASTGV---TSGTTVGAASAGTVSVS 406  
 Qy 115 -----STDEEGGLVTAKEVIDAVKAGWRMKT-----TANG-----QTQADK 154  
 Db 407 VANSSTTTGAIAVGTGTAATVAGTAGNAYNTLTQADVYVNGSSSTTAVTVQTAATA 466  
 Qy 155 FEVTVSGTN-VTF-----ASGKGTATVSKDDQGNITV---MYDVNGD----- 194  
 Db 467 GATVAGRVNCAVITDASAASATTAQKIAVTVLGSFGAATIDSSALTVMISGTSLGI 526  
 Qy 195 -----ALVNOLQNSGWLDSKVAAGS-----SGKYSQNSVSKKMD 233  
 Db 527 GRGALATPTANLTLLNGLITTTGALTDSBAADDFETTINAGSTASSSTLSLVADA 586  
 Qy 234 ETVINAGNNIEITRN-----GKNI-DIATSMTPQFSVSLGAGADAPTL 277  
 Db 587 TTLINISGDARVTTISHTAALLTGTVNSVGTALGALATGLV--FTG---GAGADSLIL 641  
 Qy 278 SVGDALNVGSKDKNRPVRTTNVAPG--VKEGDVTVNAQLKGYAQNINRIDVND----- 330  
 Db 642 GATTKAIVMGAGDVTVSSATLGAAGSVNGCDGTDV-----LVANNNGSFSADPAFGG 696  
 Qy 331 -----GNARAG-----INQAITAGLVQ---AYLPKSKMAIGGTYGGEAGYA 371  
 Db 697 FETLRVAGAAAGSHNANGFTALQLGATGATTTFTTNVAVVGLTALAAPTGTITVLANA 756  
 Qy 372 IGYSSI 377  
 Db 757 TGTSDV 762

RESULT 12

OMP\_RICTY  
ID OMP\_RICTY STANDARD: PRT; 1645 AA.  
AC P96989;  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)  
DE (Omp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
GN OMP OR SLIP.  
OS Rickettsia typhi.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=785;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Williamington;  
RX MEDLINE=94040787; PubMed=8224886;  
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;  
RT "Cloning and sequence analysis of the gene encoding the crystalline  
RT surface layer protein of Rickettsia typhi.";  
RL Gene 133:129-133(1993).  
RN [2]  
RP PARTIAL SEQUENCE.  
RC STRAIN=Williamington;  
RX MEDLINE=92114896; PubMed=1370573;  
RA Chung W.M., Carl M., Dasch G.A.;  
RT "Mapping of monoclonal antibody binding sites on OMP fragments of  
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia  
RL prowazekii.";  
RL Mol. Immunol. 29:95-105(1992).  
RN [3]  
RP IDENTIFICATION OF CLEAVAGE SITE.  
RX MEDLINE=92104668; PubMed=1729180;  
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;  
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer  
RT membrane protein of rickettsiae: identification of an avirulent  
RL mutant deficient in processing.";  
RL Infect. Immun. 60:159-165(1992).  
CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC -----  
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CC -----  
DR EMBL; L04661; AAB48987.1; -;  
DR PIR; J00896;  
DR InterPro; IPR005315; Autotransporter.  
DR Pfam; PF03797; Autotransporter; 1.  
DR TIGRfams; TIGR01414; autotrans\_bar1; 1.  
RW Antigen: S-layer; Transmembrane; Cell wall.  
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.  
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
FT CONFLICT 657 657 H -> N (IN REF. 2).  
FT CONFLICT 842 842 V -> I (IN REF. 2).  
FT CONFLICT 1071 1071 G -> A (IN REF. 2).  
FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

Query Match

6.8%; Score 141; DB 1; Length 1645;

Best Local Similarity 21.4%; Pred. No. 1.7;  
Matches 100; Conservative 67; Mismatches 172; Indels 128; Gaps 22;  
QY 14 NAMVVSELTNRHHTRASATYKTAVALAT---LFFATQASANNVFFTYDVEFLSADI 70  
DB 218 NGFVAVSDKT-----FRGKITINIGNOGIMFTTTPDAANALALOGGGNTINGRDQ 270  
QY 71 KTTVNVSSKDNKGKTEVKI-----GAKTSVIREKD-----GKL-----VTGKDKGE 112  
DB 271 TGLVLVGR--NGNTEFNVTGSLGNNLKGVIEFTTAAAGLLINGGAANNVIGTDNGA 328  
QY 113 NGS-----STDEG-----EGLVTAKEVIDAVNKKAGMRKTTTANGQT-----GOA 152  
DB 329 GRAAGFIIVSDNGNNAATISGOVYAKDIV-----IOSANAGGVFFELHVDVGLGK 379  
QY 153 DKFEFTSGTNTVFASGKGTATFATVSKDQGNITVYDVN-----VGDALNVNQLON 203  
DB 380 TNEKTAADSKVIITENASFGST-----DFGNLAVQIYVPPNNKILTGNFIDG-----KN 427  
QY 204 SGWNIDSKAVAGSSGKVIISGVNPS-----GKMDETVNI-----NAGNN 243  
DB 428 NG-NTAGVITFNANGTLVSGMTDPNIYVTNKAIEVEGAGIVQLSGIHGAEIRLGNAGSI 486  
QY 244 IETTRNGKNIDIAITSMTPQFSSVSLGACADAPTLSDGDAL---NVGSKDKNKPVRITNV 300  
DB 487 FKLA-DGTVINGPVNQNPVLVNNALAAQ---SIOLDISAITIGDIGAVNAALQDITL 541  
QY 301 APGVGEQVTVAOLKGVANQNLNNRIDVNDGAFRAGIAQATATAGLVQAVLPKSMAG 360  
DB 542 A-----NDASKILTLTSGA-----NIGANNAGAIHPQANGSTTDTLTSTONNITLDF 587  
QY 361 GGTVNGEAGVAYIGVSSISDGGNMIKGT-----ASGNSRGHFGASAS 402  
DB 588 DLDVTTDQTVGDASLTNNQTLFTINGSIGTIGANTKTLGRNNGSS 634  
RESULT 13  
OMP\_RICCN  
ID OMP\_RICCN STANDARD: PRT; 1655 AA.  
AC 09KKA3; 09KKA9; 09XC45;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)  
DE (Omp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
GN OMP OR RC1085.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cosserat P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
RL Science 293:2093-2098(2001).  
RN [2]  
RP SEQUENCE OF 33-1649 FROM N.A.  
RC STRAIN=Indian tick typhus, and Malish 7;  
RX MEDLINE=20393643; PubMed=10939649;  
RA Roux V., Raoult D.;  
RT "Phylogenetic analysis of members of the genus Rickettsia using the  
RT gene coding the outer-membrane protein rOmpB (ompB)";  
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).  
RN [3]  
RP SEQUENCE OF 353-1655 FROM N.A.  
RC STRAIN=Malish 7;  
RA Stenos J., Walker D.;

RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
RT australis, the most divergent rickettsia of the spotted fever group.",  
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
CC SIMILARITY).  
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
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CC  
-----  
DR EMBL: AF008659; AAL03623.1; -  
DR EMBL: AF123721; AAF34124.1; -  
DR EMBL: AF123726; AAF34129.1; -  
DR EMBL: AF149110; AAD39533.1; -  
DR PIR: E97835; E97835.  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR Pfam: PF03797; Autotransporter; 1.  
DR TIGRFAMs: TIGR01414; autotrans\_bar1; 2.  
KW Antigen; S-layer; Cell wall; Complete proteome.  
FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.  
FT VARIANT 61 1655 32 kDa BETA PEPTIDE.  
FT VARIANT 75 75 P -> A (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 78 78 G -> S (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 251 251 K -> N (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 413 413 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 959 959 N -> D (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 988 988 I -> V (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 1139 1139 A -> T (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
FT CONFLICT 353 354 KD -> GH (IN REF. 3).  
FT CONFLICT 776 776 F -> S (IN REF. 3).  
FT CONFLICT 1159 1159 E -> D (IN REF. 3).  
FT CONFLICT 1177 1177 G -> S (IN REF. 3).  
FT CONFLICT 1492 1492 H -> R (IN REF. 3).  
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;  
  
Query Match 6.8%; Score 141; DB 1; Length 1655;  
Best Local Similarity 24.0%; Pred. No. 1.7;  
Matches 98; Conservative 50; Mismatches 178; Indels 82; Gaps 20;  
  
QY 49 ASANNVDFVRYD---TVEFLSADTKTYYN---VESKDN-----KTEVYKIGAKT 94  
DB 426 SNPNPTAGVITFDANGTLASASADANVAVTNNITAIASGAGVQLSGTHAEELRLGNAG 485  
QY 95 SVIREKGGKLTGDKG-----ENGSTFDEGGLVTKKEYIDAVNKAQWRKKTITAN 146  
DB 486 SVFLADGTYINGVNOTALYVGLAAGTITLDSATITG---DIGNAG-----AALQ 537  
QY 147 GQTQADKFEVTV-----SGTNVTFASGKGTATVSKDQGNITVMDV----- 190  
DB 538 GITLANDATKTLTGANIGANGTINFGANGTITLTS--TQNNITVDEDLAINDQT 595  
QY 191 NVGALNVNOLONGSMULDSKAVAGSSGKVIAGVSPSKGM-DEYVIN--AGNN--I 244  
DB 596 GYVDASSLTNAQTTLTINGKIGTGVGANKKTLGQFNIGSSKTVLSDGVALINELVIGNGAV 655  
QY 245 EITNGKNIDATMTPO---FSSV-----SLGAGADAPLTVSDGALNVGSKDKKPV 295  
DB 656 QFAHNTYLTITTTAAAGQKTIIFNPVNNNTTLATGTNLGATPPLAEINIGSSGAANVD 715  
QY 296 RITNVAPGVKGDVTVNAQLKGVAQNLNRIIDNVG--NARAGIAQAIATAGLVG----- 348

DB 716 TVLWVGAVNL-VATNITTTDA---NVGSFIFNAGTNIIVSG-----TVGGQGNKRFNT 765  
QY 349 -AIVPGSMMAIGGCTRGEGAGYALIGYSSISDGGNMIITKIASGNSG 395  
DB 766 VALDNGTVYKFLGNATFNNGTITTAAN-STLDIGNGTYADAFVADGTC 812  
  
RESULT 14  
HLA\_SERMA  
ID HLA\_SERMA STANDARD; PRT; 1608 AA.  
AC P15320;  
DT 01-APR-1990 (Rel. 14, Created)  
DR 01-APR-1990 (Rel. 14, Last sequence update)  
DE 01-NOV-1990 (Rel. 16, Last annotation update)  
GN Hemolysin precursor.  
OS SHLA.  
OS Serratia marcescens.  
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC Enterobacteriaceae; Serratia.  
OX NCBI\_Taxid=615;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
RC STRAIN-SNB;  
RX MEDLINE=88257037; PubMed=3290200;  
RA Poole K., Schiebel E., Braun V.;  
RT "Molecular characterization of the hemolysin determinant of Serratia  
RT marcescens.";  
RL J. Bacteriol. 170:3177-3188(1988).  
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
CC DEFINED.  
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
CC REQUIRES SHLB FUNCTION.  
CC -1- SUBCELLULAR LOCATION: Outer membrane.  
CC -1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).  
CC  
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CC  
-----  
DR EMBL: M22618; AAA50323.1; -  
DR PIR: A28182; A28182.  
KW Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL 1 30  
FT CHAIN 1 1608 HEMOLYSIN.  
SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;  
  
Query Match 6.8%; Score 140.5; DB 1; Length 1608;  
Best Local Similarity 21.5%; Pred. No. 1.8;  
Matches 110; Conservative 50; Mismatches 188; Indels 163; Gaps 20;  
  
QY 21 ELTRNH-----TKASATVKTAVLATLTFATVQASANNVDFVRYDVEFLSADTKTIV 75  
DB 591 EVTFHGLRLDNLSTTVKIDARTGTAENITSSHKRADSYOSSSTASELKSPTNLTLY 650  
QY 76 NVEKSD-NGKKT-----EVKIGAKTSVIREKGGKLVTKGDKGKNGSSSTDEGGLVT-----A 126  
DB 651 SHKADYIGSOVASGSELVSKEKGTINVK-----AAERQONIDEQRTALTVMGYA 701  
QY 127 KEVIDAVNKAQWRM-----KTT-----TANGQTQADKFEET 157  
DB 702 KEADGQYRAGLRLEHTRDSEKTRTENSASLSGGSVKLAERKQVTFSSGKLVAADGDA 761  
QY 158 VTSNTVTFASGKTTA-----T-----T 175  
DB 762 SVSGKNVFLAADDKTASNTETQRIKGGFYVYTGIDKRLGSGVEAGYENNKTKQAOSKAIF 821

```
OY 176 VSKDQGNITWYDVNVDALNVNOLNSGMNLSKAVAGSSGCKYISGNVSPSKGMDT 235
DB 822 SCSGVKGNLT-----INARDKLTQCGASHGVAGYEMNAGVYDHLAADASTTTTKTDVG 877
OY 236 VINAGNNIETRNKNKNDIATSMTPQSSVSLGA-----GADATLTLDVDA 283
DB 878 VNI-----GANDYSAVTRPVERAKAKKLDATGYINDIGGAPNVGLDGA 926
OY 284 LNVGSRK--DNKPRVITNVAPGV-----KEGDY-----TNYAOLKGYAONIN----- 323
DB 927 QCGSSEKSSSSQAVVSSVQAGSIDIMAKGEVRDGTQVQASKG--AVNLTADSHRSEAA 985
OY 324 NRIDNVDAARAGIAQATATAGLVAYLPKSKMAIG-----GCTTREGAGTAIGTSSSD 379
DB 966 NMQDQSSRDYTR-----GSAG--VRYVYTTTGSDDLVDPAKGEQGTQNSNSASQAVTGSID 1037
OY 380 GGNW-----IIGTASGNSRGHFGASA 401
DB 1038 AANGINAVKKDAIYGTALNGRGKRTAVNA 1068

RESULT 15
APU_THETU ID APU_THETU STANDARD: PRT: 1861 AA.
AC P38536:
DB 01-OCT-1994 (Rel. 30, Created)
DB 01-NOV-1995 (Rel. 32, Last sequence update)
DB 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amylopullulanase precursor (Alpha-amyglase/pullulanase) (Pullulanase
DE type II) [includes: Alpha-amyglase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase), Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan
DE glucanohydrolase), (Alpha-dextrin endo-1,6-alpha-glucosidase)].
GN AMYP.
OS Thermoanaerobacter thermosulfurogenes (Clostridium
OS thermosulfurogenes).
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacterium.
OX NCBI_TaxID=33950;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN=DSM 3896 / EML;
RX MEDLINE=9425298; PubMed=8195085;
RA Matuschek M., Butcherdt G., Sahm K., Bahl H.;
RT Pullulanase of Thermoanaerobacterium thermosulfurogenes EML
RT (Clostridium thermosulfurogenes): molecular analysis of the gene,
RT composite structure of the enzyme, and a common model for its
RT attachment to the cell surface."
RL J. Bacteriol. 176:3295-3302(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
CC linkages in pullulan and in amylopectin and glycogen, and the
CC alpha and beta-limit dextrans of amylopectin and glycogen.
CC -1- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
CC S-LAYER ANCHOR.
CC -1- PM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M57692; AAB00841.1; .
CC DR HSSP: Q08751; 1BVZ.
CC DR InterPro: IPR006589; Alp_amy1_cat_sub.
CC DR InterPro: IPR006048; Alp_amy1_C.
```

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DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR004185; Glyco_hydro_131g.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR InterPro: IPR001119; SLH.
DR Pfam: PF00128; alpha_amyglase_1.
DR Pfam: PF02806; alpha_amyglase_C_1.
DR Pfam: PF02903; alpha-amyglase_N_1.
DR Pfam: PF00041; fn3_2.
DR Pfam: PF02922; isoamylase_N_1.
DR Pfam: PF00395; SLH_3.
DR SMART: SM00642; Amyy_1.
DR SMART: SM00632; Amyy_C_1.
DR SMART: SM00060; FN3_2.
DR PROSITE: PS01072; SLH_DOMAIN; 3.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;
KW Multifunctional enzyme; Glycoprotein.
FT SIGNAL 1 35
FT CHAIN 36 1861
FT DOMAIN 928 1018
FT DOMAIN 1157 1248
FT ACT_SITE 628 628
FT ACT_SITE 657 657
FT ACT_SITE 734 734
FT DOMAIN 1681 1739
FT DOMAIN 1740 1803
FT DOMAIN 1804 1861
FT CONFLICT 1734 1734
FT SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;
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Query Match 6.8%; Score 139.5; DB 1; Length 1861;  
Best Local Similarity 20.1%; Pred. No. 2.4;  
Matches 101; Conservative 74; Mismatches 204; Indels 123; Gaps 24;

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OY 2 NKIYRIINMSALNA-----WVYVSELTNRHNFKRASATKTVANLATLPLATQASANNDF 56
DB 1208 NEVYVIDTSYVINGVYTKVAVDLSFNRRESNVYTKPDVPIKVIJFNTVPDYTPDA 1267
OY 57 VR-----TYD--TVEFLSADTKTTVNVNESHKDKGKTEYKI--GAKTSYKREKD-- 102
DB 1268 VNLACTFPNATWDPSPAQOMTKRIDNNTYGTTL-TLDEGTQIEKVRAGSMDEVKEQYONE 1326
OY 103 ----KLVTGDKDGENSGSTDE-----GEGLVAKAYIDA VNKAG--WRMKT 142
DB 1327 FASNKRKVIIVNCGNMENMINDVYRWRDIPFIYSPSSNMVYDSNISTMEYKGNYYKGA 1386
OY 143 TTANGOTGQADKFEIVTSGFNTVPASGK-----GTFAPVSKDDGNT-----V 186
DB 1387 VTINDSFYQDKNGVFTKDVSLNIVGNKIKIHVEPNDSVYGNDGRITELTKDIEIYI 1446
OY 187 MYDVNVGDALNVNOLNSGMNLSKAVAGSSGKV-ISGNVSPSKGKMDETVNI--NAGNN 243
DB 1447 RQENNSGGGTGNNNTSTSGSN--SSSTGSGSTGSTSITSNIS--NTSNTSNTIGVITKNGNV 1504
OY 244 IEITRN--GKNIDIAISMTPO--FSSVSLGACADAPTLSDVDALNVGS-----KRD 291
DB 1505 ITLTADKAKADLIIVNSKDKKVPFITTTIGEG--QOKVVOISDILDTISAANGKDIYIKSD 1563
OY 292 NKPVRIIT-----NVAPGREGDVTVAQLKGYAONLNRRIDVNDG----- 332
DB 1564 NASIALTYDALNOLNOLNSGMNLSKAVAGSSGKV-PNTVYVSLNVDITISGISGNVTLAKVE 1623
OY 333 ----ARAGIAQATATAGLVAYLPKSKMAIGGCTYREGAG-----YA 371
DB 1624 VTLNISKANDPDKVA-----VYYNPTTQOMEVYGKVDASSGTTTFNATHSQVAAFEVD 1679
OY 372 IGYSSISDGNW-----IIGTAS 390
DB 1680 KTFNDIKD--NMAKDVIEVLAS 1699
```

Search completed: October 6, 2003, 09:24:00  
Job time : 8.28512 secs

4-11-03

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 29.8927 Seconds  
(without alignments)  
3513.485 Million cell updates/sec

Title: US-09-771-382-25

Perfect score: 2063

Sequence: 1 MNKYRIINNSALNANWVVS.....TASGNSRGHFGASVGYQW 407

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1961	95.1	591	16	09JRI8
2	1957	94.9	591	2	09JPS7
3	1956.5	94.8	591	2	09AQF0
4	1949	94.5	591	2	09JQV3
5	1909.5	92.6	600	2	09JPS6
6	1903.5	92.3	592	2	09JPS9
7	1893.5	91.8	592	16	09JQW4
8	1890.5	91.6	590	2	09JPS3
9	1890.5	91.6	598	2	09JPS7
10	1890	91.6	595	2	09JPS0
11	1888.5	91.5	594	2	09JPS2
12	1887.5	91.5	594	2	09JQY4
13	1886	91.4	599	2	09JPS8
14	1884.5	91.3	594	2	09JPI3
15	1883	91.3	599	2	09JPS8
16	1879.5	91.1	594	2	09JPH7

17	1877.5	91.0	598	2	09JPS9	09JPI9	neisseria m
18	1869.5	90.6	592	2	09JQY2	09JQY2	neisseria m
19	1865.5	90.4	600	2	09JPS5	09JPS5	neisseria m
20	1864.5	90.4	598	2	09JPS0	09JPS0	neisseria m
21	1864.5	90.4	598	2	09JPS0	09JPS0	neisseria m
22	1860	90.2	599	2	09JPI0	09JPI0	neisseria m
23	1855.5	89.9	598	2	09JQY5	09JQY5	neisseria m
24	1848	89.6	589	2	09JQY1	09JQY1	neisseria m
25	1801	87.3	526	2	09JPS4	09JPS4	neisseria m
26	1801	87.3	530	2	09JPS1	09JPS1	neisseria m
27	660.5	32.0	1098	2	048152	048152	haemophilus
28	659.5	32.0	1096	2	08GM79	08GM79	haemophilus
29	638	30.9	2353	2	P71401	P71401	haemophilus
30	592.5	28.7	1210	2	08GM74	08GM74	haemophilus
31	583.5	28.3	1210	2	08GM75	08GM75	haemophilus
32	575.5	27.9	1204	2	08GM76	08GM76	haemophilus
33	413.5	20.0	1004	2	08GM77	08GM77	haemophilus
34	393.5	19.1	1002	2	08GM78	08GM78	haemophilus
35	379	18.4	1299	16	09F3X6	09F3X6	pasteurella
36	341	16.5	1190	16	09PC04	09PC04	xyella fas
37	332.5	16.1	2059	16	09PD50	09PD50	xyella fas
38	331	16.0	1588	16	08XDG4	08XDG4	escherichia
39	331	16.0	1778	16	08FCB2	08FCB2	escherichia
40	321	15.6	1461	16	08ZL64	08ZL64	salmonella
41	320	15.5	1107	16	09F2D8	09F2D8	salmonella
42	315.5	15.3	2314	2	08KQW8	08KQW8	moraxella c
43	307.5	14.9	641	16	08CKM1	08CKM1	yersinia pe
44	307.5	14.9	658	16	08ZHJ0	08ZHJ0	yersinia pe
45	301.5	14.6	2712	16	09F3X5	09F3X5	pasteurella

## ALIGNMENTS

RESULT 1

ID 09JRI8 PRELIMINARY; PRT; 591 AA.

AC 09JRI8;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DE Outer membrane protein GNA992 (Adhesin) (Nmha outer membrane protein).  
GN GNA992 OR NM00992 OR NMHA.  
OS Neisseria meningitidis, and  
OC Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B, BZ169, BZ83, and H44/76;  
RX MEDLINE=20175756; PubMed=10710306;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.;  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B., Cotton M.D., Uitterlind T.R., Khouli H., Qin H., Vamathevan J.,

RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,  
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
RT MC58.";  
RL Science 287:1809-1815(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;  
RA Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.,  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*.";  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.  
DR EMBL; AF226375; AAF42524.1; -  
DR EMBL; AF226375; AAF41395.1; -  
DR EMBL; AF226367; AAF42516.1; -  
DR EMBL; AF226370; AAF42519.1; -  
DR EMBL; AF226374; AAF42523.1; -  
DR EMBL; AF157611; AAK68872.1; -  
DR TIGR; MMB0992; -  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;  
  
Query Match 95.1%; Score 1961; DB 16; Length 591;  
Best Local Similarity 68.9%; Pred. No. 2.1e-86;  
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;  
  
QY 1 NKKIRIIMNSALNMAVYSELTRNHTKRASATVKTAVLATLFTVQASAN----- 52  
DB 1 NKKIRIIMNSALNMAVYSELTRNHTKRASATVKTAVLATLFTVQASANNEQEEDL 60  
QY 53 ----- 52  
DB 61 YLDPVQRTAVALIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIKQ 120  
QY 53 ----- 52  
DB 121 NGTNETYSLKRDLDLTJVSGETEKLFSANGKNVITSDTKGLNFAKETAGTNGDTTHLN 180  
QY 53 -----NYDE 56  
DB 181 GIGSLTDTLLNTGATVNTNDNTVDDEKKRAASVYKDVILNAGMNIKGVKPGTTASDNDVF 240  
QY 57 VRTYDVEFLSADRTTNTVNESKDKNGKTEVKGAKTSVIREKDGKLVTKDKGENSS 116  
DB 241 VRTYDVEFLSADRTTNTVNESKDKNGKTEVKGAKTSVIREKDGKLVTKDKGENSS 300  
QY 117 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTFASGKGTATV 176  
DB 301 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTFASGKGTATV 360  
QY 177 SKDDGNTITVYDVVGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 236  
DB 361 SKDDGNTITVYDVVGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 420  
QY 237 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVSGSKDKNKPVR 296  
DB 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVSGSKDKNKPVR 480  
QY 297 ITTNAVPGKEGDVNTVAOLKGVQNLNRRINDVDCNARAAGIAQAATATAGLVQAYLPGRSM 356  
DB 481 ITTNAVPGKEGDVNTVAOLKGVQNLNRRINDVDCNARAAGIAQAATATAGLVQAYLPGRSM 540  
QY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRGASASVGYOW 407  
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRGASASVGYOW 591

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Outer membrane protein GNA92.  
GN GNA92.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RA MEDLINE=20175756; PubMed=10710308;  
RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B.  
RT *Meningococcus* by Whole-genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226366; AAF42515.1; -  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;  
  
Query Match 94.9%; Score 1957; DB 2; Length 591;  
Best Local Similarity 68.7%; Pred. No. 3.3e-86;  
Matches 406; Conservative 1; Mismatches 0; Indels 184; Gaps 1;  
  
QY 1 NKKIRIIMNSALNMAVYSELTRNHTKRASATVKTAVLATLFTVQASAN----- 52  
DB 1 NKKIRIIMNSALNMAVYSELTRNHTKRASATVKTAVLATLFTVQASANNEQEEDL 60  
QY 53 ----- 52  
DB 61 YLDPVQRTAVALIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIKQ 120  
QY 53 ----- 52  
DB 121 NGTNETYSLKRDLDLTJVSGETEKLFSANGKNVITSDTKGLNFAKETAGTNGDTTHLN 180  
QY 53 -----NYDE 56  
DB 181 GIGSLTDTLLNTGATVNTNDNTVDDEKKRAASVYKDVILNAGMNIKGVKPGTTASDNDVF 240  
QY 57 VRTYDVEFLSADRTTNTVNESKDKNGKTEVKGAKTSVIREKDGKLVTKDKGENSS 116  
DB 241 VRTYDVEFLSADRTTNTVNESKDKNGKTEVKGAKTSVIREKDGKLVTKDKGENSS 300  
QY 117 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTFASGKGTATV 176  
DB 301 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTFASGKGTATV 360  
QY 177 SKDDGNTITVYDVVGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 236  
DB 361 SKDDGNTITVYDVVGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 420  
QY 237 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVSGSKDKNKPVR 296  
DB 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVSGSKDKNKPVR 480  
QY 297 ITTNAVPGKEGDVNTVAOLKGVQNLNRRINDVDCNARAAGIAQAATATAGLVQAYLPGRSM 356  
DB 481 ITTNAVPGKEGDVNTVAOLKGVQNLNRRINDVDCNARAAGIAQAATATAGLVQAYLPGRSM 540  
QY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRGASASVGYOW 407  
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRGASASVGYOW 591

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RESULT 3
Q9AOF0 PRELIMINARY; PRT; 592 AA.
AC Q9AOF0:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales.
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF125375; AAK09243.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 94.8%; Score 1956.5; DB 2; Length 592;
Best Local Similarity 68.6%; Pred. No. 3.5e-86;
Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;

QY 1 MNKIVRIINNSALNAVVSSELRNHTKRASATVKTAVLATLTFATVOASAN----- 52
DB 1 MNKIVRIINNSALNAVVSSELRNHTKRASATVKTAVLATLTFATVOASANERPCKD 60
QY 53 ----- 52
DB 61 LYDPLVRLTAVAVLVNSDKEGTGEKEVEENSDMAVVFNEKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
DB 121 NGNTFTYSLKLDLTLSVGTETKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 180
QY 53 -----NVD 55
DB 181 NGIGSTLTDLTLNTGATTTNVTNDNVTDDEKKRAASVQDVLNAGMNIRKGVKPGTTASDNDV 240
QY 56 FVRTYDVEFLSADTKTTTVNVEESKNGKTEVKIGAKTSVKEKDKLVTGDKGENGS 115
DB 241 VRTYDVEFLSADTKTTTVNVEESKNGKTEVKIGAKTSVKEKDKLVTGDKGENGS 300
QY 116 TDEGEGLVTAKEVIDAVNKAQGMKRTTTANGQTGAQDKFETVSGTNVTFASGKGTAT 175
DB 301 STDEGEGLVTAKEVIDAVNKAQGMKRTTTANGQTGAQDKFETVSGTNVTFASGKGTAT 360
QY 176 VSKDDGNTITVMDVNVGDALNVNOLNSGWNLSKRAVAGSSGKVIISGNVSPSKGMDTV 235
DB 361 VSKDDGNTITVMDVNVGDALNVNOLNSGWNLSKRAVAGSSGKVIISGNVSPSKGMDTV 420
QY 236 VTNNAANNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKKNRPV 295
DB 421 VTNNAANNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKKNRPV 480
QY 296 RITNVAPGVKEGDTVNAQOLKQVAVONLNINRIDVNDGNARAGIAQAIATAGLVAYLPKGS 355
DB 481 RITNVAPGVKEGDTVNAQOLKQVAVONLNINRIDVNDGNARAGIAQAIATAGLVAYLPKGS 540
QY 356 MAAGGGTTRGEAGYAIIGYSSISDGGWIIKGTASGNSRHFASASVGYOW 407
DB 541 MAAGGGTTRGEAGYAIIGYSSISDGGWIIKGTASGNSRHFASASVGYOW 592

RESULT 4
Q930Y3 PRELIMINARY; PRT; 591 AA.
ID Q930Y3
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AC Q930Y3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NHHA outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales.
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157606; AAK68867.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 94.5%; Score 1949; DB 2; Length 591;
Best Local Similarity 68.5%; Pred. No. 8e-86;
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;

QY 1 MNKIVRIINNSALNAVVSSELRNHTKRASATVKTAVLATLTFATVOASAN----- 52
DB 1 MNKIVRIINNSALNAVVSSELRNHTKRASATVKTAVLATLTFATVOASANEDEEDL 60
QY 53 ----- 52
DB 61 YLDPVLRTAVAVLVNSDKEGTGEKEVEENSDMAVVFNEKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
DB 121 NGNTFTYSLKLDLTLSVGTETKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
QY 53 -----NVD 56
DB 181 GIGSTLTDLTLNTGATTTNVTNDNVTDDEKKRAASVQDVLNAGMNIRKGVKPGTTASDNDV 240
QY 57 VRTYDVEFLSADTKTTTVNVEESKNGKTEVKIGAKTSVKEKDKLVTGDKGENGS 116
DB 241 VRTYDVEFLSADTKTTTVNVEESKNGKTEVKIGAKTSVKEKDKLVTGDKGENGS 300
QY 117 TDEGEGLVTAKEVIDAVNKAQGMKRTTTANGQTGAQDKFETVSGTNVTFASGKGTAT 176
DB 301 TDEGEGLVTAKEVIDAVNKAQGMKRTTTANGQTGAQDKFETVSGTNVTFASGKGTATV 360
QY 177 SKDDGNTITVMDVNVGDALNVNOLNSGWNLSKRAVAGSSGKVIISGNVSPSKGMDTV 236
DB 361 SKDDGNTITVMDVNVGDALNVNOLNSGWNLSKRAVAGSSGKVIISGNVSPSKGMDTV 420
QY 237 NINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKKNRPV 296
DB 421 NINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKKNRPV 480
QY 297 ITNVAPGVKEGDTVNAQOLKQVAVONLNINRIDVNDGNARAGIAQAIATAGLVAYLPKGS 356
DB 481 ITNVAPGVKEGDTVNAQOLKQVAVONLNINRIDVNDGNARAGIAQAIATAGLVAYLPKGS 540
QY 357 MAAGGGTTRGEAGYAIIGYSSISDGGWIIKGTASGNSRHFASASVGYOW 407
DB 541 MAAGGGTTRGEAGYAIIGYSSISDGGWIIKGTASGNSRHFASASVGYOW 591

RESULT 5
Q9JPS6 PRELIMINARY; PRT; 600 AA.
ID Q9JPS6
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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DT 01-OCr-2002 (TREMBLrel. 22, last annotation update)  
DE Outer membrane protein GMA992.  
GN GMA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Commanduci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santilli L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226371; AAF2520.1; -.  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1  
SQ SEQUENCE 600 AA; 62762 MW; 362556963E0596CD1 CRC64;

Query Match	92.6%	Score 1909.5	-DB 2	Length 600
Best Local Similarity	66.5%	Pred. No. 6.4e-84		
Matches 399	Conservative 2	Mismatches 6	Indels 193	Gaps 1

QY	1	MNKYIRIIMNSALNAAVYVSELTNRHHTKRASVYTAVALATLFTFTVOASA-----	51
Db	1	MNKYIRIIMNSALNAAVYVSELTNRHHTKRASVYTAVALATLFTFTVOASA-----	60
QY	52	-----	51
Db	61	EEEEYLEBPVRTAPVLSFYSDAEDTGEKEVENTNMGIYFPKNGVYIKAGTITLKAGDNLK	120
QY	52	-----	51
Db	121	IKONTIDENTNASSFTYSLKKELTDLTSVGTREKLSFGANGNRKNVITSDTKGLNFAKETAGT	180
QY	52	-----	51
Db	181	NGDTTTHLNGIGSTLTDTLTFLTGATNTVNDNVDDEKKRAASVADVLNAGNNIKGVKPG	240
QY	52	---NNVDFVRTYDVEFLSADTKTTTVNVESSKDNKGKTEYKIGAKTSVIREKDDKLYTG	107
Db	241	TTASDNDVDFVHTYDVEFLSADTKTTTVNVESSKDNKGKTEYKIGAKTSVIREKDDKLYTG	300
QY	108	KDKENSSSTDEGBGLVYAKEVIDAVNKAQMRMKTYYTANGOTGQADKEETVYSGTNVTPA	167
Db	301	KGKGENSSTDEGBGLVYAKEVIDAVNKAQMRMKTYYTANGOGQADKEETVYSGTNVTPA	360
QY	168	SGKGTATVSKDDOGNITVAVGDVNVGDLANTNOLNSGAMNIDSKVAASSGKVISGNVSP	227
Db	361	SGKGTATVSKDDOGNITVAVGDVNVGDLANTNOLNSGAMNIDSKVAASSGKVISGNVSP	420
QY	228	SKGMDFTVNLNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTVSDGALNVG	287
Db	421	SKGMDFTVNLNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTVSDGALNVG	480
QY	288	SKKDNKPVRTNVAAPVKEGCVTVNAQDLKGYAONLNRFIDVNDGNARAGIAQAIATAGLV	347
Db	481	SKKDNKPVRTNVAAPVKEGCVTVNAQDLKGYAONLNRFIDVNDGNARAGIAQAIATAGLV	540
QY	348	QAYLPGKSMALGGGTYRGEAGVAILGYSSIDGGWMLIKGPAAGNSRCHFGASASVGVQW	407
Db	541	QAYLPGKSMALGGGTYRGEAGVAILGYSSIDGGWMLIKGPAAGNSRCHFGASASVGVQW	600

RESULT 6  
Q9JPS9

TD	09JPS9	PRELIMINARY;	PRT;	592 AA.
AC	09JPS9.			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Outer membrane protein GNA92.			
GN	GNA92.			
OS	Neisseria meningitidis.			
CC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID:487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=860800;			
RA	MEDLINE=20175756; PubMed=10710308;			
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,			
RA	Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,			
RA	Broeker M., Hundt E., Knapp B., Blahr E., Mason T., Tettelin H.,			
RA	Hood D.W., Ueffing A.C., Saunders N.J., Granoff D.M., Venter C.,			
RA	Moxon E.R., Grandi G., Rappuoli R.;			
RT	"Identification of Vaccine Candidates Against Serogroup B			
RT	Meningococcus by Whole-Genome Sequencing.";			
RL	Science 287:1816-1820(2000).			
DR	EMBL: AF226361; AAF42510.1; -			
DR	InterPro: IPR005594; Yada.			
DR	Pfam: PF03895; Yada; 1.			
QO	SEQUENCE 592 AA; 61917 MW; 4A347151AFD3C879 CRC64;			

Query Match	92.38;	Score 1903.5;	DB 2;	Length 592;
Best Local Similarly	67.48;	Pred. No. 1.2e-83;		
Matches 399;	Conservative 2;	Mismatches 6;	Indels 185;	Gaps 2

OY		1	MNKIYRIIMNSALNAAVVVSELTNRHTRKASVTATVALTLEFTVOASA-----	51
Dd		1	MNKIIRIIIMNSALNAAVAASELTRNHTRKASATYKTAVLATLLEFATVOANATDEDEEBEL	60
OY		52	-----	51
Dd		61	ESVGRSVGSIQASWMSGELLEJTSLSMTNDSKFEVDPIYVITLKAGDNLKIÖNTENT	120
OY		52	-----	51
Dd		121	NASSFTYSLKDDLYGLINVEITEKLSPGANGKKVNIISDTKGLNFAKETAGTNGDTYHLN	180
OY		52	-----NNDF	56
Dd		181	GIGSTLTIDMLNFCAATTNTNDNVTDDEKKRAASYKYDVLNANGMNIKGVKPCTTASDNDF	240
OY		57	VRTDPVEEFLSADPTKTTTVNYESKDNGCKTEVIKGAKTSVIREKDGKLVTKDKGENSS	116
Dd		241	VRTDPYEFLSADPTKTTTVNYESKDNGCKTEVIKGAKTSVIREKDGKLVTKDKGENSS	300
OY		117	TDEBEGVLTAKEVIDAANKAGRMKTTTANGQTGOADKFETVTSGTNYTFASGKTPATV	176
Dd		301	TDEBEGVLTAKEVIDAANKAGRMKTTTANGQTGOADKFETVTSGTNYTFASGKTPATV	360
OY		177	SKDDOGNTTWYDVNVDGDLNVNOLONGSMULDSPAIVSGSSGKITSGANVSFSKGMDETV	236
Dd		361	SKDDOGNTTWYDVNVDGDLNVNOLONGSMULDSPAIVSGSSGKITSGANVSFSKGMDETV	420
OY		237	NINANGNNEIETRKNCKNIDIATSMTPOFSSVSLGAGADPTEJSVDG-DALNYSKKDKNPV	295
Dd		421	NINANGNNEIETRKNCKNIDIATSMTPOFSSVSLGAGADPTEJSVDKGLNYSKRANKPV	480
OY		296	RITNVABGVKGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKS	355
Dd		481	RITNVABGVKGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKS	540
OY		356	MMAIIGGETYREAGYAIGYSSISDGGWNITKGTASGNSRGHFPGASASGYOM	407
Dd		541	MMAIIGGETYREAGYAIGYSSISDGGWNITKGTASGNSRGHFPGASASGYOM	592

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RESULT 7
09JOM4 PRELIMINARY; PRT: 592 AA.
ID 09JOM4;
AC 09JOM4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Putative surface fibril protein (Outer membrane protein GNA992).
GN MNA1200 OR GNA992
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=65699, 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Klee S.R., Achtmann M., James K.D., Bentley S.D., Churcher C.,
RA Davis R.M., Davis P., Devlin K., Felkwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 2491."
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=205900, B2133, F6124, AND 22491;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt B., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AL162755; CAB84461.1; -.
DR EMBL: AF226357; AAF42506.1; -.
DR EMBL: AF226365; AAF42514.1; -.
DR EMBL: AF226373; AAF42522.1; -.
DR EMBL: AF226386; AAF42535.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
KW Complete proteome.
SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match 91.8%; Score 1893.5; DB 16; Length 592;
Best Local Similarity 66.9%; Pred. No. 3.7e-83;
Matches 396; Conservative 4; Mismatches 7; Indels 185; Gaps 2;

QY 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOASA----- 51
DB 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOANATDEDEEEL 60
QY 52 ----- 51
DB 61 ESVQRSVVGSIQASMEGSGELETISLMTNDSKEFDPYIVYTLKAGDNLIKQNTNENT 120
QY 52 ----- 51
DB 121 NASSFTYSLKDLTLGLINNETEKLSPGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
QY 52 -----NNVDF 56
DB 181 GIGSTLTDLTLAGSSASHVDAGNOSTHYTRRAASIKVDLNGWNIKGVKGTGSTGQSENVDP 240

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QY 57 VRTYDVEEISADTKFTTNNVESKDNKGTTEVKGAKTSYIKERDKLVTGKNGENSS 116
DB 241 VRTYDVEEISADTKFTTNNVESKDNKGTTEVKGAKTSYIKERDKLVTGKNGENSS 300
QY 117 TDEGELVYRAKEVIDAVNNRAGRMKTTTANGQFGQADKPEFTYVSGTNVTFASRGTTATV 176
DB 301 TDEGELVYRAKEVIDAVNNRAGRMKTTTANGQFGQADKPEFTYVSGTNVTFASRGTTATV 360
QY 177 SKDDGNITFYVYVNGDALNVNQLNSGNNLSKRVAGSSGAVISGNVSPSKGMDFTV 236
DB 361 SKDDGNITFYVYVNGDALNVNQLNSGNNLSKRVAGSSGAVISGNVSPSKGMDFTV 420
QY 237 NINAGNNIETTRGNKIDATSMTPQFSVSLGAGADAPTLVSQGD-ALNVGSKKDNKPV 295
DB 421 NINAGNNIETTRGNKIDATSMTPQFSVSLGAGADAPTLVSQGDALNVGSKKDNKPV 480
QY 296 RITNVAPGVKEGVTNVAQLKGYAQLNLRNIDVNGNARAGIAQATAGLVQATYLPKGS 335
DB 481 RITNVAPGVKEGVTNVAQLKGYAQLNLRNIDVNGNARAGIAQATAGLVQATYLPKGS 540
QY 356 MMAIGGTYRGEAGYAIQVSSISDGNWITKTPASGNSRHFASASVGYQW 407
DB 541 MMAIGGTYRGEAGYAIQVSSISDGNWITKTPASGNSRHFASASVGYQW 592

RESULT 8
09JPS3 PRELIMINARY; PRT: 590 AA.
ID 09JPS3;
AC 09JPS3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt B., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 91.6%; Score 1890.5; DB 2; Length 590;
Best Local Similarity 67.1%; Pred. No. 5.1e-83;
Matches 396; Conservative 4; Mismatches 7; Indels 183; Gaps 2;

QY 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOASA----- 51
DB 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOANATDEDEEEL 60
QY 52 ----- 51
DB 61 DPOQRTAVAVLIIVNSDEKGEKEKEVENSMDAVYFNEKGVLTAGTTLKAGDNLIKQNG 120
QY 52 ----- 51
DB 121 TNFTYSLKDLTDLTGVSGETEKLSPSANGKNVNTSPTKGLNFAKETAGTNGDTTVHLNGI 180

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OY 52 -----NNVDPR 58
DB 181 GSTLTDLTLLTGATNTVNDVDEKKRAASVKDVLNAGNNIKGVPGTTASDNVDPR 240
OY 59 TYDVEFLSADTKTTTNNVESKDNKKTVEYKIGAKTSYIKEDKGLVTKDKGENGSSTD 118
DB 241 TYDVEFLSADTKTTTNNVESKDNKKTVEYKIGAKTSYIKEDKGLVTKDKGENGSSTD 300
OY 119 EGBELVTAKEVIDAVNKAQRMKTTTANGOTGQADKFEYTVSGTNVTFASGKGTATVSK 178
DB 301 EGBELVTAKEVIDAVNKAQRMKTTTANGOTGQADKFEYTVSGTNVTFASGKGTATVSK 360
OY 179 DDGQNTVPMYDYNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKGMDENYNI 238
DB 361 DDGQNTVPMYDYNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKGMDENYNI 420
OY 239 NAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLISYDGD-ALNVGSKDKPKVRI 297
DB 421 NAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLISYDDEGALNVGSKDKPKVRI 480
OY 298 TNVAPGVKEDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPKSKM 357
DB 481 TNVAPGVKEDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPKSKM 540
OY 358 AIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 407
DB 541 AIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 590
```

## RESULT 9

```
O9JPR7 PRELIMINARY: PRT: 598 AA.
AC O9JPR7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SW2107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rapunoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226385; AAF42534.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
```

```
Query Match 91.6%; Score 1890.5; DB 2; Length 598;
Best Local Similarity 66.4%; Pred. No. 5.1e-83;
Matches 397; Conservative 2; Mismatches 8; Indels 191; Gaps 2;
OY 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTPATVOASA----- 50
DB 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTPATVOASTTDDDDLYLE 60
OY 51 ----- 50
DB 61 PVQRTAPVLSFHADESGTEGKEVIGNTNLGIYFDEKRVLKAGTTTLKAGDNLKIKONTDE 120
```

```
OY 51 ----- 50
DB 121 NFDENTNASSFTYSLKAKDLDTLSYTEKLSFGANGKKNITSDTKGLNFAKETAAGTNGD 180
OY 51 ----- 50
DB 181 TTVALNGISLTFLDTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNNIKGVKGTGSTGQ 240
OY 51 ANNDVFRYTYDVEFLSADTKTTTNNVESKDNKKTVEYKIGAKTSYIKEDKGLVTKDK 110
DB 241 SENDDFVRYTYDVEFLSADTKTTTNNVESKDNKKTVEYKIGAKTSYIKEDKGLVTKDK 300
OY 111 GENGSSTDEGGLVTAKEVIDAVNKAQRMKTTTANGOTGQADKFEYTVSGTNVTFASGK 170
DB 301 GENGSSTDEGGLVTAKEVIDAVNKAQRMKTTTANGOTGQADKFEYTVSGTNVTFASGK 360
OY 171 GTTATVSKDDGQNTVPMYDYNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKG 230
DB 361 GTTATVSKDDGQNTVPMYDYNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKG 420
OY 231 KMDETVNNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLISYDGD-DLNVGSK 289
DB 421 KMDETVNNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLISYDGDGLNVGSK 480
OY 290 KDNKPVRTTNVAPGVKEDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVQ 349
DB 481 DANKPVRTTNVAPGVKEDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVQ 540
OY 350 YLPKSKMMAIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 407
DB 541 YLPKSKMMAIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 598
```

## RESULT 10

```
O9JPH0 PRELIMINARY: PRT: 595 AA.
AC O9JPH0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=528; and 1000;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rapunoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226360; AAF42509.1; -.
DR EMBL; AF226356; AAF42505.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;
```

```
Query Match 91.6%; Score 1890; DB 2; Length 595;
Best Local Similarity 66.6%; Pred. No. 5.4e-83;
Matches 396; Conservative 4; Mismatches 7; Indels 188; Gaps 2;
OY 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTPATVOASA----- 51
DB 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTPATVOANNTDDEDEL 60
```

```
QY 52 ----- 51
Db 61 EPVRSALVQFMIDKEGCEISTGDIGMSTYDDHNTLHGATVTLKADNLKIKONTD 120
QY 52 ----- 51
Db 121 ENTNASSFTYSLKKDLDTLSVGTIELSEFGANGKNVITSDTKGLNFAKKTAGTNGDTTV 180
QY 52 -----NN 53
Db 181 HLMGISTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGVKGTGSTGSEN 240
QY 54 VDFRTYDTVEFLSADTKTTTVNESKDNKKTETVKIGAKTSVKEKDGKLVTKGKGEN 113
Db 241 VDFRTYDTVEFLSADTKTTTVNESKDNKKTETVKIGAKTSVKEKDGKLVTKGKGEN 300
QY 114 GSSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGQTGAQDKFEVTSSTNTVTFASGKGT 173
Db 301 GSSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGQTGAQDKFEVTSSTNTVTFASGKGT 360
QY 174 ATYSKDDGNTTYMVTNVGDALNVNOLNSGWNLDKSAVAGSSGKVISGNSVPSKGM 233
Db 361 ATYSKDDGNTTYMVTNVGDALNVNOLNSGWNLDKSAVAGSSGKVISGNSVPSKGM 420
QY 234 ETVNINAGNIEITRNGKNIDIASMTPOFSSVSLGADAPTLSDVDG-ALNVGSKKN 292
Db 421 ETVNINAGNIEITRNGKNIDIASMTPOFSSVSLGADAPTLSDVDGALNVGSKDN 480
QY 293 KPVRTNVAPEKEDVTNVNQLKGYAQNLRNDVNGNARAGIAQAIATAGLVQAYLP 352
Db 481 KPVRTNVAPEKEDVTNVNQLKGYAQNLRNDVNGNARAGIAQAIATAGLVQAYLP 540
QY 353 GKSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
Db 541 GKSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 595
```

## RESULT 11

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Q9JPS2 PRELIMINARY; PRT; 594 AA.
ID Q9JPS2
AC Q9JPS2;
DT 01-OCT-2000 (TremBrel. 15, Created)
DT 01-OCT-2000 (TremBrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarcellì M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteil H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Grassoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
```

Query Match 91.5%; Score 1888.5; DB 2; Length 594;  
Best Local Similarity 66.7%; Pred. No. 6,4e-83;  
Matches 396; Conservative 3; Mismatches 8; Indels 187; Gaps 2;

```
QY 1 MNKIRITMNSALNAVVSSELPNHTKRASATYKAVLATLLEPATVOAS----- 50
Db 1 MNKIRITMNSALNAVVSSELPNHTKRASATYKAVLATLLEPATVOASTTDDDLYLE 60
QY 51 ----- 50
Db 61 PVQRTAPVLSFHADSEGTGKEVTEEDSNMCKVYFPDKKGLVLAGTITLAKGNLKIKNYDE 120
QY 51 ----- 50
Db 121 NTNASSFTYSLKKDLDTLSVETEKLSEFGANGKNVITSDTKGLNFAKKTAGTNGDTTVH 180
QY 51 -----ANNV 54
Db 181 LMGISTLTDLTLAGTAVTNDVTDDEKRRASVKNVYLNAGMNIKGVKPGTTASDNV 240
QY 55 DFRYTDVTEFLSADTKTTTVNESKDNKKTETVKIGAKTSVKEKDGKLVTKGKGEN 114
Db 241 DFRYTDVTEFLSADTKTTTVNESKDNKKTETVKIGAKTSVKEKDGKLVTKGKGEN 300
QY 115 SSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGQTGAQDKFEVTSSTNTVTFASGKGT 174
Db 301 SSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGQTGAQDKFEVTSSTNTVTFASGKGT 360
QY 175 TVSKDDGNTTYMVTNVGDALNVNOLNSGWNLDKSAVAGSSGKVISGNSVPSKGM 234
Db 361 TVSKDDGNTTYMVTNVGDALNVNOLNSGWNLDKSAVAGSSGKVISGNSVPSKGM 420
QY 235 TVNINAGNIEITRNGKNIDIASMTPOFSSVSLGADAPTLSDVDG-ALNVGSKKN 293
Db 421 TVNINAGNIEITRNGKNIDIASMTPOFSSVSLGADAPTLSDVDGALNVGSKDN 480
QY 294 PVRTNVAPEKEDVTNVNQLKGYAQNLRNDVNGNARAGIAQAIATAGLVQAYLP 353
Db 481 PVRTNVAPEKEDVTNVNQLKGYAQNLRNDVNGNARAGIAQAIATAGLVQAYLP 540
QY 354 KSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
Db 541 KSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594
```

## RESULT 12

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Q93QY4 PRELIMINARY; PRT; 594 AA.
ID Q93QY4
AC Q93QY4;
DT 01-DEC-2001 (TremBrel. 19, Created)
DT 01-DEC-2001 (TremBrel. 19, Last sequence update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;
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Query Match 91.5%; Score 1887.5; DB 2; Length 594;  
Best Local Similarity 66.5%; Pred. No. 7.1e-83;  
Matches 395; Conservative 5; Mismatches 7; Indels 187; Gaps 2;  
1 MNKIRITMNSALNAVVSSELPNHTKRASATYKAVLATLLEPATVOAS----- 50

```

Db 1 MNKIYRIIWSALNMAVAVSELTRNHRKRASATVATAVLAILLPATVOASTTDDDDLYLE 60
QY 51 ----- 50
Db 61 PVQRTAVVLSFRSDKEGTEKEVEDSNMGVYFDKKGVLITAGTITLKGADNLKIKONTNE 120
QY 51 ----- 50
Db 121 NTNNSPFTYSLKDLTDLTTSVTEKLSFSANSNKVNITSDTKGLNFAKTAETNGDTVH 180
QY 51 ----- 50
Db 181 LMGISGTLTDLTLTGATTNTNDVTDDEKKRAASVQDVLNAGNIGKVPCTTASDV 240
QY 55 DFPRTYDVEELADPTKTTTVNVEESKDKNGKTEVKIGAKTSVKEKDKLVTGKDGENG 114
Db 241 DFPRTYDVEELADPTKTTTVNVEESKDKNGKTEVKIGAKTSVKEKDKLVTGKDGEND 300
QY 115 SSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTVTFASGKTGA 174
Db 301 SSTKGEGLVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTVTFASGKTGA 360
QY 175 TVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSKGKMD 234
Db 361 TVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSKGKMD 420
QY 235 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVGSKDKN 293
Db 421 TVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDKN 480
QY 294 PVRTTNVAPGVKEDGVTNVAQLKGYAONLNRRIDNVGNARAGIAQAIATAGLVAYLP 353
Db 481 PVRTTNVAPGVKEDGVTNVAQLKGYAONLNRRIDNVGNARAGIAQAIATAGLVAYLP 540
QY 354 KSMAIGGCTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 407
Db 541 KSMAIGGCTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 594

RESULT 13
Q9JPR8 PRELIMINARY: PRT: 599 AA.
AC 09JPR8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhba outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RX Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16BEBF53C1970C CRC64;

Query Match          91.4%; Score 1886; DR 2; Length 599;
Best Local Similarity 66.1%; Pred. No. 8; Se-83;
Matches 396; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

QY 1 MNKIYRIIWSALNMAVAVSELTRNHRKRASATVATAVLAILLPATVOASA----- 51
Db 1 MNKIYRIIWSALNMAVAVSELTRNHRKRASATVATAVLAILLPATVOANATDEDEEEL 60
QY 52 ----- 51
Db 61 EPVRSALVLQEMIDKEGNGENESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKONTN 120
QY 52 ----- 51
Db 121 KNTNENTDSEFTYSLKDLTDLTTSVTEKLSFGANGKNVNITSDTKGLNFAKETAGTNG 180
QY 52 ----- 51
Db 181 DTTVHLNGISGTLTDLTLTGATTNTNDVTDDEKKRAASVQDVLNAGNIGKVPCTT 240
QY 52 --NNVDYFRTYDVEELADPTKTTTVNVEESKDKNGKTEVKIGAKTSVKEKDKLVTKGD 109
Db 241 ASDNVDFHTYDVEELADPTKTTTVNVEESKDKNGKTEVKIGAKTSVKEKDKLVTKGK 300
QY 110 KGENSSSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTVTFASG 169
Db 301 KGENSSSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTVTFASG 360
QY 170 KGTATVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSK 229
Db 361 KGTATVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSK 420
QY 230 GKMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSVDG-DALNVGS 288
Db 421 GKMDETVNIAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSVDGKALNVGS 480
QY 289 KDKNFPVRTTNVAPGVKEDGVTNVAQLKGYAONLNRRIDNVGNARAGIAQAIATAGLVQ 348
Db 481 KDKNFPVRTTNVAPGVKEDGVTNVAQLKGYAONLNRRIDNVGNARAGIAQAIATAGLVQ 540
QY 349 AYLPGKSMAIIGGCTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 407
Db 541 AYLPGKSMAIIGGCTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 599

RESULT 14
Q9JPI3 PRELIMINARY: PRT: 594 AA.
AC 09JPI3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88; and B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

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RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226376; AAF42525.1; -;  
DR EMBL; AF226369; AAF42518.1; -;  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 91.3%; Score 1884.5; DB 2; Length 594;  
Best Local Similarity 66.5%; Pred. No. 9, 9e-83;  
Matches 395; Conservative 3; Mismatches 9; Indels 187; Gaps 2;

QY 1 MNKIYRIIWNLSALNMAVYVSELTNRNHTKRASATVATATLLFATVOAS----- 50  
DB 1 MNKIYRIIWNLSALNMAVYVSELTNRNHTKRASATVATATLLFATVOASTTDDDDLYLE 60  
QY 51 ----- 50  
DB 61 PVQRTAPVLSFHADSEGTGEKEVTEDSNMNGVYFEDKGVLTAGTITLLKAGDNLKIKQNTD 120  
QY 51 ----- 50  
DB 121 NTNASSFTYSLKDLTDLTSVETEKLSFGANGKKNVITSDTKGLNPAKETAGTNGDTVH 180  
QY 51 -----ANV 54  
DB 181 LNCIGSTLTDTLLNTGATTNTNDVYTDDEKRAASVYKDVLANGMNKGKPGTTAASDV 240  
QY 55 DFEVRYDVEFLSADTKTTTVNVEESKDNKTEVKGATSVIKERDGLVTGDKGNG 114  
DB 241 DFEVRYDVEFLSADTKTTTVNVEESKDNKTEVKGATSVIKERDGLVTGDKGNG 300  
QY 115 SSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFEVTSGTNVTFAASKGT 174  
DB 301 SSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFEVTSGTNVTFAASKGT 360  
QY 175 TVSKDQDGNITVYVNGDALNVNOLNONGMNLDSKAVAGSSGVIISGNVSPSKGME 234  
DB 361 TVSKDQDGNITVYVNGDALNVNOLNONGMNLDSKAVAGSSGVIISGNVSPSKGME 420  
QY 235 TVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDG-ALNVGSKDNK 293  
DB 421 TVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDDEBALNVGSKDNK 480  
QY 294 PVRTINVAPEGVGVTVNAOLKGYAQNLRINDVNGNARAGIAQAIAATAGLVAYLP 353  
DB 481 PVRTINVAPEGVGVTVNAOLKGYAQNLRINDVNGNARAGIAQAIAATAGLVAYLP 540  
QY 354 KSMMAIGGTYRGEAGYALIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 407  
DB 541 KSMMAIGGTYRGEAGYALIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 15  
Q9JPS8 ID PRELIMINARY; PRT; 599 AA.  
AC Q9JPS8:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBL\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A22;  
RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scaletto V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
RA Galeotti C.L., Iuzzini E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarelli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Moxon E.R., Grandi G., Saunders N.J., Granoff D.M., Venter C.,  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226364; AAF42513.1; -;  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada; 1.  
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7E78E9 CRC64;

Query Match 91.3%; Score 1883; DB 2; Length 599;  
Best Local Similarity 66.1%; Pred. No. 1, 2e-82;  
Matches 396; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

QY 1 MNKIYRIIWNLSALNMAVYVSELTNRNHTKRASATVATATLLFATVOAS----- 50  
DB 1 MNKIYRIIWNLSALNMAVYVSELTNRNHTKRASATVATATLLFATVOANTDDEDEEYL 60  
QY 51 ----- 50  
DB 61 EPVKRTAVVLSFRSDEKTEGEKEVTEDSHMNGVYFDEKGVLLAKGTITLLKAGDNLKIKQNTD 120  
QY 51 ----- 50  
DB 121 ENTDENTNASSFTYSLKDLTDLTSVETEKLSFGANGKKNVITSDTKGLNPAKETAGTNG 180  
QY 51 ----- 50  
DB 181 DTTVHLNCGSTLTDTLLAASSSHVDAGQSTHYTAAIKVLANGMNKGKPGTTAASDV 240  
QY 51 -ANNVDEVRTYDVEFLSADTKTTTVNVEESKDNKTEVKGATSVIKERDGLVTGKD 109  
DB 241 QSENVDFVRTYDVEFLSADTKTTTVNVEESKDNKTEVKGATSVIKERDGLVTGKD 300  
QY 110 KGENGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFEVTSGTNVTFAAS 169  
DB 301 KGENGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFEVTSGTNVTFAAS 360  
QY 170 KGTATVSKDDGNTITVYVNGDALNVNOLNONGMNLDSKAVAGSSGVIISGNVSPSK 229  
DB 361 KGTATVSKDDGNTITVYVNGDALNVNOLNONGMNLDSKAVAGSSGVIISGNVSPSK 420  
QY 230 GRMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDG-DALNVGS 288  
DB 421 GRMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDKGALNVGS 480  
QY 289 KDNKRPVRTINVAPEGVGVTVNAOLKGYAQNLRINDVNGNARAGIAQAIAATAGLV 348  
DB 481 KDNKRPVRTINVAPEGVGVTVNAOLKGYAQNLRINDVNGNARAGIAQAIAATAGLV 540  
QY 349 AYLPGKSMMAIGGTYRGEAGYALIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 407  
DB 541 AYLPGKSMMAIGGTYRGEAGYALIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 599

Search completed: October 6, 2003, 09:30:39  
Job time : 32.8927 secs

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PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI: 2001-488774/53.  
 DR N-PSDB: AAS09175.  
 XX  
 PT New Nhba surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 8; 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhba  
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhba deletion mutant #3.  
 CC  
 XX  
 SQ Sequence 433 AA;

Query Match 100.0%; Score 2197; DB 22; Length 433;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-137;  
 Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIMNSALNAAWVSELTRNHTKRASATVKTAVLATLLEFATVOASANRAASVADY 60  
 DB 1 MNKIYRIIMNSALNAAWVSELTRNHTKRASATVKTAVLATLLEFATVOASANRAASVADY 60  
 QY 61 LNAAGNNTKGVKPGTASDNDVFRITDVEFLSADTKTTVNVESKNGKTEYKIGAKT 120  
 DB 61 LNAAGNNTKGVKPGTASDNDVFRITDVEFLSADTKTTVNVESKNGKTEYKIGAKT 120  
 QY 121 SVIEKDGKLVTKGDKGSGSTDEGEGLVTAKEVIDVNVKAGNRMKTTTANSGTGQADK 180  
 DB 121 SVIEKDGKLVTKGDKGSGSTDEGEGLVTAKEVIDVNVKAGNRMKTTTANSGTGQADK 180  
 QY 121 SVIEKDGKLVTKGDKGSGSTDEGEGLVTAKEVIDVNVKAGNRMKTTTANSGTGQADK 180  
 DB 121 SVIEKDGKLVTKGDKGSGSTDEGEGLVTAKEVIDVNVKAGNRMKTTTANSGTGQADK 180  
 QY 181 FEVTSGTNVTFASGKGTATVSKDDGNTVMYDVNGDALNVNQLNSGMNLSKAVA 240  
 DB 181 FEVTSGTNVTFASGKGTATVSKDDGNTVMYDVNGDALNVNQLNSGMNLSKAVA 240  
 QY 241 GSSGKVISGNVSPSKGKDETVNINAGNNEITRNGKNIDTATSTPQSSVSLGAGDA 300  
 DB 241 GSSGKVISGNVSPSKGKDETVNINAGNNEITRNGKNIDTATSTPQSSVSLGAGDA 300  
 QY 301 PTLVVDGDLNWSGSKDKNPKVRITNVAPGVKEGDVTNVAQLKGVAQNINNRIDNVGNAR 360  
 DB 301 PTLVVDGDLNWSGSKDKNPKVRITNVAPGVKEGDVTNVAQLKGVAQNINNRIDNVGNAR 360  
 QY 361 AGIAOAIATAGLVQAYLTPGKSMALIGGTYRGEAGYAIGSYSSISDGMWIIKGTASGNSR 420  
 DB 361 AGIAOAIATAGLVQAYLTPGKSMALIGGTYRGEAGYAIGSYSSISDGMWIIKGTASGNSR 420  
 QY 421 GHFGASASVGYOW 433  
 DB 421 GHFGASASVGYOW 433

RESULT 2  
 ID AAU06182 standard; Protein: 512 AA.  
 XX  
 AC AAU06182;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX

DE N. meningitidis PMC21 Nhba deletion mutant #1.  
 XX  
 KW Surface antigen Nhba; meningococcal disease; meningitis vaccine;  
 KW mutant; mutuin.  
 XX  
 OS Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FH Peptide 1..51  
 FH Protein /label= Signal\_peptide  
 FT 52..512  
 FT /label= Mature\_Nhba\_deletion\_mutant\_#1  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 XX  
 PN WO200155182-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PD 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PF 25-JAN-2000; 2000US-0177917.  
 XX  
 PR (UYOU ) UNIV QUEENSLAND.  
 XX  
 PA Peak IRA, Jennings MP;  
 XX  
 PI WPI: 2001-488774/53.  
 XX  
 DR N-PSDB: AAS09172.  
 XX  
 PT New Nhba surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12; Fig 5; 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhba  
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhba deletion mutant #1.  
 CC  
 XX  
 SQ Sequence 512 AA;

Query Match 97.7%; Score 2147.5; DB 22; Length 512;  
 Best Local Similarity 84.6%; Pred. No. 1.3e-133;  
 Matches 433; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIYRIIMNSALNAAWVSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52  
 DB 1 MNKIYRIIMNSALNAAWVSELTRNHTKRASATVKTAVLATLLEFATVOASANNETDLTSV 60  
 QY 53 ----- 52  
 DB 61 GTEKLSFGSANGKNVITSDFKGLNFAKETAGTNGDTVHLNGISLTLDTLNLTGATTNV 120  
 QY 53 ----- 101  
 DB 121 TNDNVTDEKRRASAVKDYLNAGNNTKGVKGTASDNDVFRITDVEFLSADTKTTTV 180  
 QY 102 NVESKDNKKTVEKIGAKTSYIKERDGLVTKGDKGSGSTDEGEGLVTAKEVIDAVNK 161  
 DB 181 NVESKDNKKTVEKIGAKTSYIKERDGLVTKGDKGSGSTDEGEGLVTAKEVIDAVNK 240  
 QY 162 AGWRMKTTTANGQGADKDFETVTSIGTVTASGKGTATVSKDDGNTVMYDVNGDA 221

DB 241 AGWRMKTATTANGOTGADKFEVTSCTNTVFASGKGTATVSGKDDGNTVMVDVWGDA 300  
QY 222 LNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIEITRNGKNIDI 281  
DB 301 LNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIEITRNGKNIDI 360  
QY 282 ATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKNPKPVRTNVAAPVKEGDTVAQL 341  
DB 361 ATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKNPKPVRTNVAAPVKEGDTVAQL 420  
QY 342 KGVANQLNNRINDVNDGNARAGIAQATATAGLVQAYLPGRKSMAIGGTYRGEAGYAGYS 401  
DB 421 KGVANQLNNRINDVNDGNARAGIAQATATAGLVQAYLPGRKSMAIGGTYRGEAGYAGYS 480  
QY 402 SISDGGNMIITKGTASGNSRGHFGASASVGYOW 433  
DB 481 SISDGGNMIITKGTASGNSRGHFGASASVGYOW 512

RESULT 3  
AAV27202  
ID AAV27202 standard; Protein; 591 AA.  
XX  
AC AAV27202;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX  
KM Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO936544-A2.  
PD 22-JUL-1999.  
XX  
PF 14-JAN-1999; 99MO-IB00103.  
PR 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Grandi G, Maignani V, Pizza M, Rappuoli R, Scarlato V;  
PI WPI; 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX  
PT New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX  
PS Claim 1: Page 62; 123pp; English.  
XX  
CC The invention provides proteins (AAV27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisseria  
CC bacteria, especially Neisseria meningitidis.  
XX  
SQ Sequence 591 AA;

Query Match 95.9%; Score 2108; DB 20; Length 591;  
Best Local Similarity 73.3%; Pred. No. 6.2e-131;  
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;  
QY 1 MNRIYIINMSALNANWVWVSELTNRNHTKRASATVKTAVLATLLEFATVQASAN-----52

DB 1 MNRIYIINMSALNANWVWVSELTNRNHTKRASATVKTAVLATLLEFATVQASANNEDEEDL 60  
QY 53 -----52  
DB 61 YLDPVORTAVAVLIVNSDKESTGEKEREVEENSMDAVYFNEKGYLTAREITLKAGDNLIKQ 120  
QY 53 -----52  
DB 121 NGTNFTYSLKKDLTLDSVCTEKLSPSANGKNVITSDTKGLNFAKETAGTNGDITVHLN 180  
QY 53 -----RAASVADVNLNAGNNINGVPRGTTASDNVDF 82  
DB 181 GIGSTLIDPLTLLNCGATTNTVNDVTDDEKKRAASVADVNLNAGNNINGVPRGTTASDNVDF 240  
QY 83 VRTYDVEEFLSADTKTTTVNVESSKDKGKTEVIGAKTSYIKEDKLVYTKDKGNGSS 142  
DB 241 VRTYDVEEFLSADTKTTTVNVESSKDKGKTEVIGAKTSYIKEDKLVYTKDKGNGSS 300  
QY 143 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEVTSCTNTVFASGKGTATV 202  
DB 301 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEVTSCTNTVFASGKGTATV 360  
QY 203 SKDDGNTIYMYDVNVDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKDETV 262  
DB 361 SKDDGNTIYMYDVNVDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGKDETV 420  
QY 263 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKNPKPV 322  
DB 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKNPKPV 480  
QY 323 ITNVAPEVKEGDTVAQLKGVANQLNNRINDVNDGNARAGIAQATATAGLVQAYLPGRKS 382  
DB 481 ITNVAPEVKEGDTVAQLKGVANQLNNRINDVNDGNARAGIAQATATAGLVQAYLPGRKS 540  
QY 383 MAIGGTYRGEAGYAGYSISDGGNMIITKGTASGNSRGHFGASASVGYOW 433  
DB 541 MAIGGTYRGEAGYAGYSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 4  
AAV23746  
ID AAV23746 standard; Protein; 591 AA.  
XX  
AC AAV23746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KM Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO931132-A1.  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98MO-AU01031.  
PR 12-DEC-1997; 97GB-0026398.  
PR (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
PI WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections

XX Claim 1; Page 127-128; 132pp; English.  
 PS  
 CC The present sequence represents a surface protein of *Neisseria*  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 XX  
 SQ Sequence 591 AA;

Query Match 95.9%; Score 2108; DB 20; Length 591;  
 Best Local Similarity 73.3%; Pred. No. 6 2e-131;  
 Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

QY 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVAVLATLLEFATVQASAN----- 52  
 DB 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVAVLATLLEFATVQASANNEQEDL 60  
 QY 53 ----- 52  
 DB 61 YIDPQRTVAVLIVNSDEGEGEKEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIQ 120  
 QY 53 ----- 52  
 DB 121 NGTNFTYSLKNDLJDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHIN 180  
 QY 53 -----RAASVKDVLNAGWNIKGVKPGTTASDNVE 82  
 DB 181 GIGSTLTDTLLNTGATFNTVNDNTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVE 240  
 QY 83 VETVDTVEFLSADTTTNNVESKNGKTEVYIAKTSVTEKKGKLVTKGDKENGSS 142  
 DB 241 VETVDTVEFLSADTTTNNVESKNGKTEVYIAKTSVTEKKGKLVTKGDKENGSS 300  
 QY 143 TDEGGLVTAKEVIDAVNKAQWRMKTITANGOTGADKFEYVTSNTVTFASGKGTATV 202  
 DB 301 TDEGGLVTAKEVIDAVNKAQWRMKTITANGOTGADKFEYVTSNTVTFASGKGTATV 360  
 QY 203 SKDDOGNTVTVDVNGDALNVNOLONGSWMNDSKRAVAGSSGKVTSGNVSPSKGMDTV 262  
 DB 361 SKDDOGNTVTVDVNGDALNVNOLONGSWMNDSKRAVAGSSGKVTSGNVSPSKGMDTV 420  
 QY 263 NINAGNNEITPNKGNIDIAISMTPOFSSVSLGAGADAPTLSVDGDALNVGSKKNKPVR 322  
 DB 421 NINAGNNEITPNKGNIDIAISMTPOFSSVSLGAGADAPTLSVDGDALNVGSKKNKPVR 480  
 QY 333 ITNVAQVKEGDDVTVAOLKGYAQNLLNNRIDVNDGNARAGIAQALATAGLVAYLPCKSM 382  
 DB 481 ITNVAQVKEGDDVTVAOLKGYAQNLLNNRIDVNDGNARAGIAQALATAGLVAYLPCKSM 540  
 QY 383 MAIGGGTYRGEAGYVIGYSSISDGGNMIITKGTASNSRCHFGASASVGYQW 433  
 DB 541 MAIGGGTYRGEAGYVIGYSSISDGGNMIITKGTASNSRCHFGASASVGYQW 591

XX Key  
 FH Peptide  
 FT 1..51  
 FT /label= Signal\_peptide  
 FT 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..108  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 52..591  
 FT /label= Mature\_Nhha  
 FT /note= "Predicted mature protein, specifically  
 FT claimed in claim 12"  
 FT 109..120  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 121..124  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT 125..188  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 189..210  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 211..229  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 230..236  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 237..591  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 PN WO20015182-A1.  
 PD 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF 25-JAN-2000; 2000US-0177917.  
 PR (UYOU ) UNIV QUEENSLAND.  
 PA  
 XX Peak IRA, Jennings MP;  
 PI WPI: 2001-488774/53.  
 DR N-PSDB; AAS09161.  
 DR  
 XX New Nhha surface antigen polypeptides and polynucleotides from  
 PT *Neisseria meningitidis*, useful in producing vaccines for treating or  
 PT preventing broad spectrum of *Neisseria meningitidis* -  
 PT  
 XX Claim 9, Fig 1; 91pp; English.  
 PS  
 PS The present invention relates to the isolation of novel *Neisseria*  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX  
 SQ Sequence 591 AA;

Query Match 95.9%; Score 2108; DB 22; Length 591;  
Best Local Similarity 73.3%; Pred. No. 6.2e-131;  
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

```
QY 1 MNKTYRIINMSALNANVVSSELTNRNHTKRASATVKTAVALTLLFATVOASAN----- 52
DB 1 MNKTYRIINMSALNANVVSSELTNRNHTKRASATVKTAVALTLLFATVOASANNEQEDDL 60
QY 53 ----- 52
DB 61 YLDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIKQ 120
QY 53 ----- 52
DB 121 NGTNFTYSLKKDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
QY 53 -----RAASVQDVNLNAGNINIKGVKPGTTASDNVD 82
DB 181 GIGSTLTDLTLNTGATTNTVNDVTDDEKKRAASVQDVNLNAGNINIKGVKPGTTASDNVD 240
QY 83 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENGS 142
DB 241 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENGS 300
QY 143 TDEGEGLYTAKEVYDAVNKAGWRMKTTPANGOTGQADKFEYVTSNTVTFASGKGTATV 202
DB 301 TDEGEGLYTAKEVYDAVNKAGWRMKTTPANGOTGQADKFEYVTSNTVTFASGKGTATV 360
QY 203 SKDDOGNITVMYDVNVGDLNVLNOLONGMINDSKAVAGSSGKVISGNVSPSKGMDERY 262
DB 361 SKDDOGNITVMYDVNVGDLNVLNOLONGMINDSKAVAGSSGKVISGNVSPSKGMDERY 420
QY 263 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPV 322
DB 421 NINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPV 480
QY 323 ITNVAPVKEGDTNVNVAOLKGYAQNINNRIDNVGDNARAGIAQAITAGLVQAYLPKGS 382
DB 481 ITNVAPVKEGDTNVNVAOLKGYAQNINNRIDNVGDNARAGIAQAITAGLVQAYLPKGS 540
QY 383 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 433
DB 541 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591
```

RESULT 6  
AA123737  
ID AAY23737 standard; Protein; 592 AA.

```
AC AAY23737;
XX
XX 08-SEP-1999 (first entry)
DT
XX A surface protein of Neisseria meningitidis.
DE
XX Surface protein; surface glycoprotein; infection; vaccine;
KM immunoreactive peptide.
XX
XX Neisseria meningitidis.
OS
XX
XX MO9931132-A1.
PN
XX 24-JUN-1999.
PD
XX 14-DEC-1998; 98MO-AU01031.
PE
XX 12-DEC-1997; 97GB-0026398.
PR
XX (ISIS-) ISIS INNOVATION LTD.
PA (ORQV) UNIT QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
PI
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XX WPI; 1999-418754/35.
DR N-PSDB; AAX85788.
DB
XX
XX
XX
XX Claim 1; Page 86-87; 132pp; English.
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS
```

The present sequence represents a surface protein of *Neisseria meningitidis* which is approximately 62 kDa. The *N. meningitidis* surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of *N. meningitidis* infection in humans. The *N. meningitidis* surface glycoproteins can also be used to prevent or treat *N. meningitidis* infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

Sequence 592 AA;

Query Match 95.7%; Score 2103.5; DB 20; Length 592;  
Best Local Similarity 73.0%; Pred. No. 1.2e-130;  
Matches 432; Conservative 1; Mismatches 1; Indels 159; Gaps 1;

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QY 1 MNKTYRIINMSALNANVVSSELTNRNHTKRASATVKTAVALTLLFATVOASAN----- 52
DB 1 MNKTYRIINMSALNANVVSSELTNRNHTKRASATVKTAVALTLLFATVOASANRRPRKD 60
QY 53 ----- 52
DB 61 YLDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
DB 121 QNCTNFTYSLKKDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 180
QY 53 -----RAASVQDVNLNAGNINIKGVKPGTTASDNVD 81
DB 181 NGIGSTLTDLTLNTGATTNTVNDVTDDEKKRAASVQDVNLNAGNINIKGVKPGTTASDNVD 240
QY 82 FVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENGS 141
DB 241 FVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENGS 300
QY 142 STDEGEGLYTAKEVYDAVNKAGWRMKTTPANGOTGQADKFEYVTSNTVTFASGKGTAT 201
DB 301 STDEGEGLYTAKEVYDAVNKAGWRMKTTPANGOTGQADKFEYVTSNTVTFASGKGTAT 360
QY 202 VSKDDOGNITVMYDVNVGDLNVLNOLONGMINDSKAVAGSSGKVISGNVSPSKGMDERY 261
DB 361 VSKDDOGNITVMYDVNVGDLNVLNOLONGMINDSKAVAGSSGKVISGNVSPSKGMDERY 420
QY 262 VNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPV 321
DB 421 VNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPV 480
QY 322 RITNVAPVKEGDTNVNVAOLKGYAQNINNRIDNVGDNARAGIAQAITAGLVQAYLPKGS 361
DB 481 RITNVAPVKEGDTNVNVAOLKGYAQNINNRIDNVGDNARAGIAQAITAGLVQAYLPKGS 540
QY 382 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 433
DB 541 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592
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RESULT 7  
AA57045  
ID AAY57045 standard; Protein; 591 AA.

```
AC AA57045;
XX
XX 21-FEB-2000 (first entry)
DT
```

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XX BASB029 amino acid sequence from N. meningitidis strain H44/76.
DE
XX
XX BASB029: Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KM infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 90
FT /note= "Encoded by AAT"
FT Misc-difference 92
FT /note= "Encoded by GAT"
FT Misc-difference 98
FT /note= "Encoded by AAC"
FT Misc-difference 108
FT /note= "Encoded by AATC"
FT Misc-difference 123
FT /note= "Encoded by ACA"
FT Misc-difference 269
FT /note= "Encoded by AAA"
FT Misc-difference 389
FT /note= "Encoded by CGT"
XX
XX WO958683-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
XX 13-MAY-1998; 98GB-0010276.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX
XX Ruelle J;
XX
XX WPI: 2000-053103/04.
XX
XX N-PSDB: AA239865.
XX
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal
XX
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
XX serogroup B strain H44/76. The BASB029 protein is homologous to the
XX Haemophilus influenzae surface fibril (HSF) protein. The invention
XX relates to BASB029 polynucleotide sequences (AA239864-239865) and
XX polypeptide sequences (AA237044-Y57045) and their immunogenic fragments.
XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria
XX meningitidis infection in a mammal. Compositions containing BASB029
XX polynucleotides and polypeptides are useful for generating an immune
XX response in an animal. A therapeutic composition comprising an antibody
XX directed against BASB029 is useful in treating humans with Neisseria
XX meningitidis disease. The polynucleotide is useful in the diagnosis of
XX the stage of infection, type of infection, susceptibility to an
XX infection which results from increased or decreased expression of the
XX polynucleotide, and for therapeutic or prophylactic purposes.
XX particularly genetic immunisation. Antibodies against BASB029
XX polynucleotides and polypeptides are also useful for treating infections
XX particularly bacterial infections. The protein is useful in the
XX screening and development of antibacterial drugs. Fused recombinant
XX protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX
XX
XX Sequence 591 AA:
XX
XX Query Match 95.6%; Score 2101; DB 21; Length 591;
XX Best Local Similarity 72.9%; Pred. No. 1.8e-130;
XX Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;
XX
XX 1 MKKIRITWNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVQASAN----- 52
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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Db 1 MNKIRITWNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVQASANNEQEDDL 60
QY 53 ----- 52
Db 61 YLDPYQRTAVAVLIVNSDEKGEKKEKVEDSNMAYFPEDEKGLVTRAREITLAKGDLKIKQ 120
QY 53 ----- 52
Db 121 NGSNFTYSLKKDLFDLTSVGTKEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTALN 180
QY 53 -----RAASYKDVLANGMNFKGKPGPTASDNDVF 82
Db 181 GIGSTLTDLTLLNTGATFNTVNDNTDDEKKRAASVAVDLNAGMNIKGVKPGPTASDNDVF 240
QY 83 VRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSYIKERKGLVTKGDKGENSS 142
Db 241 VRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSYIKERKGLVTKGDKGENSS 300
QY 143 TDEGGLVTAKEVIDAVKAKGRMKTTPANGOTGOADKFEETVSGTNVTFASGKTATV 202
Db 301 TDEGGLVTAKEVIDAVKAKGRMKTTPANGOTGOADKFEETVSGTNVTFASGKTATV 360
QY 203 SKDDOGNTTWTAVDVAVGALVNLQNSGMNLDKAAVAGSSGKVTISGVNPSKGMDET 262
Db 361 SKDDOGNTTWTAVDVAVGALVNLQNSGMNLDKAAVAGSSGKVTISGVNPSKGMDET 420
QY 263 NINAGNIEITRNGKNIDIASMPPOFSSVSLGACADAPTLISVDGDLNVGSKDKNRPYR 322
Db 421 NINAGNIEITRNGKNIDIASMTPOFSSVSLGACADAPTLISVDGDLNVGSKDKNRPYR 480
QY 323 ITNVAPEGKEDVTNVAOLKGAQNLNRRIDNVGDNARAGIAQATATAGLVQAVLPGKSM 382
Db 481 ITNVAPEGKEDVTNVAOLKGAQNLNRRIDNVGDNARAGIAQATATAGLVQAVLPGKSM 540
QY 383 MAIGGCTYRGEAGYALIGYSSISDGGNWTIKGASGNSRGHFGASASVGYQW 433
Db 541 MAIGGCTYRGEAGYALIGYSSISDGGNWTIKGASGNSRGHFGASASVGYQW 591

RESULT 8
AA006186
ID AA006186 standard; Protein; 502 AA.
XX
XX AA006186;
AC
XX
XX 24-OCT-2001 (first entry)
DE N. meningitidis PMC21 Nhba deletion mutant #4.
XX
XX Surface antigen Nhba; meningococcal disease; meningitis vaccine;
KM mutant; mutein.
XX
XX Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FH Peptide 1..49
FT /label= signal_peptide
FT Protein 50..502
FT /label= Mature_Nhba_deletion_mutant_#4
FT /note= "Predicted mature protein, specifically
XX claimed in claim 12"
XX
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX

```



PI Peak IRA, Jennings MP;  
 XX  
 DR WPI: 2001-488774/53.  
 N-PSDB; AAS09176.  
 XX  
 PT New Nhba surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 12: Fig 9: 91pp; English.  
 XX  
 CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhba  
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhba deletion mutant #4.  
 CC  
 XX  
 SQ Sequence 502 AA;  
 Query Match 95.5%; Score 2098.5; DB 22; Length 502;  
 Best Local Similarity 83.7%; Pred. No. 2.2e-130;  
 Matches 426; Conservative 0; Mismatches 0; Indels 83; Gaps 2;  
 QY 1 MNRIYRIINMSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASAN----- 52  
 DB 1 MNRIYRIINMSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASANLTKAGDNL 60  
 QY 53 ----- 52  
 DB 61 KIKQFTYSLKDLTDLTSVTEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 120  
 QY 53 -----RASVYKDVNLNGMNIKGVKPGTTASDNDFVETVTEFLSADTCTTVNVE 104  
 DB 121 GIGSTLTDRASVYKDVNLNGMNIKGVK-----NDFVETVTEFLSADTCTTVNVE 173  
 QY 105 SKDNGKTEYKIGAKTSVIEKDKLVTKGDKGENSSDEGEGLVTAKFVIDAVNKAQW 164  
 DB 174 SKNGKTEYKIGAKTSVIEKDKLVTKGDKGENSSDEGEGLVTAKFVIDAVNKAQW 233  
 QY 165 RAKTTTANGOTGQADFEVTSCTNVTFAVGKGTATVSKDQGNITVMDVNVGDALNV 224  
 DB 234 RAKTTTANGOTGQADFEVTSCTNVTFAVGKGTATVSKDQGNITVMDVNVGDALNV 293  
 QY 225 NOLONGSMNDSKAVVSSGKXVSGNVSPSKGMDDEVINAGNNIEITRNGKNIDTATS 284  
 DB 294 NOLONGSMNDSKAVVSSGKXVSGNVSPSKGMDDEVINAGNNIEITRNGKNIDTATS 353  
 QY 285 MPPOFSSVSLGAGADAPTLSDVDALNVGSKDKNFVRITNVAPGVKEGVTVAOLKGV 344  
 DB 354 MPPOFSSVSLGAGADAPTLSDVDALNVGSKDKNFVRITNVAPGVKEGVTVAOLKGV 413  
 QY 345 AQLNLRIDNVGNARAGIAQAIAITAGVQAYLPGKSMMAIGGGTYRGEAGVAGYSSIS 404  
 DB 414 AQLNLRIDNVGNARAGIAQAIAITAGVQAYLPGKSMMAIGGGTYRGEAGVAGYSSIS 473  
 QY 405 DGGNMIITKGTASGNSRGHGASASVGYOW 433  
 DB 474 DGGNMIITKGTASGNSRGHGASASVGYOW 502  
 RESULT 9  
 ID AAY23741  
 AC AAY23741 standard; Protein: 591 AA.  
 XX AAY23741;  
 XX

DT 08-SEP-1999 (first entry)  
 XX  
 DE A surface protein of Neisseria meningitidis.  
 XX  
 KW Surface protein; surface glycoprotein; infection; vaccine;  
 XX immunoreactive peptide.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN W09931132-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-AU01031.  
 XX  
 PR 12-DEC-1997; 97GB-0026398.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA;  
 XX  
 DR WPI: 1999-418754/35.  
 DR N-PSDB; AAX85793.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1: Page 104-106; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 XX  
 SQ Sequence 591 AA;  
 Query Match 95.4%; Score 2096; DB 20; Length 591;  
 Best Local Similarity 72.9%; Pred. No. 3.9e-130;  
 Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;  
 QY 1 MNRIYRIINMSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASAN----- 52  
 DB 1 MNRIYRIINMSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60  
 QY 53 ----- 52  
 DB 61 YLDPVLTAVAVLIIVNSDKEGTGKEKEVENSMDAVYFNEKGLTAREITLAKADNLKIKO 120  
 QY 53 ----- 52  
 DB 121 NGTINFTYSLKDLTDLTSVTEKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180  
 QY 53 -----RAASVYKDVNLNGMNIKGVKPGTTASDNVDF 82  
 DB 181 GIGSTLTDLTLNGATTNVTNDVWTDDEKRAASVYKDVNLNGMNIKGVKPGTTASDNVDF 240  
 QY 83 VRTYDIVERLSADTKTTTIVNVEKDKGKTEYKIGAKTSVIEKDKLVTKGDKGENSS 142  
 DB 241 VRTYDIVERLSADTKTTTIVNVEKDKGKTEYKIGAKTSVIEKDKLVTKGDKGENSS 300  
 QY 143 TDEGEGLVTAKFVIDAVNKAQWRAKTTTANGOTGQADFEVTSCTNVTFAVGKGTATV 202  
 DB 301 TDEGEGLVTAKFVIDAVNKAQWRAKTTTANGOTGQADFEVTSCTNVTFAVGKGTATV 360  
 QY 203 SKDDQGNITVMDVNVGDALNVNOLONGSMNDSKAVVSSGKXVSGNVSPSKGMDDEV 262  
 DB 361 SKDDQGNITVMDVNVGDALNVNOLONGSMNDSKAVVSSGKXVSGNVSPSKGMDDEV 420

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OY 263 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKPVR 322
|||
DB 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKPVR 480
|||
OY 333 ITNVA PGVEGDVTNVAOLKGVAVOQLNNRINDVGNARAGIAQAIAATAGLVQAYILPGKSM 382
|||
DB 481 ITNVA PGVEGDVTNVAOLKGVAVOQLNNRINDVGNARAGIAQAIAATAGLVQAYILPGKSM 540
|||
OY 383 MAIGGCTYRGEGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYOW 433
|||
DB 541 MAIGGCTYRGEGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYOW 591
|||
RESULT 10
AAU06175
ID AAU06175 standard; Protein: 591 AA.
XX AC AAU06175;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis EG329 surface antigen Nhha polypeptide sequence.
XX KM Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain EG329.
XX FH
XX FH Key location/Qualifiers
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..108
FT /label= V1
FT /note= "Variable region 1"
FT 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT 121..124
FT /label= V2
FT /note= "Variable region 2"
FT 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT 189..210
FT /label= V3
FT /note= "Variable region 3"
FT 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..591
FT /label= C5
FT /note= "Conserved region 5"
PN WO200155182-A1.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU00069.
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYOU ) UNITV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX DR MPI: 2001-488774/53.
XX DR N-PSDB; AAS09165.
XX PT New Nhha surface antigen polypeptides and polynucleotides from
```

```
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX SQ Sequence 591 AA;
XX
XX Query Match 95.4%; Score 2096; DB 22; Length 591;
XX Best Local Similarity 72.9%; Pred. No. 3.9e-130;
XX Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;
OY 1 MNKTYRIITWNSALNAAVYVSELTRNHTKRAATYKTAVALTLTLPATVQASAN----- 52
|||
DB 1 MNEITRIITWNSALNAAVYVSELTRNHTKRAATYKTAVALTLTLPATVQASANNEQEDTL 60
|||
OY 53 ----- 52
DB 61 YLDPVLRTAVLIVNSDEKTEGEKEKVEENSDMAVFEENEKGLTAREITLAKGNLKIQQ 120
|||
OY 53 ----- 52
DB 121 NGTNETYSLLKRLDILTSVTEKLSFSAANGKVNITSDTKLNAFAKETAGTNGDTYHLN 180
|||
OY 53 -----RAASVKDVLNAGWNIKGVKPGTASDNDVF 82
|||
DB 181 GIGSTLIDTLNLTGATNTVNDNVTDDKKRAASVKDVLNAGWNIKGVKPGTASDNDVF 240
|||
OY 83 VRTYDVEFLSADTKTTTVNVEESKDNKKEVKGAKTSYKEKDGKLVYTKDGENGSS 142
|||
DB 241 VRTYDVEFLSADTKTTTVNVEESKDNKKEVKGAKTSYKEKDGKLVYTKDGENGSS 300
|||
OY 143 TDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADKFEFVTSGTNTVTFASGKGTATV 202
|||
DB 301 TDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADKFEFVTSGTNTVTFASGKGTATV 360
|||
OY 203 SKDDGNTTVWYDVNVDGALNVNOLONGSNMILDSKAVAGSSGKVIISGNVSPSKGMDETV 262
|||
DB 361 SKDDGNTTVWYDVNVDGALNVNOLONGSNMILDSKAVAGSSGKVIISGNVSPSKGMDETV 420
|||
OY 263 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKPVR 322
|||
DB 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKPVR 480
|||
OY 323 ITNVA PGVEGDVTNVAOLKGVAVOQLNNRINDVGNARAGIAQAIAATAGLVQAYILPGKSM 382
|||
DB 481 ITNVA PGVEGDVTNVAOLKGVAVOQLNNRINDVGNARAGIAQAIAATAGLVQAYILPGKSM 540
|||
OY 383 MAIGGCTYRGEGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYOW 433
|||
DB 541 MAIGGCTYRGEGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYOW 591
|||
RESULT 11
AAU06183
ID AAU06183 standard; Protein: 513 AA.
XX AC AAU06183;
XX
```

DT 24-OCT-2001 (first entry)  
 XX N. meningitidis H41 Nhha deletion mutant.  
 DE N. meningitidis H41 Nhha deletion mutant.  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
 KM mutant; mutin.  
 XX Neisseria meningitidis strain H41.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..51  
 FT Protein /label= Signal\_peptide  
 FT 52..513  
 FT /label= Mature\_Nhha\_deletion\_mutant  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 XX  
 XX WO200155182-A1.  
 PN 02-AUG-2001.  
 PD  
 XX 25-JAN-2001: 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000: 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 XX Peak IRA, Jennings MP;  
 PI  
 XX WPI: 2001-488774/53.  
 DR N-PSDB: AAS09173.  
 XX  
 XX New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 PS Claim 12; Fig 6; 91pp: English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain H41 surface  
 CC antigen Nhha deletion mutant.  
 CC  
 SQ Sequence 513 AA:  
 Query Match 93.5%; Score 2055; DB 22; Length 513;  
 Best Local Similarity 81.7%; Pred. No. 1.6e-127;  
 Matches 419; Conservative 3; Mismatches 11; Indels 80; Gaps 2;  
 QY 1 MKKIYIINNSALNMAVYSELTRNHTKRASATVKTAVLATLFAVQASDA----- 51  
 DB 1 MKKIYIINNSALNMAVYSELTRNHTKRASATVKTAVLATLFAVQANADDEGLIN 60  
 QY 52 ----- 51  
 DB 61 ETEKLSFGANGKKVNIISDTKGLNFAKTAGTNGDTTHLNLGISTLTMMLNTGATTNV 120  
 QY 52 -----NRAASYKDVNLNAGWNITKGVKPGTTASDNVDFVETDYVEFLSADTFTTV 101  
 DB 121 TNDNVTDEKKRAASYKDVNLNAGWNITKGVKPGTTASDNVDFVETDYVEFLSADTFTTV 180  
 QY 102 NRESKNGKKTVEKTKIAKTSVIREKDGKLVGTGDKKENSSTDEGGGLYTAKEVIDAVNK 161  
 DB 181 NRESKNGKKTVEKTKIAKTSVIREKDGKLVGTGDKKENSSTDEGGGLYTAKEVIDAVNK 240

QY 162 AGMRKTTTANGOTGQADKFTVTSGTNTVTFASGKTATVSKDQGNITVAVDVAGDA 221  
 DB 241 AGMRKTTTANGOTGQADKFTVTSGTNTVTFASGKTATVSKDQGNITVAVDVAGDA 300  
 QY 222 LNVNQLNSGWNLDKRAVAGSSGKYISGVNPSKGMDEFTVINAGNNIEITRNKNIDI 281  
 DB 301 LNVNQLNSGWNLDKRAVAGSSGKYISGVNPSKGMDEFTVINAGNNIEITRNKNIDI 360  
 QY 282 ATSMTPQESSVSLGAGADAPTLSDVGD -ALNNGSKDKNKPVRITTNVAPGVKGGDYTNVAQ 340  
 DB 361 ATSMTPQESSVSLGAGADAPTLSDVGD -ALNNGSKDKNKPVRITTNVAPGVKGGDYTNVAQ 420  
 QY 341 LKGVAQNLNRRIDNDVGNARAGIAQIATAGLVQAVLPCKSMMAIGGTYRSEAGYAIQY 400  
 DB 421 LKGVAQNLNRRIDNDVGNARAGIAQIATAGLVQAVLPCKSMMAIGGTYRSEAGYAIQY 480  
 QY 401 SSISDGGNWIIRKGTASGNSRGHFGASASVGYQM 433  
 DB 481 SSISDGGNWIIRKGTASGNSRGHFGASASVGYQM 513  
 RESULT 12  
 AAU06184  
 ID AAU06184 standard; Protein: 407 AA.  
 XX  
 AC AAU06184:  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE N. meningitidis PMC21 Nhha deletion mutant #2.  
 XX  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
 KM mutant; mutin.  
 XX Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain H41 surface  
 CC antigen Nhha deletion mutant.  
 CC  
 SQ Sequence 513 AA:  
 Query Match 93.5%; Score 2055; DB 22; Length 513;  
 Best Local Similarity 81.7%; Pred. No. 1.6e-127;  
 Matches 419; Conservative 3; Mismatches 11; Indels 80; Gaps 2;  
 QY 1 MKKIYIINNSALNMAVYSELTRNHTKRASATVKTAVLATLFAVQASDA----- 51  
 DB 1 MKKIYIINNSALNMAVYSELTRNHTKRASATVKTAVLATLFAVQANADDEGLIN 60  
 QY 52 ----- 51  
 DB 61 ETEKLSFGANGKKVNIISDTKGLNFAKTAGTNGDTTHLNLGISTLTMMLNTGATTNV 120  
 QY 52 -----NRAASYKDVNLNAGWNITKGVKPGTTASDNVDFVETDYVEFLSADTFTTV 101  
 DB 121 TNDNVTDEKKRAASYKDVNLNAGWNITKGVKPGTTASDNVDFVETDYVEFLSADTFTTV 180  
 QY 102 NRESKNGKKTVEKTKIAKTSVIREKDGKLVGTGDKKENSSTDEGGGLYTAKEVIDAVNK 161  
 DB 181 NRESKNGKKTVEKTKIAKTSVIREKDGKLVGTGDKKENSSTDEGGGLYTAKEVIDAVNK 240

CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nmba deletion mutant #2.

XX Sequence 407 AA:

Query Match 92.9%; Score 2040; DB 22; Length 407;  
Best Local Similarity 94.0%; Pred. No. 1,2e-126;  
Matches 407; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MNKYRIIWSALNAAVAVVSELTRNHTKRASATVAVLATLLEFATVOASAAASVADV 60  
DB 1 MNKYRIIWSALNAAVAVVSELTRNHTKRASATVAVLATLLEFATVOASAAAN----- 52  
QY 61 LNAGNNIGVAPGTTASNDVDFVRYDVEFLSADTKTTYNVESKDKTEVYIGAKT 120  
DB 53 -----NDPVRKYDVEFLSADTKTTYNVESKDKTEVYIGAKT 94  
QY 121 SVIEKDGKLVYTKDKGENSGSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADK 180  
DB 95 SVIEKDGKLVYTKDKGENSGSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADK 154  
QY 181 FEVYTSGTNTVPASGKGTATVASKDDGNTVMTDVNVGDLNVLNQLONGSMNLDKSKAVA 240  
DB 155 FEVYTSGTNTVPASGKGTATVASKDDGNTVMTDVNVGDLNVLNQLONGSMNLDKSKAVA 214  
QY 241 GSSCKVITSGNPSPSKGMDEVTNINAGNNIEITRNGKIDIDATSMTPPFSSVSLGAGADA 300  
DB 215 GSSCKVITSGNPSPSKGMDEVTNINAGNNIEITRNGKIDIDATSMTPPFSSVSLGAGADA 274  
QY 301 PTLSDGDLNVLNAGSKDKNPKVITNVPARGVEGDVTNVAOLKGYAQNLNRIIDVNDGNAR 360  
DB 275 PTLSDGDLNVLNAGSKDKNPKVITNVPARGVEGDVTNVAOLKGYAQNLNRIIDVNDGNAR 334  
QY 361 AGIAOAIATAGLVAYLTPGKSMMAIGGTYRGEAGVAYGISISDGNWIIKGTASGNSR 420  
DB 335 AGIAOAIATAGLVAYLTPGKSMMAIGGTYRGEAGVAYGISISDGNWIIKGTASGNSR 394  
QY 421 GHFGASASVGYOW 433  
DB 395 GHFGASASVGYOW 407

RESULT 13

AAV23740  
ID AAY23740 standard; Protein: 594 AA.

XX AAY23740;  
AC AAY23740;  
DT 08-SEP-1999 (first entry)  
XX A surface protein of Neisseria meningitidis.  
DE A surface protein of Neisseria meningitidis.  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KM immunoreactive peptide.  
XX Neisseria meningitidis.  
OS Neisseria meningitidis.  
XX WO9931132-A1.  
PN 24-JUN-1999.  
PD 14-DEC-1998; 98WO-AU01031.  
PE 12-DEC-1997; 97GB-0026398.  
PR (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX Jennings MP, Moxon ER, Peak IRA;

XX WP1: 1999-418754/35.  
DR N-PSDB: AAX85792.  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PT meningitidis infections  
XX Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA:

Query Match 92.5%; Score 2032.5; DB 20; Length 594;  
Best Local Similarity 70.9%; Pred. No. 6e-126;  
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

QY 1 MNKYRIIWSALNAAVAVVSELTRNHTKRASATVAVLATLLEFATVOASA----- 51  
DB 1 MNKYRIIWSALNAAVAVVSELTRNHTKRASATVAVLATLLEFATVOASTDDDLYLE 60  
QY 52 ----- 51  
DB 61 PVORTAVVLSFRSDKEGTEKEVTEDSNMWGYFDKGVLTAGTTLAAGNMLKIKONTNE 120  
QY 52 ----- 51  
DB 121 NTNASSFTSLKDLTLTTSVTEKLSFNSANSKNVNTISDPTKGLNFAKKTAEETNGDTTVA 180  
QY 52 -----NRAASVADVNLNAGMNIKGVAPGTTASDNV 80  
DB 181 LINGISLTDLTLNLTGATTNTVNDNVDEKRAASVADVNLNAGMNIKGVAPGTTASDNV 240  
QY 81 DFVRYDVEFLSADTKTTTNNVESKDKNGKTEVYIGAKTIVIEKDGKLVYTKDKGENG 140  
DB 241 DFVRYDVEFLSADTKTTTNNVESKDKNGKTEVYIGAKTIVIEKDGKLVYTKDKGENG 300  
QY 141 SSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADKPEVYTSGTNTVPASGKGT 200  
DB 301 SSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADKPEVYTSGTNTVPASGKGT 360  
QY 201 TVSKDDGNTVMTDVNVGDLNVLNQLONGSMNLDKSKRAVAGSSGKVISGNVPSKGMDE 260  
DB 361 TVSKDDGNTVMTDVNVGDLNVLNQLONGSMNLDKSKRAVAGSSGKVISGNVPSKGMDE 420  
QY 261 TVNINAGNNIEITRNGKIDIDATSMTPPFSSVSLGAGADAPTLTVDGD-ALNNSKDKN 319  
DB 421 TVNINAGNNIEITRNGKIDIDATSMTPPFSSVSLGAGADAPTLTVDGDALNNSKDKN 480  
QY 320 PVRTTNVAPGVKEDVTVNVAOLKGYAQNLRINRINDVNDGNARAGIAOAIATAGLVAYLP 379  
DB 481 PVRTTNVAPGVKEDVTVNVAOLKGYAQNLRINRINDVNDGNARAGIAOAIATAGLVAYLP 540  
QY 380 KSMMAIGGTYRGEAGVAYGISISDGNWIIKGTASGNSRGHFGASASVGYOW 433  
DB 541 KSMMAIGGTYRGEAGVAYGISISDGNWIIKGTASGNSRGHFGASASVGYOW 594

RESULT 14

AAV57044  
ID AAY57044 standard; Protein: 594 AA.

XX AAY57044;  
AC AAY57044;  
DT 21-FEB-2000 (first entry)

XX BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
 XX  
 XX BASB029; *Neisseria meningitidis*; surface fibrin protein; HSF; diagnosis;  
 KM infection; treatment; prevent; antibacterial drug.  
 XX  
 XX *Neisseria meningitidis*.  
 OS  
 FH Key Location/Qualifiers  
 FT Misc-difference 104  
 FT /note= "Encoded by AATC"  
 XX  
 XX MO958683-A2.  
 PN  
 PD 18-NOV-1999.  
 XX  
 XX 07-MAY-1999; 99MO-EP03255.  
 PF  
 XX 13-MAY-1998; 98GB-0010276.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 XX Ruelle J;  
 PI  
 XX WPI; 2000-053103/04.  
 DR  
 DR N-SDB; AA239864.  
 XX  
 PT New polypeptide from *Neisseria meningitidis* useful for diagnosis,  
 PT treatment or prevention of bacterial infections in mammal  
 XX  
 PS Claim 4; Fig 2; 74pp; English.  
 XX

CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
 CC Hemophilus influenzae surface fibrin (HSF) protein. The invention  
 CC relates to BASB029 polynucleotide sequences (AA239864-239865) and  
 CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
 CC meningitidis infection in a mammal. Compositions containing BASB029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with *Neisseria*  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.  
 CC  
 XX

SQ Sequence 594 AA;

Query Match 92.5%; Score 2032.5; DB 21; Length 594;

Best Local Similarity 70.9%; Pred. No. 6e-126;  
 Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

OY 1 MNKIYRIIMNSALNAMYVSELTRNHTKRASATVATLTLFATVQASA----- 51  
 DB 1 MNKIYRIIMNSALNAMYVSELTRNHTKRASATVATLTLFATVQASTDDDDLYLE 60  
 OY 52 ----- 51  
 DB 61 PVORTAVVLSFRSDKEGTGEKEVTEDSNMGVYEDDKGVLTAAGTTTLKAGDNLIKIKONTNE 120  
 OY 52 ----- 51  
 DB 121 NTNASSFTYSLKKDLTDLTJVGTEKLSFSANSKNKVNITSDTKGLNFAKKAETNGDTVH 180  
 OY 52 -----NRAASYKDVLMAGWNIKGVKPGTTASDNV 80  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 181 LNCIGSTLPTDLLNTGATVTNTNDNTYDDEKKRAASYKDVLMAGWNIKGVKPGTTASDNV 240  
 OY 81 DFWRTYTVTEFLISADPTTNNVNESKNGKTEKIGAKTSVKEKXGLVTGDKGNG 140  
 DB 241 DFWRTYTVTEFLISADPTTNNVNESKNGKTEKIGAKTSVKEKXGLVTGDKGNG 300  
 OY 141 SSTDEGEGLYTAKEVIDAVKAKGRMKTTHANGCOTGADFEFTVSGTNTFFASGKCTTA 200  
 DB 301 SSTDKGEGLYTAKEVIDAVKAKGRMKTTHANGCOTGADFEFTVSGTNTFFASGKCTTA 360  
 OY 201 TVSKDQGNITVMYDVNVALNVLONSGMINDSKAVAGSGKVISGVNPSKGMDE 260  
 DB 361 TVSKDQGNITVMYDVNVALNVLONSGMINDSKAVAGSGKVISGVNPSKGMDE 420  
 OY 261 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDDEGLNAGSKPANK 319  
 DB 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDDEGLNAGSKPANK 480  
 OY 320 PVRTTNVAPGVKEDGVNVAQLKGAONLNRRIDNVGNRAGIAQAIAATAGLVQAVLP 379  
 DB 481 PVRTTNVAPGVKEDGVNVAQLKGAONLNRRIDNVGNRAGIAQAIAATAGLVQAVLP 540  
 OY 380 KSMMAIGGTYRGEAGYAGISYSSIDSGNMIKGTASGNSRGHFGASASVGYOW 433  
 DB 541 KSMMAIGGTYRGEAGYAGISYSSIDSGNMIKGTASGNSRGHFGASASVGYOW 594

# RESULT 15

AAU06174  
 ID AAU06174 standard; Protein: 594 AA.

XX AAU06174;

DT 24-OCT-2001 (first entry)

XX N. meningitidis EG327 surface antigen Nha polypeptide sequence.

XX Surface antigen Nha; meningococcal disease; meningitis vaccine.

XX *Neisseria meningitidis* strain EG327.

XX Location/Qualifiers

FT 1..50  
 /label= C1  
 /note= "Conserved region 1"

FT 51..104  
 /label= V1  
 /note= "Variable region 1"

FT 105..116  
 /label= C2  
 /note= "Conserved region 2"

FT 117..126  
 /label= V2  
 /note= "Variable region 2"

FT 127..190  
 /label= C3  
 /note= "Conserved region 3"

FT 191..212  
 /label= V3  
 /note= "Variable region 3"

FT 213..231  
 /label= C4  
 /note= "Conserved region 4"

FT 232..238  
 /label= V4  
 /note= "Variable region 4"

FT 239..594  
 /label= C5  
 /note= "Conserved region 5"

FT 02-AUG-2001.

XX W0200155182-A1.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.  
PF  
XX  
XX 25-JAN-2000; 2000US-0177917.  
PR  
XX  
XX (UYOU ) UNIV QUEENSLAND.  
PA  
XX  
PI Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
DR  
XX N-PSDB; AAS09164.  
XX

PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PS preventing broad spectrum of Neisseria meningitidis -

Claim 9; Fig 1; 91pp; English.

CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
XX

SQ Sequence 594 AA:

Query Match 92.5%; Score 2032.5; DB 22; Length 594;  
Best Local Similarity 70.9%; Pred. No. 6e-126;  
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

OY 1 MNKIRIITNSALNMVWVSELTNRNHTKRASATVTAVALTLFATVQASA----- 51  
DB 1 MNKIRIITNSALNMVWVSELTNRNHTKRASATVTAVALTLFATVQASTDDDDLYLE 60  
OY 52 ----- 51  
DB 61 PVQRTAVVLSPRSDEKGEKEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLIKONTNE 120  
OY 52 ----- 51  
DB 121 NTNASSFTYSLKKDLDTLTSVGTSEKLSANSNKVNITSDTKGLNFAKRTAETNGDITVH 180  
OY 52 -----NRAASVKDVLNAGWNKIKGKPGTTASDNV 80  
DB 181 LINGISLTLDLTLLNGATTNTVNDVTDDEKRAASVDVNLNAGNNIKGVKPGTTASDNV 240  
OY 81 DFRVTVDFVEFLSADTKTTTVNESKDKNGKTEVRIGAKTSVYKEKDKLVTKDKGENG 140  
DB 241 DFRVTVDFVEFLSADTKTTTVNESKDKNGKTEVRIGAKTSVYKEKDKLVTKDKGEND 300  
OY 141 STDGEGLVTAKEVIDAVNKGMRKTTTANGOTGOADKFEYVTSGTNVTFAKSGGTTA 200  
DB 301 SSTDGEGLVTAKEVIDAVNKGMRKTTTANGOTGOADKFEYVTSGTNVTFAKSGGTTA 360  
OY 201 TVSKDQGNITWYVNVNVDALNVNQLONGNLDKSKAVAGSSGKVISGNVSPSKGKMD 260  
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Search completed: October 6, 2003, 09:22:33  
Job time : 40.1842 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 11.5793 Seconds  
(without alignments)  
1582.188 Million cell updates/sec

Title: US-09-771-382-26  
Perfect score: 2197  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2108	95.9	591	US-09-669-974-21	Sequence 21, Appl
3	2103.5	95.7	592	US-09-377-155-2	Sequence 2, Appl
4	2103.5	95.7	592	US-09-669-974-2	Sequence 2, Appl
5	2096	95.4	591	US-09-377-155-11	Sequence 11, Appl
6	2096	95.4	591	US-09-669-974-11	Sequence 11, Appl
7	2032.5	92.5	594	US-09-377-155-9	Sequence 9, Appl
8	2032.5	92.5	594	US-09-669-974-9	Sequence 9, Appl
9	2032	92.5	599	US-09-377-155-15	Sequence 15, Appl
10	2032	92.5	599	US-09-669-974-15	Sequence 15, Appl
11	2025.5	92.2	594	US-09-377-155-7	Sequence 7, Appl
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13	2015.5	91.7	592	US-09-377-155-17	Sequence 17, Appl
14	2015.5	91.7	592	US-09-669-974-17	Sequence 17, Appl
15	2010.5	91.5	598	US-09-377-155-13	Sequence 13, Appl
16	2010.5	91.5	598	US-09-669-974-13	Sequence 13, Appl
17	2001.5	91.1	598	US-09-377-155-5	Sequence 5, Appl
18	2001.5	91.1	598	US-09-669-974-5	Sequence 5, Appl
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22	776.5	35.3	1098	US-08-685-467-2	Sequence 2, Appl
23	776.5	35.3	1098	US-09-377-155-32	Sequence 32, Appl
24	776.5	35.3	1098	US-08-913-942-2	Sequence 2, Appl
25	776.5	35.3	1098	US-09-669-974-32	Sequence 32, Appl
26	776.5	35.3	1098	US-09-268-347-44	Sequence 44, Appl
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33	734	33.4	2353	US-08-913-942-4	Sequence 4, Appl
34	734	33.4	2353	US-09-669-974-33	Sequence 33, Appl
35	734	33.4	2354	US-09-268-347-47	Sequence 47, Appl
36	676.5	30.8	607	US-08-409-995-6	Sequence 6, Appl
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38	676.5	30.8	607	US-08-913-942-6	Sequence 6, Appl
39	676.5	30.8	1912	US-08-409-995-4	Sequence 4, Appl
40	676.5	30.8	1912	US-08-685-467-4	Sequence 4, Appl
41	562	25.6	679	US-09-377-155-15	Sequence 15, Appl
42	562	25.6	679	US-09-669-974-15	Sequence 15, Appl
43	487.5	22.2	1002	US-09-268-347-26	Sequence 26, Appl
44	475.5	21.6	1004	US-09-268-347-24	Sequence 24, Appl
45	397.5	18.1	1104	US-09-268-347-30	Sequence 30, Appl

ALIGNMENTS

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US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
Query Match          95.9%; Score 2108; DB 3; Length 591;
Best Local Similarity 73.3%; Pred. No. 3,7e-165;
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;
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RESULT 2  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173

GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 95.9%; Score 2108; DB 4; Length 591;  
Best Local Similarity 73.3%; Pred. No. 3.7e-165;  
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

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; Patent No. 6197312

GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

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Best Local Similarity 73.0%; Pred. No. 8.7e-165;  
Matches 432; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

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: Patent No. 633173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
: US-09-669-974-2

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Query Match	95.7%	Score 2103.5	DB 4	Length 592
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QY 53	-----	52		
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QY 53	-----	81		
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Db 301	STDSGEGLVTAKEVYIDAVNKKAGMRKKTITTAAGGOGAOKPELVTSGTNTVTFASGKGTAT	360		
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Db 361	VSXKDDOGNITWYDVNVGDALNVNQLQSGNMNLSKAVASGSGKYSIGNVSPSKKMDET	420		
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Qy 322 RITNVA PVKEGGYTVAALKEKVAONLNRRIDNYNGNRACTAAQIATAGIYQAYLEKGS 381

Db 481 RITNVA PVKEGGYTVAALKEKVAQNLNRRIDNYNGNRACTAAQIATAGIYQAYLEKGS 540

Qy 382 MMAIGGCTTTCGAGTAIGTSSISDGGNWTIKCTASGNSRGHFPGASASYGVOM 433

Db 541 MMAIGGCTTTCGAGTAIGTSSISDGGNWTIKCTASGNSRGHFPGASASYGVOM 592

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RESULT 5
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: Sequence 11, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO. 11
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-11

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Query Match	95.4%	Score 2096	DB 3	Length 591
Best Local Similarity	72.9%	Pred. No. 3, 6e-164		
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Db	1 MNEILRIIWNLSALNMAVYVSELTNRHTRKASATVKTAVLATLTFATVQASANNEQEDL	60		
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Db	121 NGTNFTYSLKDDLDLIVSGTEKLSFSAANGKNVNTISDTKGLNPAKETAGTGDDTVHLN	180		
QY	53 -----RAASYKDVILNAGWNITKGKPGTTASDNDF	82		
Db	181 GIGSTLTDLLNTGATVNTNDNVYDDEKCRRAASYKDVILNAGWNITKGKPGTTASDNDF	240		
QY	83 VRTDYTVBELSDFTTIVNVESSKNGKRTVEKISAKTSVIREKGGKLTATGDKDGENSS	142		
Db	241 VRTDYTVBELSDFTTIVNVESSKNGKRTVEKISAKTSVIREKGGKLTATGDKDGENSS	300		
QY	143 TDEEGGLTAKAEVIDAVNKAQRMKTTTANGOTGOADRFETVTSNTNVPFASGKGTATV	202		
Db	301 TDEEGGLTAKAEVIDAVNKAQRMKTTTANGOTGOADRFETVTSNTNVPFASGKGTATV	360		
QY	203 SKDDOGNTITWADVAVGALNVLNOLONSGWNLDKSAVAGSSSKVTSGNVSPBKGMDETV	262		
Db	361 SKDDOGNTITWADVAVGALNVLNOLONSGWNLDKSAVAGSSSKVTSGNVSPBKGMDETV	420		
QY	263 NINAGNNIETIRNCKNIDIASMTPQFSSVSLGACADAPTLTSLVDDDALNVGSKKNKPPVR	322		
Db	421 NINAGNNIETIRNCKNIDIASMTPQFSSVSLGACADAPTLTSLVDDDALNVGSKKNKPPVR	480		
QY	323 ITNVAQVKEGDVTVNAOLKGVAONLNNRIDNVGDNARAGIAQAIATAGLVQVATLPKSKM	382		

Db 481 ITNAPGVKEGDVTVNAOLKGYAONLNLRIDVNDGNARAGIAQAIATATAGLVQAYLPKGS 540  
Qy 383 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

RESULT 6  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 95.4%; Score 2096; DB 4; Length 591;  
Best Local Similarity 72.9%; Pred. No. 3,6e-164;  
Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;

Qy 1 MNKIRIITNSALNMAVVVSELTNRNHTKRASATVTAVALTLFFATVOASA----- 52  
Db 1 MNKIRIITNSALNMAVVVSELTNRNHTKRASATVTAVALTLFFATVOASANEQEDL 60  
Qy 53 ----- 52  
Db 61 YLDPVLRVAVLIYNSKEGEGEKEVEBNSDMAVYFNEKGVLTAREITLAKAGDNLIKQ 120  
Qy 53 ----- 52  
Db 121 NGTNTYSLKKDLFDLTSVGTPEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
Qy 53 ----- 52  
Db 181 GIGSTLTDLTNTGATTNTNDNTYTDDEKKRAASVDVNLNAGMNKIGVYKPGTTASDNVDF 240  
Qy 83 VRTYVTEFLSADTFTTVNVESKDKNGKTEVYKIGAKTSVYKEKDKGLVTKDKGENSS 142  
Db 241 VRTYVTEFLSADTFTTVNVESKDKNGKTEVYKIGAKTSVYKEKDKGLVTKDKGENSS 300  
Qy 143 TDEGEGLTAKAEVIDAVKAGRMKTTTANGOTGADFEYVTSCTNTYTFASGKGTATV 202  
Db 301 TDEGEGLTAKAEVIDAVKAGRMKTTTANGOTGADFEYVTSCTNTYTFASGKGTATV 360  
Qy 203 SKDDOGNTTVMDVNVGDLNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDET 262  
Db 361 SKDDOGNTTVMDVNVGDLNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDET 420  
Qy 263 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKNK 322  
Db 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKNK 480  
Qy 323 ITNAPGVKEGDVTVNAOLKGYAONLNLRIDVNDGNARAGIAQAIATATAGLVQAYLPKGS 382  
Db 481 ITNAPGVKEGDVTVNAOLKGYAONLNLRIDVNDGNARAGIAQAIATATAGLVQAYLPKGS 540

Qy 383 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 92.5%; Score 2032.5; DB 3; Length 594;  
Best Local Similarity 70.9%; Pred. No. 6,1e-159;  
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

Qy 1 MNKIRIITNSALNMAVVVSELTNRNHTKRASATVTAVALTLFFATVOASA----- 51  
Db 1 MNKIRIITNSALNMAVVVSELTNRNHTKRASATVTAVALTLFFATVOASTDDDDLYLE 60  
Qy 52 ----- 51  
Db 61 PVQRTAVVLSFRDKEGTGEKEVEEDSNMGVYFDKGVLTAGTTLKAGDNLIKQNTNE 120  
Qy 52 ----- 51  
Db 121 NTNASSFTYSLKKDLTDLTLSVGTPEKLSFSANSKNVNTSDTKGLNFAKETAGTNGDTTVH 180  
Qy 52 ----- 80  
Db 181 LNGIGSTLTDLTNTGATTNTNDNTYTDDEKKRAASVDVNLNAGMNKIGVYKPGTTASDNV 240  
Qy 81 DFVRTYDTEFLSADTFTTVNVESKDKNGKTEVYKIGAKTSVYKEKDKGLVTKDKGENG 140  
Db 241 DFVRTYDTEFLSADTFTTVNVESKDKNGKTEVYKIGAKTSVYKEKDKGLVTKDKGENG 300  
Qy 141 SSTDEGELVTAKEVIDAVNAGRMKTTTANGOTGADFEYVTSCTNTYTFASGKGTATV 200  
Db 301 SSTDEGELVTAKEVIDAVNAGRMKTTTANGOTGADFEYVTSCTNTYTFASGKGTATV 360  
Qy 201 TVSKDDOGNTTVMDVNVGDLNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDET 260  
Db 261 TVSKDDOGNTTVMDVNVGDLNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDET 420  
Qy 361 TVSKDDOGNTTVMDVNVGDLNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDET 480  
Qy 421 TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKNK 319  
Db 421 TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKNK 480  
Qy 320 PVRTTNVAPGVKEGDVTVNAOLKGYAONLNLRIDVNDGNARAGIAQAIATATAGLVQAYLP 379  
Db 481 PVRTTNVAPGVKEGDVTVNAOLKGYAONLNLRIDVNDGNARAGIAQAIATATAGLVQAYLP 540  
Qy 380 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433  
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 594

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 92.5%; Score 2032.5; DB 4; Length 594;  
Best Local Similarity 70.9%; Pred. No. 6.1e-159;  
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;  
QY 1 MNKIRITMSALNANWVSELTRNHTKRASATVKTAVLTLLFATVQAASA----- 51  
Db 1 MNKIRITMSALNANWVSELTRNHTKRASATVKTAVLTLLFATVQAASATDDDLXLE 60  
QY 52 ----- 51  
Db 61 PVQRTAVVLSFRSDKEGTGEVTEEDSNMGVYFDKKGVLTAGTTTLKAGDNLIKONTNE 120  
QY 52 ----- 51  
Db 121 NTNASSFTYSLKKDLTDLTSVTEKLSFGANSKNVNTSDTKGLNFAKKTAEINGDTTVH 180  
QY 52 ----- 80  
Db 181 LNCIGSTLTDLTLLNTGATTVTNDNTDDEKRRASVYKDVLANGMNKGKVPETASDNV 240  
QY 81 DEVRTYDVEFLSADTKTTTVNVEESKNGKRTVEKIGAKTSVIEKDKGLVTGKDGENG 140  
Db 241 DEVRTYDVEFLSADTKTTTVNVEESKNGKRTVEKIGAKTSVIEKDKGLVTGKDGEND 300  
QY 141 SSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSTNTVTFASGKTGA 200  
Db 301 SSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSTNTVTFASGKTGA 360  
QY 201 TVSKDOGNITTVADVNGDALNVNOLONGSNLDSKAVAGSSGKTVSGNVSPSKGKME 260  
Db 361 TVSKDOGNITTVADVNGDALNVNOLONGSNLDSKAVAGSSGKTVSGNVSPSKGKME 420  
QY 261 TVNINAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKDNK 319  
Db 421 TVNINAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDANK 480  
QY 320 PVRTITNAPGVKSGDVTNVNOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVOAALPG 379  
Db 481 PVRTITNAPGVKSGDVTNVNOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVOAALPG 540  
QY 380 KSMALIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433  
Db 541 KSMALIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594

RESULT 9

US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 92.5%; Score 2032; DB 3; Length 599;  
Best Local Similarity 70.5%; Pred. No. 6.7e-159;  
Matches 422; Conservative 2; Mismatches 9; Indels 166; Gaps 2;  
QY 1 MNKIRITMSALNANWVSELTRNHTKRASATVKTAVLTLLFATVQAASA----- 51  
Db 1 MNKIRITMSALNANWVSELTRNHTKRASATVKTAVLTLLFATVQAASATDDDEEEL 60  
QY 52 ----- 51  
Db 61 EPVYRSALVLOFMIDKEGNEBENSTGNGSIYTDNHTLHGATVYTLKAGDNLIKONTN 120  
QY 52 ----- 51  
Db 121 KTNENTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKKTAEING 180  
QY 52 ----- 75  
Db 181 DTVHLNGISTLTDLTLLNTGATTVTNDNTDDEKRRASVYKDVLANGMNKGKVPET 240  
QY 76 ASDNVDPVRYDYVEFLSADTKTTTVNVEESKNGKRTVEKIGAKTSVIEKDKGLVTGKD 135  
Db 241 ASDNVDPVRYDYVEFLSADTKTTTVNVEESKNGKRTVEKIGAKTSVIEKDKGLVTGKG 300  
QY 136 KGENGSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSGTVTFASG 195  
Db 301 KGENGSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTVSGTVTFASG 360  
QY 196 KGTATYVSKDOGNITTVADVNGDALNVNOLONGSNLDSKAVAGSSGKTVSGNVSPSK 255  
Db 361 KGTATYVSKDOGNITTVADVNGDALNVNOLONGSNLDSKAVAGSSGKTVSGNVSPSK 420  
QY 256 GKMDETVNIAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPTLSDVDG-DALNVGS 314  
Db 421 GKMDETVNIAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPTLSDVDGKALNVGS 480  
QY 315 KDNKPVRTITNAPGVKSGDVTNVNOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVO 374  
Db 481 KDNKPVRTITNAPGVKSGDVTNVNOLKGVNOLNLRIDNVGNARAGIAQAIAATAGLVO 540  
QY 375 AYLPGRKSMALIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433  
Db 541 AYLPGRKSMALIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599

RESULT 10  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 599  
TYPE: PRF  
ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 92.5%; Score 2032; DB 4; Length 599;  
Best Local Similarity 70.5%; Pred. No. 6,7e-159;  
Matches 422; Conservative 2; Mismatches 9; Indels 166; Gaps 2;

QY 1 NKKIYRIIWSALNMAVVSSELTRNHTKRASATVKTAVLATLLFATVOASA----- 51  
DB 1 NKKIYRIIWSALNMAVVSSELTRNHTKRASATVKTAVLATLLFATVOANATDDEDEEL 60  
QY 52 ----- 51  
DB 61 EPPVSALVLPQIMDKEGNGENESTGNIGMSIYYDNHNTLHGATVTLKAGDNLKIKONTN 120  
QY 52 ----- 51  
DB 121 KNTNENTNDSFTYSLAKKDLTLFSETEKLSFGANGKNVNTSDTKGNLPAKETAGTNG 180  
QY 52 ----- 51  
DB 181 DTTVHLNGIGSTLTDTLLNTGATTVNTNDNTDDKKRAASVDVNLNAGMNIKGVPGTT 240  
QY 76 ASDNDVFTVTVTEFLSADTKTTTVNVESKDNCKTEVKIGAKTSYIKERDKLVTKGD 135  
DB 241 ASDNDVFTVTVTEFLSADTKTTTVNVESKDNCKTEVKIGAKTSYIKERDKLVTKG 300  
QY 136 KGENSGSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADFEFTVTSCTNTFFAG 195  
DB 301 KGENSGSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADFEFTVTSCTNTFFAG 360  
QY 136 KGTATVSKDDGNTTVMYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSK 255  
DB 361 KGTATVSKDDGNTTVMYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSK 420  
QY 256 GMDTETVNIAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLVSVDG-DALNVS 314  
DB 421 GMDTETVNIAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGKGLNVS 480  
QY 315 KKDNPVRTTNAVPVKEGVDYTNVAOLKGYAONLNRRIDNVGNNRAGIAQAATATAGLVQ 374  
DB 481 KKDNPVRTTNAVPVKEGVDYTNVAOLKGYAONLNRRIDNVGNNRAGIAQAATATAGLVQ 540  
QY 375 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGHFGASASVGYOW 433  
DB 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGHFGASASVGYOW 599

RESULT 11  
US-09-377-155-7  
Sequence 7, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 594  
TYPE: PRF  
ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 92.2%; Score 2025.5; DB 3; Length 594;  
Best Local Similarity 70.9%; Pred. No., 2.3e-158;  
Matches 421; Conservative 2; Mismatches 10; Indels 161; Gaps 2;

QY 1 NKKIYRIIWSALNMAVVSSELTRNHTKRASATVKTAVLATLLFATVOASA----- 51  
DB 1 NKKIYRIIWSALNMAVVSSELTRNHTKRASATVKTAVLATLLFATVOANATDDEDEEL 60  
QY 52 ----- 51  
DB 61 PVOGTAVVLSFRSDEKGEKTEGTEGSDSNMAYVFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
QY 52 ----- 51  
DB 121 NTNDSFTYSLAKKDLTLFSETEKLSFGANGKNVNTSDTKGNLPAKETAGTNGDPVH 180  
QY 52 ----- 51  
DB 181 LMGISTLTDLTLNTGATTVNTNDNTDDEKRAASVDVNLNAGMNIKGVPGTTASDNV 240  
QY 81 DEVRTVTVTEFLSADTKTTTVNVESKDNCKTEVKIGAKTSYIKERDKLVTKGDENG 140  
DB 241 DEVRTVTVTEFLSADTKTTTVNVESKDNCKTEVKIGAKTSYIKERDKLVTKGDENG 300  
QY 141 SSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADFEFTVTSCTNTFFAG 200  
DB 301 SSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADFEFTVTSCTNTFFAG 360  
QY 201 TVSKDDGNTTVMYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGKDE 260  
DB 361 TVSKDDGNTTVMYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGKDE 420  
QY 261 TVNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSKDNK 319  
DB 421 TVNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGKGLNVS 480  
QY 320 PVRTTNAVPVKEGVDYTNVAOLKGYAONLNRRIDNVGNNRAGIAQAATATAGLVQ 379  
DB 481 PVRTTNAVPVKEGVDYTNVAOLKGYAONLNRRIDNVGNNRAGIAQAATATAGLVQ 540  
QY 380 KSMMAIGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGHFGASASVGYOW 433  
DB 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGHFGASASVGYOW 594

RESULT 12  
US-09-669-974-7  
Sequence 7, Application US/09669974  
Patent No. 6333173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974

;; CURRENT FILING DATE: 2000-09-26  
;; PRIOR APPLICATION NUMBER: US 09/377,155  
;; PRIOR FILING DATE: 1999-08-19  
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
;; PRIOR FILING DATE: 1998-12-14  
;; PRIOR APPLICATION NUMBER: GB 9726398.2  
;; PRIOR FILING DATE: 1997-12-12  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 7  
;; LENGTH: 594  
;; TYPE: PRT  
;; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 92.2%; Score 2025.5; DB 4; Length 594;  
Best Local Similarity 70.9%; Pred. No. 2.3e-158;  
Matches 421; Conservative 2; Mismatches 10; Indels 161; Gaps 2;

QY 1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOASA----- 51  
Db 1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDDDLYLE 60  
QY 52 ----- 51  
Db 61 PVQRTAVLSEFSRDEKTEGTEGEDSDSNMNAVYFDEKRVLKAGATILKAGDNLIKQNTNE 120  
QY 52 ----- 51  
Db 121 NTNDSFTYSLKKDLTGLTGLINVEETKLSFGANGKVNIIISDFKGLNFAKETAGTNGDTVHLN 180  
QY 52 ----- -NRASVADVLNAGNNIKGVKPGTTASDNV 80  
Db 181 LNCIGSTLFDLLNTGATNTNDVNTDEKKRAASVADVLNAGNNIKGVKPGTTASDNV 240  
QY 81 DVRTDYVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKLVTKGKGENG 140  
Db 241 DVRTDYVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKLVTKGKGENG 300  
QY 141 SSTDEGGLVTAKEVIDAVNKGAMKTTTANGOTGQADKEFTVSGTNTVTFASGKTATV 200  
Db 301 SSTDEGGLVTAKEVIDAVNKGAMKTTTANGOTGQADKEFTVSGTNTVTFASGKTATV 360  
QY 201 TVSKDDQGNITVYDVNVDALNVQNLONSGNMLDSKAVAGSSGKVIISGVNPSKGMDE 260  
Db 361 TVSKDDQGNITVYDVNVDALNVQNLONSGNMLDSKAVAGSSGKVIISGVNPSKGMDE 420  
QY 261 TVNINAGNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDGD-ALNVGSKKNKP 319  
Db 421 TVNINAGNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKKNKP 480  
QY 320 PVRTVAPGVKEGDTVNAOLKGVANLNRRIDNVGNARAGIAQAIATAGLVQAYLPKG 379  
Db 481 PVRTVAPGVKEGDTVNAOLKGVANLNRRIDNVGNARAGIAQAIATAGLVQAYLPKG 540  
QY 380 KSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYOM 433  
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYOM 594

RESULT 13  
US-09-377-155-17  
;; Sequence 17, Application US/09377155  
;; Patent No. 6197312  
;; GENERAL INFORMATION:  
;; APPLICANT: PEAK, Ian Richard Anselm  
;; APPLICANT: JENNINGS, Michael Paul  
;; APPLICANT: MOXON, E. Richard  
;; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
;; FILE REFERENCE: 065064/0128  
;; CURRENT APPLICATION NUMBER: US/09/377,155  
;; CURRENT FILING DATE: 1999-08-19  
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031

;; PRIOR FILING DATE: 1998-12-14  
;; PRIOR APPLICATION NUMBER: GB 9726398.2  
;; PRIOR FILING DATE: 1997-12-12  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 17  
;; LENGTH: 592  
;; TYPE: PRT  
;; ORGANISM: Neisseria meningitidis  
US-09-377-155-17

Query Match 91.7%; Score 2015.5; DB 3; Length 592;  
Best Local Similarity 70.8%; Pred. No. 1.5e-157;  
Matches 419; Conservative 3; Mismatches 11; Indels 159; Gaps 2;

QY 1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOASA----- 51  
Db 1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEBEL 60  
QY 52 ----- 51  
Db 61 ESQVRSVGSIQASMEGSEVLEETISLMTNDSKEFVDPIVTLKAGDNLIKQNTNENT 120  
QY 52 ----- 51  
Db 121 NASSFTYSLKKDLTGLTGLINVEETKLSFGANGKVNIIISDFKGLNFAKETAGTNGDTVHLN 180  
QY 52 ----- -NRASVADVLNAGNNIKGVKPGTTASDNV 82  
Db 181 GIGSTLTDMLNTGATNTNDVNTDEKKRAASVADVLNAGNNIKGVKPGTTASDNV 240  
QY 83 VRTDYVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKLVTKGKGENGSS 142  
Db 241 VRTDYVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVKEKDKLVTKGKGENGSS 300  
QY 143 TDEGGLVTAKEVIDAVNKGAMKTTTANGOTGQADKEFTVSGTNTVTFASGKTATV 202  
Db 301 TDEGGLVTAKEVIDAVNKGAMKTTTANGOTGQADKEFTVSGTNTVTFASGKTATV 360  
QY 203 SKDDQGNITVYDVNVDALNVQNLONSGNMLDSKAVAGSSGKVIISGVNPSKGMDE 262  
Db 361 SKDDQGNITVYDVNVDALNVQNLONSGNMLDSKAVAGSSGKVIISGVNPSKGMDE 420  
QY 263 NINAGNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDGD-ALNVGSKKNKP 321  
Db 421 NINAGNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKKNKP 480  
QY 322 RITNVAPEGVKEGDTVNAOLKGVANLNRRIDNVGNARAGIAQAIATAGLVQAYLPKGS 381  
Db 481 RITNVAPEGVKEGDTVNAOLKGVANLNRRIDNVGNARAGIAQAIATAGLVQAYLPKGS 540  
QY 382 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYOM 433  
Db 541 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRCHFGASASVGYOM 592

RESULT 14  
US-09-669-974-17  
;; Sequence 17, Application US/09669974  
;; Patent No. 633173  
;; GENERAL INFORMATION:  
;; APPLICANT: PEAK, Ian Richard Anselm  
;; APPLICANT: JENNINGS, Michael Paul  
;; APPLICANT: MOXON, E. Richard  
;; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
;; FILE REFERENCE: 065064/0128  
;; CURRENT APPLICATION NUMBER: US/09/669,974  
;; CURRENT FILING DATE: 2000-09-26  
;; PRIOR APPLICATION NUMBER: US 09/377,155  
;; PRIOR FILING DATE: 1999-08-19  
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
;; PRIOR FILING DATE: 1998-12-14  
;; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentl Ver. 2.0  
 ; SEQ ID NO 17  
 ; LENGTH: 592  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria meningitidis  
 US-09-669-974-17

Query Match 91.7%; Score 2015.5; DB 4; Length 592;  
 Best Local Similarity 70.8%; Pred. No. 1.5e-157;  
 Matches 419; Conservative 3; Mismatches 11; Indels 159; Gaps 2;

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QY 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVTAVALTLFFATVOASA----- 51
DB 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVTAVALTLFFATVOANATDEDEEEL 60
QY 52 ----- 51
DB 61 ESVORSVVSIOASMEGSVELETTISLSMTNDSKEFVDEYIVVTLKAGDNLKIKQNTNENT 120
QY 52 ----- 51
DB 121 NASSFTYSLKQDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
QY 52 ----- 82
DB 181 GIGSTLTMDLNTGATNTVNDNTVDDEKKRAASVYKDVNLNAGWNIKGVKPGTTASDNVDF 240
QY 83 VRTYTVTFEFLSADPTTVTVNVESSKNGKTEVYKIGAKTSVIREKDGKLVYTGKKEENSS 142
DB 241 VRTYTVTFEFLSADPTTVTVNVESSKNGKTEVYKIGAKTSVIREKDGKLVYTGKKEENSS 300
QY 143 TDEGGLVTAKEVIDAVNKAQWRMKTTFANGOTGADKFEYVTSNTYTFASGKGTATV 202
DB 301 TDEGGLVTAKEVIDAVNKAQWRMKTTFANGOTGADKFEYVTSNTYTFASGKGTATV 360
QY 203 SKDDGNTTVYMDVNVGDLNVLNOLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETIV 262
DB 361 SKDDGNTTVYMDVNVGDLNVLNOLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETIV 420
QY 263 NINNGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGD-ALNVGSKDNMFPV 321
DB 421 NINNGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGD-ALNVGSKDNMFPV 480
QY 322 RITNAPGVKESGDVTNVAOLKGVANLNNRIDNVGNNRAGIAQAIAATAGLVAOATLPKGS 381
DB 481 RITNAPGVKESGDVTNVAOLKGVANLNNRIDNVGNNRAGIAQAIAATAGLVAOATLPKGS 540
QY 382 MAAIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 433
DB 541 MAAIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 592
  
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RESULT 15  
 US-09-377-155-13  
 ; Sequence 13, Application US/09377155  
 ; Patent No. 6197312  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/377, 155  
 ; CURRENT FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398.2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentl Ver. 2.0  
 ; SEQ ID NO 13

; LENGTH: 598  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria meningitidis  
 US-09-377-155-13

Query Match 91.5%; Score 2010.5; DB 3; Length 598;  
 Best Local Similarity 69.9%; Pred. No. 3.9e-157;  
 Matches 418; Conservative 3; Mismatches 12; Indels 165; Gaps 2;

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QY 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVTAVALTLFFATVOASA----- 51
DB 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVTAVALTLFFATVOANATDEDDDLYLE 60
QY 52 ----- 51
DB 61 PVQRTAAVLSFRSDEKTEGTEKGTEDSNMAYVFDEKRVLKAGAITLAKAGDNLKIKQNTNE 120
QY 52 ----- 51
DB 121 NTNENTNDSFTYSLKQDLTDLTSVETKLSFGANGKNVNIISDTKGLNFAKETAGTNGD 180
QY 52 ----- 76
DB 181 PTVHLNIGSTLTDLTGLINVEETKLSFGANGKNVNIISDTKGLNFAKETAGTNGD 240
QY 77 SDNVDFVRYDVEFLSADPTTVTVNVESSKNGKTEVYKIGAKTSVIREKDGKLVYTGKDK 136
DB 241 SDNVDFVRYDVEFLSADPTTVTVNVESSKNGKTEVYKIGAKTSVIREKDGKLVYTGKDK 300
QY 137 GENSSTDEGGLVTAKEVIDAVNKAQWRMKTTFANGOTGADKFEYVTSNTYTFASGK 196
DB 301 DENGSSTDEGGLVTAKEVIDAVNKAQWRMKTTFANGOTGADKFEYVTSNTYTFASGK 360
QY 197 GTTATVSKDDGNTTVYMDVNVGDLNVLNOLNSGWNIDSKAVAGSSGKVISGNVSPSKG 256
DB 361 GTTATVSKDDGNTTVYMDVNVGDLNVLNOLNSGWNIDSKAVAGSSGKVISGNVSPSKG 420
QY 257 KMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGD-ALNVGSK 315
DB 421 KMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDGD-ALNVGSK 480
QY 316 KDNKRVRTNVAQVKEGSDVTNVAOLKGVANLNNRIDNVGNNRAGIAQAIAATAGLVAO 375
DB 481 DANKRVRTNVAQVKEGSDVTNVAOLKGVANLNNRIDNVGNNRAGIAQAIAATAGLVAO 540
QY 376 YLPKGSMAAIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 433
DB 541 YLPKGSMAAIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 598
  
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Search completed: October 6, 2003, 09:35:49  
 Job time : 15.5793 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 12.3947 Seconds  
(Without alignments)  
3359.577 Million cell updates/sec

Title: US-09-771-382-26

Perfect score: 2197

Sequence: 1 MNKIYRIIWSALNANWVVS.....TASGNSRGHPGASVGYQW 433

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2108	95.9	591	2 G81133	adhesin NMB0992 [i
2	2009.5	91.5	592	2 A81888	probable surface f
3	345	15.7	298	2 I64138	adhesin homolog HI
4	340.5	15.5	2059	2 D82671	surface protein XF
5	335	15.2	1150	2 A82615	surface protein XF
6	329.5	15.0	1588	2 A86036	probable adhesin z
7	329.5	15.0	1588	2 H91188	probable adhesin E
8	326	14.8	1107	2 AC0976	probable autotrans
9	315.5	14.4	658	2 AH0110	surface p
10	214	9.7	1004	2 C82672	surface-exposed ou
11	189	8.6	1286	2 S28634	adhesin AIDA-I pre
12	186.5	8.5	1018	2 H83135	probable adhesin p
13	186.5	8.5	1091	2 G64964	hypothetical prote
14	186	8.5	364	2 A81019	adhesin/Invasin, p
15	185	8.4	365	2 AB3486	cell surface prote
16	182	8.3	1325	2 A64305	yeast protein - Esc
17	178	8.1	385	2 F90961	flagellin [importe
18	178	8.1	585	2 F85809	hypothetical prote
19	177.5	8.1	3705	2 AD0123	probable autotrans
20	175	8.0	1910	2 AF0394	flagellin - Escher
21	167.5	7.6	584	2 C48658	high-molecular-we
22	167	7.6	1477	2 B43855	Aida-I adhesin-lik
23	165.5	7.5	949	2 D90803	probable adhesin z
24	165.5	7.5	1005	2 H85611	high-molecular-we
25	165.5	7.5	1536	2 A43855	190k surface anti
26	165.5	7.5	2249	2 A41477	hypothetical prote
27	165	7.5	1343	2 E90893	probable RTX fami
28	165	7.5	1388	2 B85547	hypothetical prote
29	165	7.5	5291	2 F90696	hypothetical prote

30	164.5	7.5	936	2 I40711	sapB protein - Cam
31	164	7.5	4919	2 T31105	hypothetical prote
32	163.5	7.4	338	2 D90697	adhesin/Invasin-11
33	163.5	7.4	338	2 D90697	adhesin/Invasin-11
34	162.5	7.4	1635	2 A10452	hemolysin [importe
35	162	7.4	1335	2 T17508	glycoprotein Vp260
36	162	7.4	1343	2 D85724	hypothetical prote
37	160.5	7.3	2015	2 B81989	hypothetical prote
38	160	7.3	1655	2 E97835	hypothetical prote
39	159	7.2	1417	2 A83080	hypothetical prote
40	158.5	7.2	595	2 A48658	flagellin - Escher
41	158	7.2	2020	2 C48399	ABC-type transport
42	157.5	7.2	1461	2 E90696	hypothetical prote
43	157	7.1	3013	2 AB0480	probable invasiv
44	156.5	7.1	933	2 S41539	fibrinogen-binding
45	156	7.1	920	2 I40614	surface array prot

#### ALIGNMENTS

##### RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Accession: G81133

R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masigian, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoli, R.

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175753; PMID:10710307

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <TEXT>

A:Cross-references: GB:AE002450; GB:AE002098; NID:97226229; PIDN:AAE41395.1; PID:9722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match	Score	2108	DB 2	Length	591
Best Local Similarity	73.3%				
Matches	433	Conservative	0	Mismatches	0
				Indels	158
				Gaps	1
QY	1	MNKIYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASAN-----	52		
DB	1	MNKIYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL	60		
QY	53	-----	52		
DB	61	YLDPVORTAVAVLIIVNSDEKTEGTEKEKEVENSMAVYFNEKGVLTAREITLKAGDNLIKQ	120		
QY	53	-----	52		
DB	121	NGNFIYSLKKDLTDLTLSVTEKLSFNSANGKNKNTISDTGLNFAKTTAGTNGDTTYHLN	180		
QY	53	-----	82		
DB	181	GIGSTLTDLLNTGATNTVNDVTDDEKRRASVSKVLAAGNMIKGVKPGTTASDNDVF	240		
QY	83	VRIYDVEEFSADPTKTTTAVVESKDKKTEVIGATSVIKEDGGLVYGRKGEKSS	142		
DB	241	VRIYDVEEFSADPTKTTTAVVESKDKKTEVIGATSVIKEDGGLVYGRKGEKSS	300		
QY	143	TDEGEGLVTAKEVYIDAVNKRGMKTTTAGGOTGQADKFTVNSGTVTFASGKGTATV	202		
DB	301	TDEGEGLVTAKEVYIDAVNKRGMKTTTAGGOTGQADKFTVNSGTVTFASGKGTATV	360		
QY	203	SKDDGNTIYVYVNDGALNVQNLONGSNGLDSKAVAGSSGKVGISGNSPSKGMDET	262		

Db 361 SKDDGNTVWYDVNVGDLNVNQLONGSNMLDSKAVAGSSGKVIYSGNVSPSKGMDETV 420  
Qy 263 NINAGNNETIRNKNIDDIATSMTPQFSVSLGAGADPTLSVGDALNVGSKDKNRPV 322  
Db 421 NINAGNNETIRNKNIDDIATSMTPQFSVSLGAGADPTLSVGDALNVGSKDKNRPV 480  
Qy 323 ITNVAPGVKEGDVNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVAQVLPCKSM 382  
Db 481 ITNVAPGVKEGDVNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVAQVLPCKSM 540  
Qy 383 MAIGGGYRGEAGYAGYSSISDGNWIKGTASGNSRGHFGASASVGYOM 433  
Db 541 MAIGGGYRGEAGYAGYSSISDGNWIKGTASGNSRGHFGASASVGYOM 591  
RESULT 2  
A:1888  
Probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis (strain 2249)  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,  
; Holtroyd, S.; Jørgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajadream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: A81888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:A162755; GB:A157959; NID:97379742; PIDN:CA884461.1; PID:9737989  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match 91.5%; Score 2009.5; DB 2; Length 592;  
Best Local Similarity 70.4%; Pred. No. 3.6e-105;  
Matches 417; Conservative 7; Mismatches 9; Indels 159; Gaps 3;

Qy 1 MNKIYRIIWSALNMAVWVSELTNRHNRKASATVTAVALTLTFAVTA----- 51  
Db 1 MNKIYRIIWSALNMAVWVSELTNRHNRKASATVTAVALTLTFAVTAANATDEDEEEL 60  
Qy 52 ----- 51  
Db 61 ESYQSVSVGIQASMEGSELETISLSMTNDSKEFVDPIYVTLKAGNLKIKONTNENT 120  
Qy 52 ----- 51  
Db 121 NASSFTYSLKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180  
Qy 52 -----NRAASVKKVLANGNWIKGVKPGTTA--SDNVDF 82  
Db 161 GIGSLTTLTGLSSASHVDAGNQSTHYTRASIKYVLNAGNWKIKVKTGGSTTGGSENVDF 240  
Qy 83 VRTYDVEFLSADTKTTTVNWSKDNKGRKTEVIGAKTSVYKEKDKLVTGKDGKNGSS 142  
Db 241 VRTYDVEFLSADTKTTTVNWSKDNKGRKTEVIGAKTSVYKEKDKLVTGKDGKNGSS 300  
Qy 143 TDEGGGLVTAKEVIDAVNKAQKRMKTTTANGOTGADKFEYVTSSTNTVTFASGKGTATV 202  
Db 301 TDEGGGLVTAKEVIDAVNKAQKRMKTTTANGOTGADKFEYVTSSTNTVTFASGKGTATV 360  
Qy 203 SKDDGNTVWYDVNVGDLNVNQLONGSNMLDSKAVAGSSGKVIYSGNVSPSKGMDETV 262  
Db 361 SKDDGNTVWYDVNVGDLNVNQLONGSNMLDSKAVAGSSGKVIYSGNVSPSKGMDETV 420  
Qy 263 NINAGNNETIRNKNIDDIATSMTPQFSVSLGAGADPTLSVGDALNVGSKDKNRPV 321  
Db 421 NINAGNNETIRNKNIDDIATSMTPQFSVSLGAGADPTLSVGDALNVGSKDKNRPV 480  
Qy 322 RTTNVAPGVKEGDVNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVAQVLPCKS 381

Db 481 RTTNVAPGVKEGDVNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVAQVLPCKS 540  
Qy 382 MAIGGGYRGEAGYAGYSSISDGNWIKGTASGNSRGHFGASASVGYOM 433  
Db 541 MAIGGGYRGEAGYAGYSSISDGNWIKGTASGNSRGHFGASASVGYOM 592

RESULT 3  
A:16138  
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: J164138  
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.;  
Science 269, 486-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: J164138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:I42023; NID:91574588; PID:91574589; TIGR:HI1732

Query Match 15.7%; Score 345; DB 2; Length 298;  
Best Local Similarity 29.9%; Pred. No. 1.9e-12;  
Matches 87; Conservative 19; Mismatches 41; Indels 144; Gaps 2;

Qy 1 MNKIYRIIWSALNMAVWVSELTNRHNRKASATVTAVALTLTFAVTA----- 49  
Db 1 MNKIYRIIWSALNMAVWVSELTNRHNRKASATVTAVALTLTFAVTAINDAGTFFVKVQ 60  
Qy 50 ----- 49  
Db 61 STEDDIEDSAATKDDNKQALKAGDTLTLKAGKNLAKLDDGSGSVTFALAKDDVKTAK 120  
Qy 50 ----- 49  
Db 121 VSDTLTIGNTPPAGGATPKVSTSTADGLAKTNGDTVAHLNGLASTLPDYTTNTGA 180  
Qy 50 -----SANRAASVKKVLANGNWIKGVKPGTTA--SDNVDF 98  
Db 181 STSVTFSPDIEKFAATIKDVLNAGNWKIKAKVAGGTFENVDLVAGDNEFFITGDKNT 240  
Qy 99 TTVNWSKDNKGRKTEVIGAKTSVYKEKDKLVTGKDGKNGSSSTDEGE 147  
Db 241 LDVYLTAKENGTTEVKTPTKTSYKDNNGKLLTGKQLKDANTGTATNATE 291

RESULT 4  
A:82671  
surface protein Xfi529 [Imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: D82671  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2059 <SIM>  
A:Cross-references: GB:AE003982; GB:AE003849; NID:9106554; PIDN:AAF4338.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, L.E.A.; Carriero, D.M.; Carrier  
as-Neto, E.; Docena, C.; El-Poriry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Fr



J.D.: Junqueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigz, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.C.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.C.; Miyaki, C.V.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, E.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasata, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
.:Gene: XF1529

	Query Match	15.5%	Score 340.5;	DB 2;	Length 2059;
	Best Local Similarity	24.6%;	Pred. No. 3.6e-11;		
	Matches 137;	Conservative	70;	Mismatches 177;	Indels 173; Gaps 20;
QY	17 VVSELTNRNHTKRASATPVKTAVLTLLEFAYOASA-----NRASVKDKVLNAWNI- 67	:::	:::	:	: ::   :::
Db	1536 VVVNDLGLSIYGASLFTSGINAGSHK.TTNTACTGEPDADAVNFQSLKSVSVAVDKGWILT 15955	:::	:::	:	: ::   :::
QY	68 -----KGVPFGTTASDNV-----FVTTFDTVEFLSDPKT-----TTTVNWESK 106				
Db	1596 ASGANGSVVSGGVTDLKTNDGNLAISKSGDSNVFPLSKDFVEDEYTAGNTVYNTDGV 16555				
QY	107 DNGAKTEVKIGAKTSVIKEKDGLVTKDKCEN-----GSSTDEEGCLVTAKEVIDAV 159	: :	: : :   :	:	: : :   :
Db	1656 KVG--SDVSICAMGLFIANGPSVYASCPNAGDKYISHAVGMADPTDAVNSQLQAQVSY 17133	: :	: : :   :	:	: : :   :
QY	160 NKACWRMKTTT-----ANGOTGO--ADFETVYSTNV-----TFPASKGTGA 200	:	:	:	:
Db	1714 TVKATRYRYSYTGDDGGTGGNYDGDGATGSKAIAAGVGTQASEGEAAAVSSGAAGAAGSTGA 17737	:	:	:	:
QY	201 -----TYS-----KDDQGNTIVM 213	----	----	----	----
Db	1774 IGRNALISADGSVALGDGAKDGCGRAESTYCKYSGCVNNYVCTVSGVDAAGKETRSLSNV 18333	:::	:::	:	: ::   :::
QY	214 YDVNVG-DALNVNOL-----QNSGNLDS-----KAFA 240	: :	: : :   :	:	: : :   :
Db	1834 ADAKEAMDADVNLRLQDLDAVAQRKSNLOTPDMREHINNIEDVFRTKDGDSASSVKGMGVNMA 18933	: :	: : :   :	:	: : :   :
QY	241 GSSGSKVISCNVPSPKKMDDEVININAGNIIIEITRNKRIIDATISTPTPFSSVSLCAGADA 300	: :	: : :   :	:	: : :   :
Db	1894 IGYNAAAISGTESVALRG--NTNVSADAAVAI-GNG-----SVADRANSVSGSG-- 19399	: :	: : :   :	:	: : :   :
QY	301 PTLTSDVDGALNVGSKDKRKPVRIINVAPGVLEGEDVTNVAOLKGVAQNLMNRINDVNGAR 360	: :	: : :   :	:	: : :   :
Db	1940 -----GSEER-----QVINVAAGTADPTDAVNVNSQLNOGLITRKQYTDDGAVGHLR 1982	: :	: : :   :	:	: : :   :
QY	361 ---AGTAAQTATAGLVQAVLPGRSMALIGGGTYRGEAGVALIGVSSISDGGNMIIKTGAS 416	:	:   :   :	:	:   :   :
Db	1983 RETSGGVAAAIATATANTLPQAVYQGRGMTSVGSSVYOGGALIAVGSVAESEGHWFKFSGS 20424	:	:   :   :	:	:   :   :
QY	417 GNSRGHPFASASGYOW 433	:	:   :   :	:	:   :   :
Db	2043 ANTRSHVGVGAGVGIYW 2059	:	:   :   :	:	:   :   :

RESULT 5  
A82615  
surface protein xrl1981 [imported] - xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-1190 <STM>  
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN000

A:Experimental source: strain 9a5c  
R:Rimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
B:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier  
as-Neto, E.; Docena, C.; El-Dority, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; La  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.S.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.U. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1981

[illegible]

RESULT 6  
AB6036  
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL936)  
C.Species: Escherichia coli  
C.Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C.Accession: AB6036  
R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, M.L.; Miller, L.; Grobbeck, E.J.; Davis, N.W.; Jim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.;  
Nature 409, 529-533, 2001  
A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A.Reference number: AB5480; MUID:21074935; PMID:11206551  
A.Accession: AB6036  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 11588 <STO>  
A.Cross-References: GB:AB005174; NID:912518349; PIDN:AA658749.1; GSPEDB:GN00145; UMGP:EDL936  
A.Experimental source: strain O157:H7, substrain EDL936  
C.Genetics:

**A;Gene: Z5029**

Query Match	15.0%;	Score 329.5;	DB 2;	Length 1588;
Best Local Similarity	26.1%;	Pred. No. 1.1e-10;		
Matches 118;	Conservative 63;	Mismatches 177;	Indels 94;	Gaps 177;

[illegible]

## RESULT 7

H91188  
 probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMM)  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
 R:Hagashi, T.; H91188  
 gasavara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome  
 A:Reference number: A99629; MUID:21156231; PMID:11558796  
 A:Accession: H91188  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1588 <NRY>  
 A:Cross-references: GB:BA000007; PTDN:BAB37903.1; PTD:g136363955; GSPDB:GN00154  
 A:Experimental source: Strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: ECs4480

```

Query March 15.0%: Score 329.5; DB.2: Length 1588;
Best Local Similarity 26.1%: Pred. No.1.1e-10;
Matches 118; Conservative 63; Mismatches 177; Indels 94; Gaps 17;

QY 49 ASANRAASVKDVLNAGNMKGVKPGTASDNDVDFRYDVE-FLSADTKTTTVNVESKD 107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1164 SEADDAVTYRLOLONA-----IGAVATPTPTKFFHANSTREDSLAVGTDSLAKGARTIY 1215
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 108 NGKK-----TEVKIGAKTSVTKKDKGKLVNGKDGKSGNSRDEDEGLVTA 152
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1216 NGDKGIGIGICATYDANALNGLAIGSNAQYIHV--NSTAIG-----NSTITTRRAQNIYT 1268
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 153 KEVIDAVNKAGWRMKTTTANQO-----TGQADKFTVTSGLTVTFASGKGTATVASC 205
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db      1269  AYNNDAPQNSGFEVSGSADGQROITNNAGSAD-----TFAVNV--GQLVTPAQVSON 1321
Qy      206  DQGMITVA-----YDNNNGDAL-----NVNQLQNSGMMLLDKSAVAGS 242
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1322  TQ-SITNLNDNRVYMLDSREVTINENGIGIVYTGSTKFKFTKNTDQVDASQAGKDSVALIGSG 1380

```

```

OY      243  GKVXISGVSPSKKM---DETVINNGNNIEIRN---GKN---IDITSMPQSSV 292
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1381  STAADNSVALGCTSSVATEENTIVGSSSTNORRTITNVAAGKNATDAVNAQLKSEAGV 1440

OY      293  SLGAGADAPLTIVDGDALNVGSKKDNKPRVTRITNAPGVKEGDVTNVAQLKGAO----- 346
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1441  RYDFRKAD---SIDYSNTLGG-GNGGTTIRISVAGANNNDVYNAQLKQSVQETROYT 1496

OY      347  -----NLNLRIDNVGNAKAGIAQAIATAGLVQAYLPDGKSMALIGGTYRGEAGYALGYS 401
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1497  DÖRVEVENDNKLKSTESKLGGIASAMAMGTGIPQAYTPQASWASIGGTYMGESAVALGVS 1556

OY      402  SISDGMMIITKGTASGSRGHFGASASVGYOM 433
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1557  MVSANGRWVYKLGSTINSQGEYSALAGAIOW 1588

```

RESULT 8  
AC0976

Probable autotransporter sagB [imported] *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 A:Note: This species has also been called *Salmonella typhimurium*  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AC091976  
 R:Parkhill, J., Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, T.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, P.; S. Moulé, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.; White, J.  
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium  
 #:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Residues: 1-1107 <PAR>  
A:Cross-references: GB:AL513382; PID:916504923; GSPDB:GN00176  
C:Genetics:  
C:Gene: sap3  
  
Query Match 14.8%; Score 326; DB 2; Length 1107;  
Best Local Similarity 20.5%; Pred.No.1.le-10;  
Matches 142; Conservative 89; Mismatches 18; Indels 278; Gaps 25;

[illegible]





QY 362 GAAQAIAAT-----AGLQAVLPEKSM--MAIGGTYRGEAGYAGYSSISDGN 408  
 Db 473 SLGANAATYVSGGYTYVONLQAIKINKLIDGLVGLGNTLGGSYCTALGSLG-GR 511  
 QY 409 WIIKCTAS--GNSRGHFGS 426  
 Db 532 GVFSGLDGLGNSIGLSTIS 551

RESULT 13

hypothetical protein b2000 - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: G64964  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: G64964  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1091 <BLAT>  
 A:Cross-references: GB:AE000291; GB:U00096; NID:q1788298; PIDN:AACT5061.1; PID:q1788309;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Keywords: nucleotide binding; P-loop  
 F:683-690/Region: nucleotide-binding motif A (P-loop)

Query Match 8.5%; Score 186.5; DB 2; Length 1091;  
 Best Local Similarity 21.8%; Pred. No. 0.0067;  
 Matches 112; Conservative 56; Mismatches 201; Indels 145; Gaps 20;

QY 1 MKKIYIINNSALNAVYVSELRNTRKASATVRAVLATLFAVYQASANRAAVKDY 60  
 Db 57 LNTCYRLVNMHTGAFVASELARAKRGVAV-----ASTLAIVTSLPVLAAOI--V 108  
 QY 61 LNAAGNIKGVKPGTASDVNDFV-----RTYDFVEFLSADTKTTVNVESKDN--KKT 112  
 Db 109 VHRGEVYNG---GTLANHNOIVFGTNGMTISTGLEYPDNANANGGQWQVGGTANKT 165  
 QY 113 EVKIG-----AKTSVIEKDKGLYTK--DKENGSSYDEEGGLYTAKEVIDAVN 160  
 Db 166 TVTSGGLQRYVNPGSYSDTVISAGGQSLOGRAVNTTLNGGEQMHGALATGTVL--N 222  
 QY 161 KQWR-----KMTTA-----NGTGOADKPEYV-----TS 186  
 Db 223 DKGMQVVKPGYATDTVNTGAEAGDAENGDTGDFVRGDAVRTTINKNGROIYRAEGTA 282  
 QY 187 GENVFASGKGTATVSKDDOGNITVMDVNVGDALNVNOLONGMNL-DSKAVAGSSGK 245  
 Db 283 NITTVYVAGDDQYHGAIDLTLTLNGYQYHNGSTASD-IYVNSDGMQIYKNGVAAAGTIV 341  
 QY 246 VISGNVSPSKMDETVINAG-----NNIEITRNGKN 278  
 Db 342 NQKGRLOVDAGGATATVTEKQGALVTSPATVTGINRLGAFSVEGKADNV-VLENGGR 400  
 QY 279 IDIATMTPOFSSVSLGA-----GADAPTLV-----DDDALNVGSKKNKPYRIT 324  
 Db 401 LDVLTHTATNTRKVDGGLDVNRNGGTATVSGNGSVLLADGAAGVSGRSDGK----- 455  
 QY 325 NVAPEGKEDVTVAOLKGAQNLNRRIDVNDNARAGIAQATATAGLVQAVLPKSMMA 384  
 Db 456 --AFSTGGQADALMEKGSFTLN-----AGDAPDTT----- 487  
 QY 385 IGGTYRGEAGYAGYSSISDGNWIIKCTASGN 418  
 Db 488 VNGGLTARGGLAGTTTLNCAITLISGKTVNN 521

RESULT 14

AB1019  
 adhesin/Invasin, probable NMB1994 [Imported] - Neisseria meningitidis (strain MC58 serog

C:Species: Neisseria meningitidis  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
 C:Accession: AB1019  
 R:Reitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Hart, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scaliato, V.; Masiagnan, V.; Piazza, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A:Reference number: AB1000; MUID:20175755; PMID:10710307  
 A:Accession: AB1019  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-364 <RET>  
 A:Cross-references: GB:AE002548; GB:AE002098; NID:97227249; PIDN:AAAF42321.1; PID:9722  
 A:Experimental source: serogroup B, strain MC58  
 A:Genetics:  
 A:Gene: NMB1994

Query Match 8.5%; Score 186; DB 2; Length 364;  
 Best Local Similarity 25.7%; Pred. No. 0.0019;  
 Matches 112; Conservative 56; Mismatches 156; Indels 112; Gaps 24;

QY 31 SATVKTAVLATI---LFAIVQASANRAASVKDY--LNGWNIVKVPPTASDVNDFVR 84  
 Db 8 SKVLTATLALTFCSGALAAATSDDDVKKAATVAIVAAYNNGQETNGFKAGET----- 58  
 QY 85 TYDFVEFLSADTKTTVNVESKD--NGKTEVYIGAKTSYIKKDKLTYGKRGENGSS 142  
 Db 59 IYDIGEDGTYTQDADTAADVADDFRG-----LGK-----KVYINLTQYVEN- 102  
 QY 143 TDEGEIYTAKEVIDAVNKNAG---WRMKTTTANGTQGAOKPEFVTSCTNVTFAAGKGT 198  
 Db 103 -----KQVNDKAVRAESEIEKLTTLKADTPAALADTPAALDETTNALNKGENT 152  
 QY 199 TATVSKDDGNTVMDVNVGDALNVNOLONGMNLDSKAVAGSSCK-----VISGNVS 252  
 Db 153 T-TFAEETKTNI-----VKIDEKL-----EAVADTVDKHAEFNDIADSLD 192  
 QY 253 PSKGMKDETVNI--NAGNNEITRNGKNIDTASMTPOFSSVSLGACADAPTLISVGDAL 310  
 Db 193 EYTKADEAVKTAENEKQTAETKR--QND-----AKVAAETAAKABRAAGTAN 241  
 QY 311 NVGSKKDNKPYRITTVNAPGVEGDTVNVQOLKGAQNLNRRIDVNDG-----ARAGI 363  
 Db 242 TAADKAEVAAKATD-----IKADIATNKAD---IAKN-SKIDSLDKRVANLKEKTRGL 293  
 QY 364 AQAIAATAGLVQAVLPKSMMAIGGTYRGEAGYAGYSSISDGNWIIK-----GTASGN 418  
 Db 294 AEGQALISGLFQPYNNGRFTVTAAVGVKSSSAVAIG-TGRFTENFAAKGAVAVGTSSGS 352  
 QY 419 SRG-HFGASASVGTOW 433  
 Db 353 SAAVHWG---VNYEW 364

RESULT 15

AB3486  
 cell surface protein [Imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: AB3486  
 R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, Mazur, M.; Goltsman, E.; Sekov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AB3486  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-365 <KUR>  
 A:Cross-references: GB:AE008917; PIDN:AAL53053.1; PID:q17983913; GSPDB:GN00190  
 A:Experimental source: strain 16M



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 6.68663 Seconds  
(without alignments)

3045.266 Million cell updates/sec

File: US-09-771-382-26

Perfect score: 2197  
Sequence: 1 MNKIRIINNSALNANWVVS.....TASGNSRGHFGASASVGYQW 433

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	8.6	1286	1 AIDA_ECOLI	Q03155 escherichia
2	186.5	8.5	1039	1 AGA3_ECOLI	P39180 escherichia
3	182	8.3	1325	1 YDEK_ECOLI	P32051 escherichia
4	165.5	7.5	2249	1 OMPA_RICRI	P15921 rickettsia
5	160	7.3	1655	1 OMPB_RICCN	O9K433 r outer mem
6	158	7.2	2003	1 YDBA_ECOLI	P33666 escherichia
7	150	6.8	1300	1 120K_RICRI	P14914 rickettsia
8	150	6.8	1654	1 OMPB_RICRI	Q53047 r outer mem
9	148	6.7	550	1 FLIC_SHIFL	O08860 shigella fl
10	147.5	6.7	2021	1 OMPA_RICCN	Q52657 rickettsia
11	147	6.7	1025	1 SLAP_CAUCR	P35828 caulobacter
12	145.5	6.6	1861	1 APD1_THERU	P38336 t anlytopull
13	145	6.6	497	1 FLIC_ECOLI	P04949 escherichia
14	142.5	6.5	1007	1 Y741_CHILMD	O9P156 chlamydia m
15	142	6.5	1608	1 HLVA_SERMA	P15320 serratia ma
16	142	6.5	1953	1 BIGA_SALTY	P25927 salmonella
17	141.5	6.4	737	1 ALYS_EMTPA	P37710 enterococcu
18	141.5	6.4	1567	1 ICERX_XANCT	P18127 xanthomonas
19	140.5	6.4	930	1 PMPB_CHLPN	O9Z993 chlamydia p
20	140	6.4	1577	1 HLVA_PROMI	P16466 proteus mir
21	138.5	6.3	365	1 FLIC1_PROMI	P42262 proteus mir
22	138.5	6.3	2660	1 YEBL_ECOS7	O08897 escherichia
23	138	6.3	507	1 FLIC_SALON	O06974 salmonella
24	137.5	6.3	367	1 FLIC2_PROMI	P42273 proteus mir
25	137	6.2	933	1 SLAP_CAMEE	P33527 campylobact
26	136.5	6.2	1656	1 OMPB_RICJA	O06653 r outer mem
27	136	6.2	507	1 FLIC_SALBE	O06968 salmonella
28	136	6.2	1228	1 SLAP_BACST	P35825 bacillus st
29	134.5	6.1	444	1 SLAP_IACAC	P35829 lactobacilli
30	134.5	6.1	1148	1 ICERX_PSESX	O30611 pseudomonas
31	134.5	6.1	1569	1 YPDA_ECOLI	P52143 escherichia
32	133.5	6.1	504	1 FLIC_SALRO	O06982 salmonella
33	133	6.1	464	1 FLIC_ECO57	P58397 escherichia

34	133	6.1	642	1 FLIC2_CAMEE	Q9P166 campylobact
35	133	6.1	918	1 YMBJ_CAEEL	P34487 caenorhabdi
36	133	6.1	928	1 P40B_CHLPN	O9R065 chlamydia p
37	133	6.1	1258	1 ICERX_ERMHE	P16239 erwinia her
38	133	6.1	1645	1 OMPB_RICRY	P96889 r outer mem
39	132.5	6.0	445	1 G6PL_BACTN	O8A5W2 bacteroides
40	132.5	6.0	523	1 P60_LISSE	O01638 listeria se
41	132.5	6.0	1196	1 ICERX_PSESX	O33479 pseudomonas
42	132.5	6.0	3178	1 YS89_CAEEL	O06624 caenorhabdi
43	132	6.0	484	1 P60_LISMO	P21171 listeria mo
44	131.5	6.0	461	1 US45_LACIC	P22865 lactococcus
45	131.5	6.0	504	1 FLIC_SALBU	O06969 salmonella

#### ALIGNMENTS

```

RESULT 1
ID AIDA_ECOLI STANDARD: PRT: 1286 AA.
AC 003155,
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adhesin aidA-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Plasmid pIB6.
OC Bacteria: Proteobacteria; Gammaproteobacteria: Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 50-56.
RC STRAIN=0126:H27 / 2787;
RX MEDLINE=92326538; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X65022; CAA46156.1; -
CC PIR: S28634; S28634.
CC InterPro: IPR006315; Autotransport.
CC InterPro: IPR005546; Autotransporter.
CC InterPro: IPR004899; Pertactin.
CC Pfam: PF03797; Autotransporter; 1.
CC TIGRPFAMs: TIGR01414; autotrans_Par1; 2.
CC Cell adhesion; Signal; Outer membrane; Plasmid.
CC
CC SIGNAL 1 49
CC CHAIN 50 2 ADHESIN AIDA-I.
CC PROPEP ? 1286
CC SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
Query Match 8.6%; Score 189; DB 1; Length 1286;
Best Local Similarity 24.7%; Pred. No. 0.0043;
Matches 111; Conservative 57; Mismatches 189; Indels 92; Gaps 23;
QY 1 MNKIRIINNSALNANWVVSLETRNHTKRASATVKTAVLA--TLLEFAVQASANRAASYK 58
||| | ||| : ||:| ||| | || | ||| | : : |

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Db 1 MNKAYSTIWSHROAMIVASELARGH-----GVLAKNLTLLVIAVSTIGMAPAV- 50
QY 59 DVLAGNNGKGV--KPGTASDNVDFRTYDFELSDTKTTVN--VESKNGKTE 113
Db 51 -----NISGTSSGSGTSGEQIV-----YSGRGNMNAVNSGGIOIVANGCKT- 95
QY 114 VKIKAKSVIKKDKGLVTKDKKENGSSDDEGGLYAKVIDAVNKAQRMTTTRANG 173
Db 96 -----TATVNSSG-----SQNVGTSAGTI-----STIVNSGGIORVSSG-----VASATIN 137
QY 174 OTGQADFEIVTSGTNTFASGKTATFVSKDDGNTVMDVAVGALANN--OLONS 230
Db 138 LSGAQNIVNLGHSNVIFSG-----GNQTI-FSGGIDTSTNSSGQOQVRS 184
QY 231 GWNIDSKAVAGSSGKIVSGNVSPSKMDKDETVINAGNNIETIRNGKNIDATSMPTQFS 290
Db 185 SGVAVSWTTINSSG---AQNTLSEGAII--STHSSGNGQISA-GANATEETIVNSGGFQ 238
QY 291 SVSLGAGADAPTLSDVDALNVGSKKDNKPRITNVAPGKEGVTVAOLKVAQNLNN 350
Db 239 RVNSGAVATGTVLGGTQNVSSGSAISTVYNSGVGTVFAGATVTTVNSGNGONISS 298
QY 351 RIDNVDNARAGIQ--AIIAGLVQAYLPKSKMAA-IGGTYGEGAVATGYSISDGG 407
Db 299 -----GGIVSETTVNSGTQNTYSGGSAISANIKSQIVNSEGTAIN-TLVSDG 347
QY 408 NMIIK--GTASG---NSRGHGASAVGY 431
Db 348 YOHIRNGIASGTIVNOSGYNIS-SGGY 375

RESULT 2
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P3180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluifling protein).
GN Flv OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-9742661; PubMed-9278503;
RA Blatter F.R., Plunkett G., Iii, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97251358; PubMed-9097040;
RA Itoh T., Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiochi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN-ML 308-225;
RX MEDLINE-89291704; PubMed-2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
RT 43, a unique protein complex associated with the outer membrane of
RT Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN-K12 / EMG2;
RX MEDLINE-97443975; PubMed-9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RP GENE NAME.
RX MEDLINE-97257509; PubMed-9103983;
RA Henderson I.R., Meehan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
RT determines colony morphology and autoaggregation in Escherichia coli
RT K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
CC FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
CC -1- SIMILARITY: TO ADHESIN ALDI-1 AND TO BORDETELLA PERTACTIN.
CC
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CC
DR EMBL: AE000291; AAC75061.1; ALT INIT.
DR EMBL: D90838; BAA15825.1; ALT INIT.
DR EMBL: D90839; BAA15832.1; ALT INIT.
DR EMBL: U24429; AAB47869.1; -.
DR HSSP: P07505; ISRD.
DR EcoGene; EG12686; flv.
DR InterPro: IPR006315; Autotransporter.
DR InterPro: IPR005546; Autotransporter.
DR InterPro: IPR004899; Pertactin.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
KW Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551
FT CHAIN 552 1039
FT VARIANT 2
FT VARIANT 41 42
FT VARIANT 46 46
FT VARIANT 157 157
FT VARIANT 188 188
FT VARIANT 303 305
FT VARIANT 320 320
FT VARIANT 372 372
FT VARIANT 493 493
FT VARIANT 497 497
FT VARIANT 585 585
FT VARIANT 709 709
FT VARIANT 721 721
FT VARIANT 751 753
FT VARIANT 803 803
FT VARIANT 815 815
FT VARIANT 824 824
FT ANTIGEN 43 ALPHA CHAIN.
FT ANTIGEN 43 BETA CHAIN.
FT K -> N (IN STRAIN ML 308-225).
FT SL -> FE (IN STRAIN ML 308-225).
FT T -> K (IN STRAIN ML 308-225).
FT W -> L (IN STRAIN ML 308-225).
FT V -> F (IN STRAIN ML 308-225).
FT ATN -> STI (IN STRAIN ML 308-225).
FT A -> T (IN STRAIN ML 308-225).
FT N -> Q (IN STRAIN ML 308-225).
FT E -> V (IN STRAIN ML 308-225).
FT S -> N (IN STRAIN ML 308-225).
FT H -> Y (IN STRAIN ML 308-225).
FT E -> K (IN STRAIN ML 308-225).
FT M -> T (IN STRAIN ML 308-225).
FT GHL -> SHF (IN STRAIN ML 308-225).
FT S -> P (IN STRAIN ML 308-225).
FT A -> V (IN STRAIN ML 308-225).
FT C -> S (IN STRAIN ML 308-225).

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FT  VARIANT      829      835      LNLVHTS -> MNLIVNA (IN STRAIN ML 308-
FT  VARIANT      845      847      OGN -> LGA (IN STRAIN ML 308-225).
FT  VARIANT      855      855      S -> T (IN STRAIN ML 308-225).
FT  VARIANT      888      888      Q -> L (IN STRAIN ML 308-225).
FT  VARIANT      1025     1025      S -> I (IN STRAIN ML 308-225).
FT  CONFLICT      61       63       ETV -> TTT (IN REF. 5).
SQ  SEQUENCE      1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;

Query Match
Best Local Similarity 21.8%; Score 186.5; DB 1; Length 1039;
Matches 112; Conservative 56; Mismatches 201; Indels 145; Gaps 20;

OY 1 MNKRIIINSALNANVAVVSELTRNHTKASATVKAVALATLLEFATVOASNRASVKVY 60
DB 5 LNTCTRLVNMHTGAFVVASSELARAGKGGVAV-----ALSLAATVLPVLAADI--V 56
OY 61 LNAGNNIKVKGKGTASDNDV-----RTYDVEFLSADTKTTTVNESKDNQ--KKT 112
DB 57 VHPGETVNG---GTLANHDNQIYFGTNGMTISTGLEYGPRDEANTGGQWDDGDTANKT 113
OY 113 EVKIG-----AKTSVKEKDKLVTKG--DKGEGSSSTDEBEGVLTAKVETDAVN 160
DB 114 TTTSGGLORVNDGGSVSDTVISAGGQSLOGRAVNTTLNGSGQWMEGAIATGTVI--N 170
OY 161 KAGWR-----MKTTTA-----NGOTGQADKFEYV-----TS 186
DB 171 DKGWQVVKPGYATVDVVTGTAEGGPDANGDTCGVRBDARTITNKGRQIVRAEGTA 230
OY 187 GNNVTFASGKGTATVAVSKDDGNTIVYDVNVGDALNVNOLONGMNL-DSKAVAGSSGK 245
DB 231 NTFVYVAGGDDQTVHGHALDTTLNGGYQYVHNGGTASD--TVVNSDGMQIVKNGVAGNTIV 289
OY 246 VTSQNVSPSKGMDHEVNINAG-----NNEIFTRNGKN 278
DB 290 NOKGRLOVDAGGTATNVTLKOGALVTSTAATVYTGINRLGAPSVYEGKADNV-VLENGR 348
OY 279 IDIATSMTPQFSSVSIGA-----GADAPPLISV-----DGDALNVGSKDKNPKVRIT 324
DB 349 LQVLGHTATNTRVDDGGLVDVRNGSTATTVMGNGCVLLADSGAIVSGTSTRSGK----- 403
OY 325 NVAPEGVEGDTNVNAOLKQVANOINNRIDNVGNARAGIAQATAGLVQAVYLPGKSKMA 384
DB 404 --AFSIGGGQADALMEKSSSFTLN-----AGDTATDDT----- 435
OY 385 IGGGTYRGAAGYAIGSSISISDGNMIRKGTASGN 418
DB 436 VNGGLTFARGGLAGTTTLNNGAIIITLTSKTYVNN 469

RESULT 3
YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).

```

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakano S., Nakamura Y., Nishimoto H., Nishio Y., Oshino T., Saito N.,
RA Sempel G., Seki Y., Sivasubaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Tjims M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: TO E. COLI YEAL.
CC -1- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -1- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000248; AAC74583.1; -
DR EMBL: D90793; BAA15190.1; ALT_INIT.
DR EMBL: D90794; BAA15197.1; ALT_INIT.
DR EMBL: X73295; CAA51730.1; ALT_FRAME.
DR PIR: A64905; A64905.
DR Ecogene: Egl1780; ydek.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal.
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHEICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 884 N -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
FT FT
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19ADVD CRC64;

Query Match
Best Local Similarity 8.3%; Score 182; DB 1; Length 1325;
Matches 125; Conservative 60; Mismatches 216; Indels 172; Gaps 23;

OY 1 MNKRIIINSALNANVAVVSELTR-----NHTRASATVTAVALATLLEFATVOASAN 52
DB 1 MNRIYVNWCTLOVFOACSELTRRAGKSTVNLKSSGLTKFSRLTGLVLLALSAS 60
OY 53 RAA-----SVKDVNLAGW-----NIKGVFPGTASDNDVFPRTYDVEFLSAD 95
DB 61 GASLEVDNDQIINIDVDVAVDAVGVYGTGVNIIAGNAS-----LTTITTSVIGANE 115
OY 96 TKTITVNV-----ESKDNKRTVEY-RIGAKTSVYKEK-----DGLKVTGDKGNGSS 142
DB 116 DSEGTAVNVAGTWRLDSDNNAPLNVGSGSTGLNIKQKHGVDGGLRSGSTGCVTV 175
OY 143 TDEGDEGLVYAKVYID-----AVNKAQ-WRM 166
DB 176 NVEGEDSVLTLELFGSYGTGSLNITDKGYTSSITVAIIIGYQAGSNGGVYVEKGEWLI 235

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QY 167 KTTTA-----NCOTGADKFEVTVSGTNTVF-----ASGKTTATVSKDQGNIT 211
D 236 KNDSSIEFOJIGNOGTGEA-----TIRREGGLVTAENTIGGNATIGLWVODDSDVITVR 291
QY 212 VMVD-----VWGDALN--VNOLONGMWL----- 234
D 292 RLIVGTYGNGTVAINNGLINNKKEYSLVGVODGSHGVVNTDKHMFNLGEGEAFRIYI 351
QY 235 ----DSKAVAGSSGKVIISGVNPSKGMDEF-----VNINANNIEITRNKN 278
D 352 GDADGDGLNVSSEKGVDSGITTAG--MKETGTGNTIYVKOKNSVITNLGTLGYDGHGEM 408
QY 279 IDITSMTPPESSVSLGAGADAPTLSDGALNAGSKKD--NKPVRIITNVAFCVKEGDYTN 337
D 409 NISNOGLVNSGSSSLGYG---ETGVGNVSITTGGMWEVKNVYTTIGVAGVGNLNSD 464
QY 338 VAQLKGAQNLMNRIDVNDGNARAGIAQAITAGLYOAYLP--GSKMAIGGTYRGAG 395
D 465 GG--KFSQNTFTFGDKASGIGTLNMDATSSFTVGLVNGNFGSGIVNNSGATLNSGTG 522
QY 396 YAI-----GYSSISDGGNMIKGTASGNSR 420
D 523 YGFIGNAGSGKIVINISTDSLMLNK--TSSTNAQ 554

```

## RESULT 4

OMPA\_RICRI

ID OMPA\_RICRI STANDARD; PRT; 2249 AA.

AC P15921;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmpA A).

GN OMPA.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI\_TaxID=783;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90354033; PubMed=2117568.

RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;

RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";

RL Infect. Immun. 58:2760-2769(1990).

CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.

CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.

CC -1- PFM: GLYCOSYLATED (PROBABLE).

CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

CC -----

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CC -----

CC EMBL, M31227; AAA26380.1; -.

DR PIR; A41477; A41477.

DR InterPro; IPR006315; Autotransport.

DR InterPro; IPR005546; Autotransport.

DR Pfam; PF03797; Autotransporter; 1.

DR TIGRPFAMS; TIGR01414; autotrans\_ber1.3.

KM Antigen; Repeat; Cell wall; S-layer; Glycoprotein.

FT SIGNAL 1 28 POTENTIAL.

FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.

FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.

FT REPEAT 212 286 A (TYPE I).

FT REPEAT 287 358 B (TYPE II).

```

FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE I).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE I).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MM; A9D646C089DF087 CRC64;

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Query Match 7.5%; Score 165.5; DB 1; Length 2249;  
 Best Local Similarity 25.1%; Pred. No. 0.15;  
 Matches 127; Conservative 46; Mismatches 180; Indels 153; Gaps 27;

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QY 32 ATYAT-AVLATLLEFATYQASANR---AASYVDVYNAGNINIKGVKPGTTASDNDVFRTYD 87
D 807 ATISVGATATLGGAVIKATTTKLTNAAASVLTITNANAVLGAVDNTGGDNGVNLNG 866
QY 88 TVEFLSADTKTTTVNVESKDKGKTEVIGAKT---SVIKERDKL----- 130
D 867 ALSQVTDIGNT-----NSLAT-ISVGAGTATLGGAVIKATTTKLTNAAASVLTITLNA 917
QY 131 -----VTGKDKGENGSST-DEGEGLVT-----AREVI 156
D 918 NAVLTGAIDNTGGDNGVNLNGLALSOVTDIGNTNSLATISVGAGTATLGGAVIKATTT 977
QY 157 DAVKAGKRAKTTTANQOTGADKFEVTVSGTNTFPASGKGTATYVSKDQGNITWAYDV 216
D 978 TKLTDASAVKFTVPVYVGTGIDNTGNANNGI-VTFGNSTVTVGN-----GNTNALATV 1031
QY 217 NVGDALNVNOLONGMWNLDSKAVAGSSGKVIISGVNPSKGMDEFVNIINAG-----NNIE 271
D 1032 NVGAGL--LOYQGVVAVANTINLTDNASAVFTTPVYVGTGIDNTGNANNCIYTFGTNST 1089
QY 272 ITRNGKNIDATSMTPPESSVSLGAGADAPTLSDGAL--NVGSKRDN-KPVRIITNVA 328
D 1090 VTGVGN-----TNLATVAVNGAG--LLQYQGVVAVKANTINLTDNASAVVFTN--P 1136
QY 329 CVKCGDVATNVAQLKGVQNLNRIDVNDGNARA---GIAQAIAT---AGL-VQAYLPG 379
D 1137 VVVYGAIDNNG-----NANNGIVTFEGNSTVGTGIDNTGNALATVAVNGAGITLQA--G 1186
QY 380 KSWMA-----IGGTYRGEAGVAYIG---SSISDGGNMIK----- 412
D 1187 GSLAANNIDEGARLTLENGPLDGG-----GKAIPYFGKALANGNNAIILNVTKILTA 1240
QY 413 ----GTASGNSRGH---FGASASVG 430
D 1241 SHLTGTVAELINIGAGNLTIDASVG 1266

```

## RESULT 5

OMPB\_RICCN

ID OMPB\_RICCN STANDARD; PRT; 1655 AA.

AC O9KKA3; O9KKA3; O9KKA3; O9KKA3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein)

DE (Surface protein antigen) (Cell surface antigen 5) (Scab) (rOmpB)

DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].

GN OMPB OR RC1085.

OS Rickettsia conorii.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI\_TaxID=781;

RN [1]

RP SEQUENCE FROM N.A.

```

FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 1655 OUTER MEMBRANE PROTEIN B.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).

```



RT Escherichia coli K-12.  
RL Blochmle 73:1361-1374(1991).  
CC -1- SIMILARITY: TO S. TYPHIMURUM ORF NEAR CYS6 (AC P25928).  
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR  
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
CC BETWEEN AMINO ACIDS 839 AND 840.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AE000237; AC074483.1; ALT\_SEQ.  
DR EMBL: AE000237; AC074487.1; ALT\_SEQ.  
DR EMBL: D90778; BAA15009.1; ALT\_SEQ.  
DR EMBL: D90778; BAA18880.1; ALT\_SEQ.  
DR EMBL: D90779; BAA18881.1; ALT\_SEQ.  
DR EMBL: X62680; -; NOT\_ANNOTATED\_CDS.  
DR EcoGene: EG1307; ydbA.  
KM Hypothetical protein: Complete proteome.  
FT CONFLICT 489 489 I -> V (IN REF. 2).  
FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;  
  
Query Match 7.2%; Score 158; DB 1; Length 2003;  
Best Local Similarity 23.2%; Pred. No. 0.34;  
Matches 112; Conservative 61; Mismatches 111; Indels 138; Gaps 26;  
  
QY 33 TVKTAVIATLLEFATVQASANRPAASVKVLYNAGNIKVKPGTTASDN--VDEVRYDTV 89  
DB 151 TEKLTITRDSVF--TYTENADGTTSLD-----SNORKATIMLMQIDEANNTVAL 198  
QY 90 EPLSADIKT-----TTYNVESKONKKEVKGAKKTV--IKENKDKLYTK 134  
DB 199 EGVASADATKQYHNHSELVITGNATVNNNGKTT--VDEKSTGEIINGNNKRVYDGG 255  
QY 135 DKENG-----SSTDEGEGLVYAKE-----VIDA-----VNRAGWEMKTTTANQ 174  
DB 256 DLVSGGGHGDIDTGSATVNDKGTMTVTDPESGIDIDGKALVNNBG--ESTIINGG 312  
QY 175 TGQADKREYV-----SGTNTVFASGK-----GTTAT 201  
DB 313 TGTQINDGDDATANNNGKTVYDGDKSTGEIINGNNKVIYDGGDLVSSGGHGDIDTGSAT 372  
QY 202 VSKDGNITVYMYDVNVDGALNVNQ--LQNSGMNLDKAVAGSSGKVISGN--VSPSKG 257  
DB 373 V--DNKGTMTVTDPESIGIYDGDQAVVNNNG--ESAITNGGTQIINGDADATANNNGK 427  
QY 258 -----MDETVINAGNN-----IEITRNGKNIDI-AUSMTPQFSSVSLGAGADAPTL 303  
DB 428 TTVYDGRKSTGTELAGNNKVIYDGGDLVSSGGHGDIDTGSATVNDKGTMTVTDPESIGI 487  
QY 304 SVYDGDALVNSKDKNKRVTITNVAPEKEDVYTNVADKVAQNLNLR-IDNVGNAKAG 362  
DB 488 QIDDDQALVNNES--TTINGGTG-----TQINGDADATANNNGKTVYDGGKSTG 535  
QY 363 IAAQIAVAGLVQAVLPKSMMAIGGTYRGEAGVATYSSISDGGNNILIGTAGNSRGH 422  
DB 536 -TKIAGNIGIVN--LDG-SLIVTGG-----AHGEVENTIGDNGTVNNKNDIYVDSGS 582  
QY 423 FG 424  
DB 583 IG 584

DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 120 kDa surface-exposed protein.  
GN P120.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R:  
RA MEDLINE=90136087; PubMed=2515418;  
RX Gilmore R.D. Jr., Joste N., McDonald G.A.;  
RT "Cloning, expression and sequence analysis of the gene encoding the  
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
RL Mol. Microbiol. 3:1579-1586(1989).  
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS  
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES  
CC CONFERRING ANTIGENICITY TO THE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X16353; CAA34402.1; -.  
DR PIR: S07575; S07575.  
DR InterPro: IPR006315; Autotransport.  
DR InterPro: IPR005546; Autotransporter.  
DR Pfam: PF03797; Autotransporter; 1.  
DR TIGRFAMs: TIGR01414; autotrans\_bar1. 2.  
KW Antigen; Glycoprotein; Cell wall; S-layer.  
FT CARBOHYD 7  
FT CARBOHYD 66  
FT CARBOHYD 86  
FT CARBOHYD 103  
FT CARBOHYD 103  
FT CARBOHYD 147  
FT CARBOHYD 268  
FT CARBOHYD 330  
FT CARBOHYD 375  
FT CARBOHYD 415  
FT CARBOHYD 424  
FT CARBOHYD 430  
FT CARBOHYD 436  
FT CARBOHYD 444  
FT CARBOHYD 515  
FT CARBOHYD 547  
FT CARBOHYD 593  
FT CARBOHYD 653  
FT CARBOHYD 698  
FT CARBOHYD 710  
FT CARBOHYD 799  
FT CARBOHYD 800  
FT CARBOHYD 826  
FT CARBOHYD 844  
FT CARBOHYD 861  
FT CARBOHYD 879  
FT CARBOHYD 920  
FT CARBOHYD 926  
FT CARBOHYD 926  
FT CARBOHYD 1116  
FT CARBOHYD 1128  
FT CARBOHYD 1140  
FT CARBOHYD 1146  
FT CARBOHYD 1211  
FT CARBOHYD 1211  
SQ SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;

Query Match 6.8%; Score 150; DB 1; Length 1300;  
 Best Local Similarity 23.0%; Pred. No. 0.57;  
 Matches 104; Conservative 50; Mismatches 172; Indels 126; Gaps 22;

QY 52 NNAASVKK--DVLNACNINIG--VKPQTASDNVDVRYTD---TYEFLSADPKRTTVN-- 102  
 DB 50 NLAADIKVPNATLTGNFTGDSNPGNTAG-----VITFDANGTLESASADANVAVTNMI 104  
 QY 103 --VESKDNQ-----KTEVKIGAKTSYIKKEDGLVYKDK-----GENGSSTDEGE 147  
 DB 105 TAIEASGAGVYOLSGTHAAELRLGNAGSIFKLADGVINGKYNQFALVGGALAACTITTD 164  
 QY 148 GLVTAKVIDAVNKAQWKRKTTTANGQTGOADKFEVTV--SGTNVTFASG-----KGT 199  
 DB 165 GSATITGIDGNAGAAALQRTILAN-----DAKKTLLTGANNITIGAGGCTIDLQANGST 218  
 QY 200 ATVSXDDGNTIVMYDV-----NVGDALNNQOLNSGN-----LDSKAVA-----G 241  
 DB 219 IKLT-STONNIYVDEDLAIALATDQGVDASSLTNAQTLLINCKIGTIGANNKTLGQFNIG 277  
 QY 242 SSGKYIS-GNV-----SPSKKMEDEVINAGNIEIT 273  
 DB 278 SSKTYLSNKNVAINELVINGDCAVOPAHDTYLTTRTNNAAGOKIIFNVPVANGTTILAA- 336  
 QY 274 RNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVSKKDKNPVRIT---NVAPG 329  
 DB 337 --GTNLGSATNPPLAEINFGSKGVNVD-----VLNNGEGVNLATNTITTTDANVGSF 386  
 QY 330 VKEGVTNVAQLKQVQNNLRIDVNDGNARAGIAOAIATAGLVQAYLFGKSMMAIGGT 389  
 DB 387 VFNAGGTNTIVS-GTVGGGQGNKFNIV-----ALENGTVYKFLGNAT 426  
 QY 390 YRGEAGYALGYSISDGNWMIKGTASGNSRG 421  
 DB 427 FNGNTTIAAN-STLQIGNTYADCVASADGTG 457

## RESULT 8

OMP\_RICKRI  
 ID OMP\_RICKRI STANDARD; PRT; 1654 AA.

AC 053047:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (rOmpB)  
 DE (rOmp B) [contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RA MEDLINE=92167802; PubMed=1724278;  
 RA MEDLINE=90136087; PubMed=2515418;  
 RA "Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii.";  
 RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame:  
 RT evidence for protein processing from a large precursor.";  
 RT Mol. Microbiol. 5:2361-2370(1991).  
 RN [2]  
 RP SEQUENCE OF 279-1654 FROM N.A.  
 RC STRAIN=R;  
 RA MEDLINE=90136087; PubMed=2515418;  
 RA "Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii.";  
 RT Mol. Microbiol. 3:1579-1586(1989).  
 CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY.  
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
 CC -----  
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 CC -----

DR EMBL: X16353; CAA34403.1; -  
 DR FIR: S18227; S18227.  
 DR InterPro: IPR006315; Autotransport.  
 DR InterPro: IPR005546; Autotransporter.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR TIGRPFAMs: TIGR01414; autotrans\_bar1; 2.  
 DR Antigen; S-layer; Cell wall.  
 FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.  
 FT DOMAIN 1181 1188 POLY-PHR.  
 SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.8%; Score 150; DB 1; Length 1654;  
 Best Local Similarity 23.0%; Pred. No. 0.75;  
 Matches 104; Conservative 50; Mismatches 172; Indels 126; Gaps 22;

QY 52 NNAASVKK--DVLNACNINIG--VKPQTASDNVDVRYTD---TYEFLSADPKRTTVN-- 102  
 DB 404 NLAADIKVPNATLTGNFTGDSNPGNTAG-----VITFDANGTLESASADANVAVTNMI 458  
 QY 103 --VESKDNQ-----KTEVKIGAKTSYIKKEDGLVYKDK-----GENGSSTDEGE 147  
 DB 459 TAIEASGAGVYOLSGTHAAELRLGNAGSIFKLADGVINGKYNQFALVGGALAACTITTD 518  
 QY 148 GLVTAKVIDAVNKAQWKRKTTTANGQTGOADKFEVTV--SGTNVTFASG-----KGT 199  
 DB 519 GSATITGIDGNAGAAALQRTILAN-----DAKKTLLTGANNITIGAGGCTIDLQANGST 572  
 QY 200 ATVSXDDGNTIVMYDV-----NVGDALNNQOLNSGN-----LDSKAVA-----G 241  
 DB 573 IKLT-STONNIYVDEDLAIALATDQGVDASSLTNAQTLLINCKIGTIGANNKTLGQFNIG 631  
 QY 242 SSGKYIS-GNV-----SPSKKMEDEVINAGNIEIT 273  
 DB 632 SSKTYLSNKNVAINELVINGDCAVOPAHDTYLTTRTNNAAGOKIIFNVPVANGTTILAA- 690  
 QY 274 RNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVSKKDKNPVRIT---NVAPG 329  
 DB 691 --GTNLGSATNPPLAEINFGSKGVNVD-----VLNNGEGVNLATNTITTTDANVGSF 740  
 QY 330 VKEGVTNVAQLKQVQNNLRIDVNDGNARAGIAOAIATAGLVQAYLFGKSMMAIGGT 389  
 DB 741 VFNAGGTNTIVS-GTVGGGQGNKFNIV-----ALENGTVYKFLGNAT 780  
 QY 390 YRGEAGYALGYSISDGNWMIKGTASGNSRG 421  
 DB 781 FNGNTTIAAN-STLQIGNTYADCVASADGTG 811

## RESULT 9

FLIC\_SHIFL  
 ID FLIC\_SHIFL STANDARD; PRT; 550 AA.

AC 008860:  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Flagellin.  
 GN FLIC OR SF1966.  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.

[illegible]

Db 347 SIFS-TGNSTPDDITITYSVTAK---VQAAAFDKRAVTSIGNNVDPFTTAGISVNGTTGAVT 402

Qy 361 AGI-----AOAIATAGLVQAVTLPKGSMAIGGG 388

Db 403 KGVDSVYVDNNNEALITSDTVDFEYLQDDGSYVINGSG 437

RESULT 10

OMPA\_RICCN

ID OMPA\_RICCN STANDARD: PRT: 2021 AA.

AC Q52657; P95591; P95592; P95594; Q52667; Q52669; Q52670; Q52674;

NC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).

GN OMPA OR RC1273.

OS Rickettsia conorii.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

OC Rickettsiaceae; Rickettsiaseae; Rickettsia.

OX NCBI\_TaxID=781;

[1]

RP SEQUENCE FROM N.A.

RP STRAIN=Malish 7;

RC MEDLINE=94171067; PubMed=8125327;

RA Crocquet-Valdes P.A., Weiss K., Walker D.H.;

RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";

RL Gene 140:115-119(1994).

[2]

RP SEQUENCE FROM N.A.

RP STRAIN=Malish 7;

RC MEDLINE=21442074; PubMed=11557893;

RA Ogata H., Audic S., Rencoste-Audiffren P., Fournier P.-E., Barbe V., Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;

RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.;"

RL Science 293:2093-2098(2001).

[3]

RP SEQUENCE OF 8-204 FROM N.A.

RP STRAIN=Indian tick typhus 'M1, Malish 7, and Moroccan;

RC MEDLINE=97015921; PubMed=8662558;

RA Roux V., Fournier P.-E., Raoult D.;

RT "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA.;"

RL J. Clin. Microbiol. 34:2058-2065(1996).

[4]

RP SEQUENCE OF 953-2012 FROM N.A.

RP STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;

RA Raoult D., Fournier P.-E., Roux V.;

RT "Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rOmpA.;"

RL Submitted (Dec-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.

CC -1- PTR: GLYCOSYLATED (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

CC -----

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CC -----

DR EMBL; U01028; AAA17405.1; -

DR EMBL; AE008674; AAL03811.1; -

DR EMBL; U43794; AAB49549.1; -

DR EMBL: U43798; AAB49550.1; -  
 DR EMBL: U43806; AAB49551.1; -  
 DR EMBL: U45244; AAB49566.1; -  
 DR EMBL: U46918; AAB49566.1; -  
 DR EMBL: U83440; AAC35176.1; -  
 DR EMBL: U83443; AAC35179.1; -  
 DR EMBL: U83448; AAC35184.1; -  
 DR EMBL: U83453; AAC35189.1; -  
 DR InterPro: IPR006315; Autotransport.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR TIGRfam: TIGR01414; autotrans\_bar1; 1.  
 DR Antigen: Repeat; Signal; Cell wall; S-layer; Glycoprotein;  
 KW Complete proteome.  
 FT CHAIN 1 38  
 FT SIGNAL 39 2021  
 FT DOMAIN 238 946  
 FT DOMAIN 1424 1528  
 FT VARIANT 60 60  
 FT VARIANT 76 76  
 FT VARIANT 86 137  
 FT VARIANT 126 133  
 FT VARIANT 953 954  
 FT VARIANT 1243 1245  
 FT VARIANT 1308 1308  
 FT VARIANT 1877 1877  
 FT CONFLICT 10 10  
 FT CONFLICT 92 92  
 FT CONFLICT 126 126  
 FT CONFLICT 137 137  
 FT CONFLICT 157 157  
 FT CONFLICT 368 369  
 FT CONFLICT 374 388  
 FT CONFLICT 640 640  
 FT CONFLICT 669 669  
 FT CONFLICT 793 793  
 FT CONFLICT 803 804  
 FT CONFLICT 809 823  
 FT CONFLICT 898 898  
 FT CONFLICT 908 908  
 FT CONFLICT 985 985  
 FT CONFLICT 1009 1009  
 FT CONFLICT 1013 1013  
 FT CONFLICT 1182 1182  
 FT CONFLICT 1314 1314  
 FT CONFLICT 1451 1451  
 FT CONFLICT 1624 1624  
 FT CONFLICT 1628 1628  
 FT CONFLICT 1872 1872  
 FT CONFLICT 1875 1875  
 FT CONFLICT 1878 1878  
 FT CONFLICT 1936 1936  
 FT CONFLICT 1965 1970  
 FT CONFLICT 1997 1997  
 SO SEQUENCE 2021 AA; 203328 MM; 327FC42D7CB24668 CXC64;  
 Query Match 6.78; Score 147.5; DB 1; Length 2021;  
 Best Local Similarity 21.04; Pred. No. 1.3;  
 Matches 125; Conservative 70; Mismatches 192; Indels 207; Gaps 29;

QY 163 ---GWRKTTAN-----GOTGOADK-----FETV---SGTN 189  
 DB 811 RVGGVYKSTNTILTDNASAVTTPNPVVTGAIDNTGNMANGIVTFTGDSVTGNGNTN 870  
 QY 190 ---VTFASGKT-----TATVSKDDGNTITVADVVDGALVNVQLONSGWNLSK 237  
 DB 871 ALATISVAGKATLGAIKATTTKLTLDNASAVTFNPVVTGAID-----NMG-NANN 924  
 QY 238 AVAGSGKATISGVNSPSKGMDETVINAG-----NNIEI----- 272  
 DB 925 IVFTGDSVTGNGNTNAL--ATVNVGAGVTLTQAGSLDANNIDGARSTLEFNGPLDG 982  
 QY 273 -----TRNKN--IDTATSMTPQ-----SSVSGAGDAPTLSDGDALN 311  
 DB 983 GGNALPYRKGAITANGNAILNVNTKLLATVHLITGTVAETINIGAG--NLRAIDASAGD 1039  
 QY 312 V-----GSKDKRPVITNVAVGVEGDV-----T 336  
 DB 1040 VTLTNMODIHFRLDSALVLSNLTGVGVNNILLAADLVAGVDEGTVPDGVNGLNIGS 1099  
 QY 337 NVAQLKGVQNLNN-----RIDVNGNARAGIAQAIATAG 371  
 DB 1100 NVA---GAAMNIDVGKNKENTLLIYNAVITTDVNLGEGIONVLINNADFTSTAFNAG 1156  
 QY 372 LVQAYLPKSKMAIGGTY-----REBAGYALIGYSSISDGMNIIIGTASGNSR 420  
 DB 1157 TIO-----INDATYITDANGMLNIPAGNIKFAHADQOLIIONSSGND 1200  
 RESULT 11  
 SLAP\_CAUCR STANDARD; PRT; 1025 AA.  
 ID P35828; Q46015; Q9RF12;  
 AC 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE S-layer protein (Paracrystalline surface layer protein).  
 GN R5A OR CCL1007.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_Taxid=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=93007489; PubMed=1393820;  
 RA Gilchrist A., Fisher J.A., Smit J.K.;  
 RT "Nucleotide sequence analysis of the gene encoding the Caulobacter  
 RT crescentus paracrystalline surface layer protein.";  
 RL Can. J. Microbiol. 38:193-202(1992).  
 RN [2]  
 RP REVISIONS TO 376; 636 AND 842-843.  
 RA Awram P.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J53001;  
 RA Bingle W.H., Awram P.A., Nornellini J.F., Smit J.K.;  
 RT "The secretion signal of C. crescentus S-layer protein is located in  
 RT the C-terminal 82 amino acids of the molecule.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Debock I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA Peboy R.T., Dodson R.D., Durkin A.S., Gwin M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Osterback T., Tran K., Wolf A., Vamathevan J., Emsolava M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of *Caulobacter crescentus*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
RN [1]  
RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.  
RC STRAIN-ATCC 19089 / CB15;  
RX MEDLINE=89008089; PubMed=3049545;  
RA Fisher J.A., Smit J.K., Agabian N.;  
RT "Transcriptional analysis of the major surface array gene of  
RT *Caulobacter crescentus*.";  
RL J. Bacteriol. 170:4706-4713(1988).  
RP [6]  
RC CHARACTERIZATION  
RC STRAIN-ATCC 19089 / CB15;  
RX MEDLINE=98292737; PubMed=9620954;  
RA Awram P., Smit J.K.;  
RT "The *Caulobacter crescentus* paracrystalline S-layer protein is  
RT secreted by an ABC transporter (type I) secretion apparatus.";  
RL J. Bacteriol. 180:3062-3069(1998).  
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A  
CC PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER  
CC (TYPE I) SECRETION APPARATUS.  
CC -1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE  
CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A  
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; AF062345; AAC38665.2; -  
DR EMBL; AF193063; AAF19365.1; -  
DR EMBL; AE005779; AAK22991.1; ALT\_INIT.  
DR PIR; A48995; A48995.  
DR HSSP; P22629; ISWC.  
DR TIGR; CC1007; -  
DR InterPro; IPR001343; HemIysn\_Ca\_bind.  
DR Pfam; PF00353; HemolysinCabin; 3.  
DR PRINTS; PR00313; CABNDNGRP.  
DR Cell wall; S-layer; Calcium-binding; Complete proteome.  
FT INIT MET 0  
SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;  
  
Query Match 6.7%; Score 147; DB 1; Length 1025;  
Best Local Similarity 24.1%; Pred. No. 0.63;  
Matches 114; Conservative 50; Mismatches 189; Indels 120; Gaps 22;  
  
OY 13 LNWAVVSELT--NNHTRASATKTNVLAFLFATVQASNRASVADVLAAGNT--- 67  
DB LNTSSGVTGLPALTNTSSGAAQVYTAGAGNMLRTTAAQANVVA---VDGANNVVA 382  
OY 68 -KGKPGTTASDNVDFVTFVEFISADTKTTTVNVESSKNGKTEVIGAKTSV-IKE 125  
DB STGVTSSTT-----TVGANSASGTSVSANSSSTTTTGALAIVGGAIVYAAQ 430  
OY 126 KDKGLV-----TGKDKGENSGSTDEG-----EGLVTAKEYIDAVNKAQMRKTTTA 171  
DB 431 TAGNAVNTTLTQADVTVTGNSSSTAIVTQTAATAGATVAGRVGAVT-----ITDSA 484  
OY 172 NGQVGAQDKETVTSG-----TNTFASGKTTATVSKDDOGNTVWADVAVG 219  
DB 485 AASATYAGKATVTLGSGAATIDSSALTTVNL-SGTGTSLGIGR--GALTATPTANT- 539  
OY 220 DALVNVNOLONGSMILDSKAVAGS-----SGKTVSGNVSPSKGMDFTVINAGNNIET 272  
DB 540 LTLVNLGLTTTGALTIDSEAAADGFTTININGSTASSITIASLVAAADATTLINISGDARTI 599

OY 273 TRN-----GKNI--DIATSMTPQFSVSLGACADAPTLISVDGALNVGSK 316  
DB 600 TSHTAALITGITVTVNSVATGAEIATGLV--FTG---GAGADSTILGATTKAIVMGAD 654  
OY 317 DNKPVRIINVAPG--VKRGDVTNVAQKGVANQNLNRIDVND-----GNARAG 362  
DB 655 DFTVVSATLGAAGSVNGGDDTDV-----LVANNGSSFSADPAFGFETLRVAGAAAG 709  
OY 363 -----IAQATITAGLVQ-----AYLPKSMMAIGGCTYRGAGYAIGYSSI 403  
DB 710 SHNANGFTALDLAGATAGTFTTNVAVNVGLVLAAPRTTTLVLANAGTSDV 762  
  
RESULT 12  
APU\_THETU  
ID APU\_THETU STANDARD; PRT; 1861 AA.  
AC P38536;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase  
DE type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan  
DE glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan  
DE glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].  
GN AMTB.  
OS Thermomicrobacter thermosulfurogenes (Clostridium  
OS thermosulfurogenes).  
OC Bacteria; Firmicutes; Clostridia; Thermomicrobacteriales;  
OC Thermomicrobacteriaceae; Thermomicrobacterium.  
OX NCBI\_TaxID=33950;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DSM 3896 / EMI;  
RX MEDLINE=94252998; PubMed=8195085;  
RA Matuschek M., Burchardt G., Sahn K., Bahl H.;  
RT "Pullulanase of *Thermomicrobacterium thermosulfurogenes* EMI  
RT (Clostridium thermosulfurogenes): molecular analysis of the gene,  
RT composite structure of the enzyme, and a common model for its  
RT attachment to the cell surface.";  
RL J. Bacteriol. 176:3295-3302(1994).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic  
CC linkages in pullulan and in amylopectin and glycogen, and the  
CC alpha- and beta-limit dextrins of amylopectin and glycogen.  
CC -1- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN  
CC S-LAYER ANCHOR.  
CC -1- PTM: GLYCOSYLATION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -1- SIMILARITY: Contains 3 S-layer homology (SLH) domains.  
CC -----  
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CC -----  
DR EMBL; M57692; AAB00841.1; -  
DR HSSP; Q08751; IBYZ.  
DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
DR InterPro; IPR006048; Alpha\_amy1\_C.  
DR InterPro; IPR006047; Alpha\_amy1\_cat.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR004185; Glyco\_hydro\_131g.  
DR InterPro; IPR004193; Glyco\_hydro\_13N.  
DR InterPro; IPR001119; SLH.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR Pfam; PF02806; alpha-amylase\_C; 1.  
DR Pfam; PF02903; alpha-amylase\_N; 1.



DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF02922; Isoamylase\_N; 1.  
 DR Pfam; PF00395; SLH; 3.  
 DR SMART; SM00642; Amy; 1.  
 DR SMART; SM00632; Amy\_C; 1.  
 DR SMART; SM00600; FN3; 2.  
 DR PROSITE; PS01072; SLH\_DOMAIN; 3.  
 KM Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;  
 KM Multifunctional enzyme; Glycoprotein.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1861  
 FT DOMAIN 928 1018  
 FT DOMAIN 1157 1248  
 FT ACT\_SITE 628 628  
 FT ACT\_SITE 657 657  
 FT ACT\_SITE 734 734  
 FT DOMAIN 1681 1739  
 FT DOMAIN 1740 1803  
 FT DOMAIN 1804 1861  
 FT CONFLICT 1734 1734  
 SQ SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;  
 Query Match 6.68; Score 145.5; DB 1; Length 1861;  
 Best Local Similarly 19.94; Pred. No. 1.5;  
 Matches 103; Conservative 76; Mismatches 210; Indels 129; Gaps 24;

OY 2 NKIYRIWNSALNA-----WVYSELTRHRTKRASATVTRAVLATILFATVQASANAAS 56  
 DB 1208 NEVYNTIDTSVINGVYNYKVVAVDLSFNRTESNVYIKDPVPIKIFNV-----T 1259  
 OY 57 VKDVLNAGWNKIGKVPCTASDNVDFRYDVEFLSADPKTTTVNESKDKKEVKI 116  
 DB 1260 VPDYTPDAVNLACGFPAATMDPSAQ-----QMTKIDNNTSITL-TLDEGQIEYKY 1310  
 OY 117 --GAKSVIEKKG-----KLVTKGKXGSGSTDE-----GECVLTAK 154  
 DB 1311 ARGSMDKVEKDEGENEFASNRKATYVNOGNEMTINDYRMRDIPFIYSPSSNMTVDS 1370  
 OY 155 VIDAVERNAG--WRMKTANGOTGOADKFEVTVSGTVTFASGK-----GTTATVSKD 206  
 DB 1371 NISMVEKGYTKGAKTYTNGVDSVODKNGVFTKDSVLANGVNKKIKIHPENDGSSVYGN 1430  
 OY 207 QGNIT-----VWYDVNVGDALNVNOLNSGNMLDSKAVAGSSGKY-ISCNVSPSK 255  
 DB 1431 QGRITELTKDIEIDVHQENNSGSGGTNNMTSTSGSN-SSSTGSGSGTSTISNIS-NT 1488  
 OY 256 GKADERYNT--MAGNNIEITRN-GKNTDIATSMTPQ---FSSVSLGADAPILSDGDA 309  
 DB 1489 SMTSNTIGVITKNGNVITLTDAGKADKLIVNSKDKKVPFDITTTIGEG--QOKVVOISKDI 1547  
 OY 310 LNVGS-----KKOKKPYRIT-----NVAAPYKREGDVTVAQLKGVAQNLNN 350  
 DB 1548 LDTSAANGKDIIVIKSDASTALTTRDALNOMQIONGVASTIKDNGKPVNTVYSLNVVDI 1607  
 OY 351 RIDNVQDN-----ARAGIAQAIATAGLVQAYLPGKSMALGGCTYGEAG-- 395  
 DB 1608 TISGISCVTLAKPVEVTLNISKANDPRKVA---YVYPTNTQMEYVGKQVADASSGTI 1663  
 OY 396 -----YALGYSISDGNW---IITKGNAS 416  
 DB 1664 TFNATHPSOYAAFEYDFTFDIKD--NMARDVIEVLAS 1699

RESULT 13  
 FLIC\_ECOLI  
 ID FLIC\_ECOLI STANDARD; PRT; 497 AA.  
 AC P04949;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Flagellin.  
 GN FLIC OR FLAF OR HAG OR B1923.  
 OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=87057066; PubMed=3536885;  
 RA Kuwajima G., Asaka J.-I., Fujiwara T., Fujiwara T., Node K., Kondo E.;  
 RT "Nucleotide sequence of the hag gene encoding flagellin of  
 RT Escherichia coli.";  
 RL J. Bacteriol. 168:1479-1483(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=89281489; PubMed=2659972;  
 RA Hanafusa T., Sakai A., Tomlinaga A., Enomoto M.;  
 RT "Isolation and characterization of Escherichia coli hag operator  
 RT mutants whose hag48 expression has become repressible by a Salmonella  
 RT H1 repressor.";  
 RL Mol. Gen. Genet. 216:44-50(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97251358; PubMed=9097040;  
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,  
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
 RA Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H.,  
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horikuchi T.;  
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 40.1-50.0 min region on the linkage map.";  
 RL DNA Res. 3:379-392(1996).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=83238225; PubMed=6305924;  
 RA Szekely E., Simon M.;  
 RT "DNA sequence adjacent to flagellar genes and evolution of flagellar-  
 RT phase variation.";  
 RL J. Bacteriol. 155:74-81(1983).  
 RN [6]  
 RP SEQUENCE OF 1-12.  
 RC STRAIN-K12 / EWG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 RT in the genome of Escherichia coli K-12.";  
 RL Electrophoresis 18:1259-1313(1997).  
 RN [7]  
 RP SEQUENCE OF 1-4.  
 RC STRAIN-K12 / W3110;  
 RX MEDLINE=98263247; PubMed=9600841;  
 RA Wilkins M.R., Gasteliger E., Tonella L., Ou K., Tyler M.,  
 RA Sanchez J.-C., Gooley A.A., Walsh B.J., Balroch A., Appel R.D.,  
 RA Williams K.L., Hochstrasser D.F.;  
 RT "Protein identification with N and C-terminal sequence tags in  
 RT proteome projects.";  
 RL J. Mol. Biol. 278:599-608(1998).  
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO  
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.  
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.  
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QY 395 GYAIGYSSISDGNMIIKGTAS-----GNSRGH 422  
 DB 858 -----KLVKNGN--IPGETTIAELLPLRGH 882

RESULT 15

HLA.SERMA STANDARD; PRT; 1608 AA.  
 ID HLVA--SERMA  
 AC P15320;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Hemolysin precursor.  
 GN SHLA.  
 OS Serratia marcescens.  
 OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales;  
 OC Enterobacteriaceae; Serratia.  
 OX NCBI\_TaxID=615;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
 RC STRAIN-SN8;  
 RX MEDLINE=88257037; PubMed=3290200;  
 RA Poole K., Schiebel E., Braun V.;  
 RT "Molecular characterization of the hemolysin determinant of Serratia marcescens.";  
 RL J. Bacteriol. 170:3177-3188(1988).  
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.  
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane.  
 CC -1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).  
 CC -----  
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 CC -----  
 DR EMBL: M22618; AAA50323.1; -  
 DR PIR: A28182; A28182.  
 KM Hemolysis; Toxin; Outer membrane; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 1608 HEMOLYSIN.  
 SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.5%; Score 142; DB 1; Length 1608;  
 Best Local Similarity 21.9%; Pred. No. 2;  
 Matches 98; Conservative 53; Mismatches 156; Indels 140; Gaps 20;

QY 26 HFKRASATVKTAVLATLFAVQASANRAASVADVLNAGMNIKGVKPGTTASDNVDFVRT 85  
 DB 717 HTRDSEKTRTEMSA-----SLSGGSVKLKAEDVTFSSKLYADKGDASVSGN----- 766  
 QY 86 YDTEFLSADITTYVNVESKDKNGKTEVKGAKTSVIEKDGKLVGDKDGENSSSTDE 145  
 DB 767 --KVSFLAADDKTAS--NTE-----QTKIGG-----GFYYTG----- 794  
 QY 146 GEGLVYAKEVDAVNKAGWRMKTNTTANGOTGADKFEVTSGMTVFASGKGTATVSKD 205  
 DB 795 -----GIDKLGSGVEAGYENKNT-QAOSKAITSGSDV----- 826  
 QY 206 DQGNITVMYDVNVGALNVNOLNSGMNLSKAVAGSSGVISGNVSPSKMKDETVNIN 265  
 DB 827 -KGNLT-----INARDKLTQGAQHVSAGVQENAAQVDHLLAADTASTTTTKTDVGVT- 880  
 QY 266 AGNNITITRNGKNIDTATSMTPFSSVSLGA-----GADAPTLSDVDGDLNMG 313  
 DB 881 -----GANVDYSAVTRPEYRAVGAAKADATGVINDIGIGAPNVGIDIGAQGS 930

QY 314 SKK--DNKEPVRTTNVAPGV-----KEGDV-----TNVAQLKGVQNLN-----NRID 353  
 DB 931 SEKRSSSQAVYSSVQAGSIDINAKGEVNDQGTQYQASKG-AVNLTADSHRSEAANRQD 989  
 QY 354 NVDGNARAGIAQAIATAGLVQAVLPGKSMMAIG---GGTYRGEAGYAIGYSSISDGNM 409  
 DB 990 EOSRDR-----GSAG-VRYVTTTGSIDLTVDAKGEGETQSRNSSSAQAVTGSIDAANG 1041  
 QY 410 -----LIKGTASGNSRGHFGASA 427  
 DB 1042 INVNVKKA1YOGTALNGRGKTAANA 1068

Search completed: October 6, 2003, 09:24:03  
 Job time : 9.68663 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 31.8023 Seconds  
(without alignments)  
3513.485 Million cell updates/sec

Title: US-09-771-382-26  
Perfect score: 2197  
Sequence: 1 MNKXRIINSLAMVWVS.....FASGNRGHFGASASVGYQW 433

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.unclassified:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2108	95.9	591	09JRI8	09JRI8 neisseria m
2	2104	95.8	591	09JPS7	09JPS7 neisseria m
3	2103.5	95.7	592	09AQF0	09AQF0 neisseria m
4	2096	95.4	591	093QY3	093QY3 neisseria m
5	2056.5	93.6	600	09JPS6	09JPS6 neisseria m
6	2049.5	93.3	592	09JPS9	09JPS9 neisseria m
7	2036.5	92.7	590	09JPS3	09JPS3 neisseria m
8	2033.5	92.6	594	09JPS2	09JPS2 neisseria m
9	2032.5	92.5	599	093QY4	093QY4 neisseria m
10	2032	92.4	594	09JPI3	09JPI3 neisseria m
11	2029.5	92.4	594	09JPI3	09JPI3 neisseria m
12	2025.5	92.2	594	09JPI7	09JPI7 neisseria m
13	2023.5	92.1	598	09JPI9	09JPI9 neisseria m
14	2015.5	91.7	592	093QY2	093QY2 neisseria m
15	2010.5	91.5	598	09JPS0	09JPS0 neisseria m
16	2010.5	91.5	598	09JPT0	09JPT0 neisseria m

17	2009.5	91.5	592	16	09JQW4	09JQW4 neisseria m
18	2006	91.3	595	2	09JPH0	09JPH0 neisseria m
19	2005.5	91.3	598	2	09JPR7	09JPR7 neisseria m
20	2001.5	91.1	598	2	093QY5	093QY5 neisseria m
21	1998	90.9	599	2	09JPS8	09JPS8 neisseria m
22	1981.5	90.2	600	2	09JPS5	09JPS5 neisseria m
23	1976	89.9	589	2	09JPI0	09JPI0 neisseria m
24	1964	89.4	589	2	093QY1	093QY1 neisseria m
25	1920	87.4	596	2	09JPS4	09JPS4 neisseria m
26	1920	87.4	530	2	09JPS1	09JPS1 neisseria m
27	776.5	35.3	1098	2	048152	048152 haemophilus
28	775.5	35.3	1096	2	08GM79	08GM79 haemophilus
29	734	33.4	2353	2	P71401	P71401 haemophilus
30	687.5	31.3	1204	2	08GM76	08GM76 haemophilus
31	664.5	30.2	1210	2	08GM74	08GM74 haemophilus
32	655.5	29.8	1210	2	08GM75	08GM75 haemophilus
33	509.5	23.2	1004	2	08GM77	08GM77 haemophilus
34	489.5	22.3	1002	2	08GM78	08GM78 haemophilus
35	382	17.4	1299	16	09F3X6	09F3X6 pasteurella
36	355.5	16.2	2314	2	08KOM8	08KOM8 moraxella c
37	340.5	15.5	2059	16	09PD50	09PD50 xyella fas
38	335	15.2	1190	16	09PC04	09PC04 xyella fas
39	329.5	15.0	1588	16	08XD64	08XD64 escherichia
40	328	14.9	1461	16	08ZL64	08ZL64 salmonella
41	326	14.8	1107	16	09F2D8	09F2D8 salmonella
42	326	14.8	1778	16	08FCB2	08FCB2 escherichia
43	315.5	14.4	641	16	08CKM1	08CKM1 yersinia pe
44	315.5	14.4	658	16	08ZHU0	08ZHU0 yersinia pe
45	301.5	13.7	2712	16	09F3X5	09F3X5 pasteurella

## ALIGNMENTS

RESULT 1  
ID 09JRI8 PRELIMINARY; PRT; 591 AA.  
AC 09JRI8:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA92 (Adhesin) (Nha outer membrane protein).  
GN GNA92 OR NMB0992 OR NHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B, B2169, B283, and H447/6;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scariato V., Maignan V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.,  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*  
RL Science 287.1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
RA Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Clecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,  
RA Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,

RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,  
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
MC58";  
RL Science 287:1809-1815(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;  
RA Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.,  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RU EMBL: AF226375; AAF42524.1; -  
DR EMBL: AF226375; AAF41395.1; -  
DR EMBL: AF226367; AAF42516.1; -  
DR EMBL: AF226370; AAF42519.1; -  
DR EMBL: AF226374; AAF42523.1; -  
DR EMBL: AF157611; AAK68872.1; -  
DR TIGR: MMB0992; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
DR Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 95.9%; Score 2108; DB 16; Length 591;  
Best Local Similarity 73.3%; Pred. No. 5.9e-90;  
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

OY 1 MNKIYRIIWSALNAAVYVSELTRNHTKRASATYKAVLATLLEFATVOASAN----- 52  
DB 1 MNKIYRIIWSALNAAVYVSELTRNHTKRASATYKAVLATLLEFATVOASANNEOEEDL 60  
OY 53 ----- 52  
DB 61 YLDPVORTAVAVLIYNSDEKTEGKEKYEENSDMAVYFNEKGYLTAREITLAKGNLKIQ 120  
OY 53 ----- 52  
DB 121 NGTNYFSLKDLTDLISVTEKLSFSAANGKVNITSDTKLNFARAKETAGNGDTTVALN 180  
OY 53 -----RAASVQDVNLNAGNMIKGVKPGTTASDNVDF 82  
DB 181 GIGSTLFDTLNTGATTVTNDNTDDEKRRASVQDVNLNAGNMIKGVKPGTTASDNVDF 240  
OY 83 VRTDYVEFLSADTKTTTVNVEESKDNKGKTEVKIGAKTSVYKEDGKLVTKGDKGENSS 142  
DB 241 VRTDYVEFLSADTKTTTVNVEESKDNKGKTEVKIGAKTSVYKEDGKLVTKGDKGENSS 300  
OY 143 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKGTATV 202  
DB 301 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKGTATV 360  
OY 203 SKDDGNTTVWYDVNAGDALVNOLONSGMNLSKAAVAGSSGKVIISGNVSPSKKMDETV 262  
DB 361 SKDDGNTTVWYDVNAGDALVNOLONSGMNLSKAAVAGSSGKVIISGNVSPSKKMDETV 420  
OY 263 NINAGNNIETIRNKNKNDIATSMTPQFSSVSLGAGADAPTLISVGDALNVSSKKDKNRPV 322  
DB 421 NINAGNNIETIRNKNKNDIATSMTPQFSSVSLGAGADAPTLISVGDALNVSSKKDKNRPV 480  
OY 323 ITTNAAPGKEGDVTVNVAQLKGAONLNRRIDNVGNAAGIAQAATATAGLVQAVLPKSM 382  
DB 481 ITTNAAPGKEGDVTVNVAQLKGAONLNRRIDNVGNAAGIAQAATATAGLVQAVLPKSM 540  
OY 383 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 433  
DB 541 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 591

RESULT 2  
O9JPS7  
AC O9JPS7;  
PRELIMINARY; PRT; 591 AA.

DT 01-OCT-2000 (TREMBlrel. 15; Created)  
DT 01-OCT-2000 (TREMBlrel. 15; Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22; Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hunt E., Knapp B., Blair E., Mason T., Tettein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
DR Complete proteome.  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 95.8%; Score 2104; DB 2; Length 591;  
Best Local Similarity 73.1%; Pred. No. 9e-90;  
Matches 432; Conservative 1; Mismatches 0; Indels 158; Gaps 1;

OY 1 MNKIYRIIWSALNAAVYVSELTRNHTKRASATYKAVLATLLEFATVOASAN----- 52  
DB 1 MNKIYRIIWSALNAAVYVSELTRNHTKRASATYKAVLATLLEFATVOASANNEOEEDL 60  
OY 53 ----- 52  
DB 61 YLDPVORTAVAVLIYNSDEKTEGKEKYEENSDMAVYFNEKGYLTAREITLAKGNLKIQ 120  
OY 53 ----- 52  
DB 121 NGTNYFSLKDLTDLISVTEKLSFSAANGKVNITSDTKLNFARAKETAGNGDTTVALN 180  
OY 53 -----RAASVQDVNLNAGNMIKGVKPGTTASDNVDF 82  
DB 181 GIGSTLFDTLNTGATTVTNDNTDDEKRRASVQDVNLNAGNMIKGVKPGTTASDNVDF 240  
OY 83 VRTDYVEFLSADTKTTTVNVEESKDNKGKTEVKIGAKTSVYKEDGKLVTKGDKGENSS 142  
DB 241 VRTDYVEFLSADTKTTTVNVEESKDNKGKTEVKIGAKTSVYKEDGKLVTKGDKGENSS 300  
OY 143 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKGTATV 202  
DB 301 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKGTATV 360  
OY 203 SKDDGNTTVWYDVNAGDALVNOLONSGMNLSKAAVAGSSGKVIISGNVSPSKKMDETV 262  
DB 361 SKDDGNTTVWYDVNAGDALVNOLONSGMNLSKAAVAGSSGKVIISGNVSPSKKMDETV 420  
OY 263 NINAGNNIETIRNKNKNDIATSMTPQFSSVSLGAGADAPTLISVGDALNVSSKKDKNRPV 322  
DB 421 NINAGNNIETIRNKNKNDIATSMTPQFSSVSLGAGADAPTLISVGDALNVSSKKDKNRPV 480  
OY 323 ITTNAAPGKEGDVTVNVAQLKGAONLNRRIDNVGNAAGIAQAATATAGLVQAVLPKSM 382  
DB 481 ITTNAAPGKEGDVTVNVAQLKGAONLNRRIDNVGNAAGIAQAATATAGLVQAVLPKSM 540  
OY 383 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 433  
DB 541 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 591

RESULT 3  
Q9AOF0 PRELIMINARY; PRT; 592 AA.  
AC Q9AOF0;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein.  
GN NHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF125375; AAK09243.1;  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada.  
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 95.7%; Score 2103.5; DB 2; Length 592;  
Best Local Similarity 73.0%; Pred. No. 9.5e-90;  
Matches 432; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

QY 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLTFATVOASAN----- 52  
DB 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLTFATVOASANNEPRKKD 60  
QY 53 ----- 52  
DB 61 LYDPVQRTAVLIYNSDKEGTGEKEVEENSDMAVYENEKGLTAREITLKAGDNLIK 120  
QY 53 ----- 52  
DB 121 QNCTNFTYSLKDDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGDTVHL 180  
QY 53 ----- 81  
DB 181 NGIGSTLTDLTLLNTGATTNTNDVTDDEKRRASVADVLNAGNINIGKRGTTASDNVD 240  
QY 53 ----- 81  
DB 82 FVRDYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 141  
DB 241 FVRDYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 300  
QY 142 STEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEFVTSCTNVTFAAGKGTAT 201  
DB 301 STEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEFVTSCTNVTFAAGKGTAT 360  
QY 202 VSKDDGNTVMTDVNVDALNVNOLONGSNLDSKAVAGSSGKVISGNVSPSKKMD 261  
DB 361 VSKDDGNTVMTDVNVDALNVNOLONGSNLDSKAVAGSSGKVISGNVSPSKKMD 420  
QY 262 VTNAGNNIETTRNKNIDIAITSMTPQFSSVSLGAGADAPTLSTVDGALNVGSKDKPV 321  
DB 321 VTNAGNNIETTRNKNIDIAITSMTPQFSSVSLGAGADAPTLSTVDGALNVGSKDKPV 480  
QY 421 VTNAGNNIETTRNKNIDIAITSMTPQFSSVSLGAGADAPTLSTVDGALNVGSKDKPV 480  
DB 481 RITNVAAGVEGADVTNVAOLKGVANLNRRIDNDVGNARAGIAOAIATAGLVQAVLPCKS 540  
QY 382 MAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433  
DB 541 MAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 592

RESULT 4  
Q930Y3 PRELIMINARY; PRT; 591 AA.

AC Q930Y3;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE NHA outer membrane protein.  
GN NHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157606; AAK68867.1;  
DR InterPro; IPR005594; Yada.  
DR Pfam; PF03895; Yada.  
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 95.4%; Score 2096; DB 2; Length 591;  
Best Local Similarity 72.9%; Pred. No. 2.1e-89;  
Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;

QY 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLTFATVOASAN----- 52  
DB 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLTFATVOASANNEQEEDL 60  
QY 53 ----- 52  
DB 61 YLDPVLTAVLIYNSDKEGTGEKEVEENSDMAVYENEKGLTAREITLKAGDNLIKQ 120  
QY 53 ----- 52  
DB 121 NGTNTYSLKDDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKETAGTNGDTVHLN 180  
QY 53 ----- 82  
DB 181 GIGSTLTDLTLLNTGATTNTNDVTDDEKRRASVADVLNAGNINIGKRGTTASDNVD 240  
QY 83 VRYDYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 142  
DB 241 VRYDYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 300  
QY 143 TDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEFVTSCTNVTFAAGKGTAT 202  
DB 301 TDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEFVTSCTNVTFAAGKGTAT 360  
QY 203 SKDDGNTVMTDVNVDALNVNOLONGSNLDSKAVAGSSGKVISGNVSPSKKMD 262  
DB 361 SKDDGNTVMTDVNVDALNVNOLONGSNLDSKAVAGSSGKVISGNVSPSKKMD 420  
QY 263 NINAGNNIETTRNKNIDIAITSMTPQFSSVSLGAGADAPTLSTVDGALNVGSKDKPV 322  
DB 421 NINAGNNIETTRNKNIDIAITSMTPQFSSVSLGAGADAPTLSTVDGALNVGSKDKPV 480  
QY 323 ITNVAAGVEGADVTNVAOLKGVANLNRRIDNDVGNARAGIAOAIATAGLVQAVLPCKS 382  
DB 481 ITNVAAGVEGADVTNVAOLKGVANLNRRIDNDVGNARAGIAOAIATAGLVQAVLPCKS 540  
QY 383 MAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433  
DB 541 MAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

RESULT 5  
Q9JPS6 PRELIMINARY; PRT; 600 AA.  
AC Q9JPS6;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria: Betaproteobacteria: Neisseriales:  
OC Neisseriaceae: Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42520.1; --  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;  
  
Query Match 93.6%; Score 2056.5; DB 2; Length 600;  
Best Local Similarity 70.8%; Pred. No. 1.4e-87;  
Matches 425; Conservative 2; Mismatches 6; Indels 167; Gaps 1;  
  
QY 1 MNKIRITWNSALNMAVYSELTRNHRKRASATVTAVALTLFPATVOASAN----- 52  
DB 1 MNKIRITWNSALNMAVYSELTRNHRKRASATVTAVALTLFPATVOASADN 60  
QY 53 ----- 52  
DB 61 EEEETLEPVVKTAPVLSFSAEDTGEKEVTENTMGIYFKNGYIKAGTTLKAGDNLK 120  
QY 53 ----- 52  
DB 121 IKONTDENTNASSFTYSLKKELTDLTSVGTETKLSFGANGKNKVNITSDPKGLNFAKETAGT 180  
QY 53 ----- 240  
DB 181 NGDTTVHLNGIGSTLTDLTLNTGATTNTNDVNDDEKRRASASVDVYLNAGNINIGVXPG 240  
QY 74 TTSADNVFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDKLYTG 133  
DB 241 TTSADNVFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDKLYTG 300  
QY 134 KDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSNTNTPA 193  
DB 301 KDKGENSGSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSNTNTPA 360  
QY 194 SKGTATATVSKDDGNITVMDVYNGDALNVLNOLNSGWNLDKSAVAGSSGKVIYGNVSP 253  
DB 361 SKGTATATVSKDDGNITVMDVYNGDALNVLNOLNSGWNLDKSAVAGSSGKVIYGNVSP 420  
QY 254 SKGKDEFTVNTNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDGALANG 313  
DB 421 SKGKDEFTVNTNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDGALANG 480  
QY 314 SKDKKPVRTNVAQVKEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLV 373  
DB 481 SKDKKPVRTNVAQVKEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLV 540  
QY 374 QAYLPKSKMAIIGGTYRGEAGYATGYSISIDGGWIIKGTASGNSRGHFGASASVGYOM 433  
DB 541 QAYLPKSKMAIIGGTYRGEAGYATGYSISIDGGWIIKGTASGNSRGHFGASASVGYOM 600

ID 09JPS9 PRELIMINARY; PRT: 592 AA.  
AC 09JPS9;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria: Betaproteobacteria: Neisseriales:  
OC Neisseriaceae: Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=860800;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42510.1; --  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 592 AA; 61917 MW; 4A347151AFD3C879 CRC64;  
  
Query Match 93.3%; Score 2049.5; DB 2; Length 592;  
Best Local Similarity 71.8%; Pred. No. 3e-87;  
Matches 425; Conservative 1; Mismatches 7; Indels 159; Gaps 2;  
  
QY 1 MNKIRITWNSALNMAVYSELTRNHRKRASATVTAVALTLFPATVOASA----- 51  
DB 1 MNKIRITWNSALNMAVYSELTRNHRKRASATVTAVALTLFPATVOANATDEDEEEL 60  
QY 52 ----- 51  
DB 61 ESVQSVYSGISQASMEGSELETISLSMTNDSKEFVPIYVTLKAGDNLIKONTNENT 120  
QY 52 ----- 51  
DB 121 NASSFTYSLKKELTGLINVEETKLSFGANGKNKVNITSDPKGLNFAKETAGTNGDTTVHLN 180  
QY 52 ----- 240  
DB 181 GIGSTLTMLNTGATTNTNDVNDDEKRRASASVDVYLNAGNINIKYKPGTTASDNDVF 240  
QY 83 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDKLYTGKDKGENSS 142  
DB 241 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDKLYTGKDKGENSS 300  
QY 143 TDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSNTNTPASGKTTATV 202  
DB 301 TDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSNTNTPASGKTTATV 360  
QY 203 SKDDGNTVMDVYNGDALNVLNOLNSGWNLDKSAVAGSSGKVIYGNVSPSKGMDFTV 262  
DB 361 SKDDGNTVMDVYNGDALNVLNOLNSGWNLDKSAVAGSSGKVIYGNVSPSKGMDFTV 420  
QY 263 NINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDGALANGSKDKNRPV 321  
DB 421 NINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDGALANGSKDKNRPV 480  
QY 322 RTTNVAPGVKESDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLVQAYLPKS 381  
DB 481 RTTNVAPGVKESDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLVQAYLPKS 540  
QY 382 MMAIGGTYRGEAGYATGYSISIDGGWIIKGTASGNSRGHFGASASVGYOM 433  
DB 541 MMAIGGTYRGEAGYATGYSISIDGGWIIKGTASGNSRGHFGASASVGYOM 592



## RESULT 7

09JPS3 PRELIMINARY; PRT: 590 AA.  
AC 09JPS3: 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DE Outer membrane protein GMA992.  
CN GMA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC30D800C CRC64;

Query Match 92.7%; Score 2036.5; DB 2; Length 590;  
Best Local Similarity 71.5%; Pred. No. 1.2e-86;  
Matches 422; Conservative 3; Mismatches 157; Gaps 2;

QY 1 MNKIYRIIWNLSALNAAWVVSSELTNRNHTKASATKATVATLTLFATVOASA----- 51  
DB 1 MNKIYRIIWNLSALNAAWVVSSELTNRNHTKASATKATVATLTLFATVOANATDEDEBDL 60  
QY 52 ----- 51  
DB 61 DPVORTAVAVLVNSDKKESTGEKEVEENSDMAVYFNEKGVLTAGTITLKAGDNLKIKONG 120  
QY 52 ----- 51  
DB 121 TNFTYSLKKDLTDLTSVTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGI 180  
QY 52 ----- 84  
DB 181 GSTLTDLTLTGATTTNTNDVTDDEKRRASVSKDVLNAGWNIGVKRGTTASDVVDVR 240  
QY 85 TYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDKLVTKGDKGENGSTD 144  
DB 241 TYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDKLVTKGDKGENGSTD 300  
QY 145 EGBELVTAKEVIDAVNKAQGRMKTTTANGOTGQADKRETVTSGTNVTFASGKTATVSK 204  
DB 301 EGBELVTAKEVIDAVNKAQGRMKTTTANGOTGQADKRETVTSGTNVTFASGKTATVSK 360  
QY 205 DDGQNTIYMYDVNVDALNVQNLNSGWNLSKAVAGSSGKVISGNVSPSGKMDETVNI 264  
DB 361 DDGQNTIYMYDVNVDALNVQNLNSGWNLSKAVAGSSGKVISGNVSPSGKMDETVNI 420  
QY 265 NAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKKNKPVRI 323  
DB 421 NAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKANKPVRI 480  
QY 324 TNVAPGVKEGDTVNVQOLKGYAONLNRIIDVNDGNARAGIAQAIATAGLVQAVYLPKSSMM 383  
DB 481 TNVAPGVKEGDTVNVQOLKGYAONLNRIIDVNDGNARAGIAQAIATAGLVQAVYLPKSSMM 540

QY 384 AIGGTYRGEAGYAIAGVSSISDGNWIKITAGSNGRCHFGASASVGYOM 433  
DB 541 AIGGTYRGEAGYAIAGVSSISDGNWIKITAGSNGRCHFGASASVGYOM 590

## RESULT 8

09JPS2 PRELIMINARY; PRT: 594 AA.  
AC 09JPS2: 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DE Outer membrane protein GMA992.  
CN GMA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 92.6%; Score 2033.5; DB 2; Length 594;  
Best Local Similarity 71.0%; Pred. No. 1.6e-86;  
Matches 422; Conservative 1; Mismatches 10; Indels 161; Gaps 2;

QY 1 MNKIYRIIWNLSALNAAWVVSSELTNRNHTKASATKATVATLTLFATVOASA----- 51  
DB 1 MNKIYRIIWNLSALNAAWVVSSELTNRNHTKASATKATVATLTLFATVASTTDDDDLYLE 60  
QY 52 ----- 51  
DB 61 PVORTAPVLSFHADSEGTGEKEVTEEDSNMGVYFDPKGVLTAGTITLKAGDNLKIKONTDE 120  
QY 52 ----- 51  
DB 121 NFNASSFTYSLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDTTVH 180  
QY 52 ----- 80  
DB 181 LINGISTLTDLTLTGATTTNTNDVTDDEKRRASVSKDVLNAGWNIGVKRGTTASDVNI 240  
QY 81 DFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDKLVTKGDKGENG 140  
DB 241 DFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDKLVTKGDKGENG 300  
QY 141 SSTDEGBELVTAKEVIDAVNKAQGRMKTTTANGOTGQADKRETVTSGTNVTFASGKTAT 200  
DB 301 SSTDEGBELVTAKEVIDAVNKAQGRMKTTTANGOTGQADKRETVTSGTNVTFASGKTAT 360  
QY 201 TVSKDDGNTIYMYDVNVDALNVQNLNSGWNLSKAVAGSSGKVISGNVSPSGKMDKDE 260  
DB 361 TVSKDDGNTIYMYDVNVDALNVQNLNSGWNLSKAVAGSSGKVISGNVSPSGKMDKDE 420  
QY 261 TVNINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKKDNK 319  
DB 421 TVNINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKDNK 480

QY	320	PVRLTNVAPGKEGVTVNAOLKGYAQNLMNRIDVNDGNARAGIAQALATAGLVOAYLPG	379
Db	481	PVRLTNVAPGKEGVTVNAOLKGYAQNLMNRIDVNDGNARAGIAQALATAGLVOAYLPG	540
QY	380	KSMALIGGGTYRGEAGTVAIGYSSISDGGNMIIKGTASGNSRCHFGASASVGYQW	433
Db	541	KSMALIGGGTYRGEAGTVAIGYSSISDGGNMIIKGTASGNSRCHFGASASVGYQW	594
RESULT 9			
Q930Y4	PRELIMINARY:	PRT:	594 AA.
Q930Y4	AC	Q930Y4	
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Nhha outer membrane protein.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
CC	Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EG327;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RL	membrane protein of Neisseria meningitidis";		
DR	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF157605; AAK6866.1; -		
DR	InterPro; IPR005594; Yada.		
DR	Pfam; PF03895; Yada; 1.		
SQ	SEQUENCE 594 AA; 62297 MW; 9DDDA6B04B3A8EA2 CRC64;		
Query Match 92.5%; Score 2032.5; DB 2; Length 594;			
Best Local Similarity 70.9%; Pred. No. 1.8e-86;			
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;			
QY	1	MNKIYRIIWNALNMAVVVSELTNRHTRKASATVTAVALTLEFATVQASA-----	51
Db	1	MNKIYRIIWNALNMAVAVSELTRNHTKRASATVATAVALTLEFATVQASTTDDDDLYLE	60
QY	52	-----	51
Db	61	PVGRTAVALSPRSDEKTEGKEVTEEDSNMGYFDDKGVLTAGTITLKAQDNLKIKQNTNE	120
QY	52	-----	51
Db	121	NTNASSFTYSLKKDLTDLTSVETKLSFANSNKVNIITSDTKGLNFAAKTAETNGDTTVH	180
QY	52	-----	80
Db	181	LNIGSGITLDTLTLNTGATTNTNDNVYDDEKKRAASVADVNLAGNNIKGVKFGTTASDNV	240
QY	81	DEVFRTYDVEFLSADTKTTTVNVESKDGKTEVYIGAKTSYIKEDKLVYTKDGKENG	140
Db	241	DFVFRTYDVEFLSADTKTTTVNVESKDGKRTYVYIGAKTSYIKEDKLVYTKDGKENG	300
QY	141	SSTDEGSELVYAKREVYDAVNAKGRMKTTTANGQIGQADKREYVYSGTNVTFASKGTTA	200
Db	301	SSTDEGSELVYAKREVYDAVNAKGRMKTTTANGQIGQADKREYVYSGTNVTFASKGTTA	360
QY	201	TYSKDDGNGTIVMDVNVGDALANVNOLOSGMNLDSKRVASSGGVIGSNVSPSKGKME	260
Db	361	TYSKDDGNGTIVMDVNVGDALANVNOLOSGMNLDSKRVASSGGVIGSNVSPSKGKME	420
QY	261	TVINAGNNIEITRNGKNIDTASKTPOFSSVSLGAGADAPTLVSVDG-ALNVGSKDKNK	319
Db	421	TVINAGNNIEITRNGKNIDTASKTPOFSSVSLGAGADAPTLVSVDGALNVGSKDKNK	480
QY	320	PVRLTNVAPGKEGVTVNAOLKGYAQNLMNRIDVNDGNARAGIAQALATAGLVOAYLPG	379

[illegible]

Db 301 KGENSSSTDEGEGLVTAKEVIDAYNKAGWEMKTTTANGOTGQADKEFTYVSGTNVTFASG 360  
QY 196 KGTATVSKDDGDNITVMDVYNGDALNVNQLONSGWMLDSKAVAGSSGKVISGNVSPSK 255  
Db 361 KGTATVSKDDGDNITVMDVYNGDALNVNQLONSGWMLDSKAVAGSSGKVISGNVSPSK 420  
QY 256 GKMEFTVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDG-DALNVGS 314  
Db 421 GKMEFTVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGKALNVGS 480  
QY 315 KKNKRVRTTNVAPKVEGVTVAQLKGVAQNLRNIDVNDGNARAGIAQAIATAGLVQ 374  
Db 481 KKNKRVRTTNVAPKVEGVTVAQLKGVAQNLRNIDVNDGNARAGIAQAIATAGLVQ 540  
QY 375 AYPGKSMMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433  
Db 541 AYPGKSMMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599

## RESULT 11

Q9JPT3 PRELIMINARY; PRT; 594 AA.  
AC Q9JPT3; 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, and BZ232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tellelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.D., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -;  
DR EMBL: AF226369; AAF42518.1; -;  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D04B46 CRC64;

Query Match 92.4%; Score 2029.5; DB 2; Length 594;  
Best Local Similarity 70.9%; Pred. No. 2, 5e-86;  
Matches 421; Conservative 1; Mismatches 11; Indels 161; Gaps 2;

QY 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATLTLFAVYQASA----- 51  
Db 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATLTLFAVYQASTTDDDLYLE 60  
QY 52 ----- 51  
Db 61 PVOPTAPVLSFHADSEGTGEKVEYEDSNMVGFDKGVLAGTTTLKAGDNLIKQNTDE 120  
QY 52 ----- 51  
Db 121 NTNASSFTYSLKDLTDLFVETEKLSFGANGKKNVITSDPKGLNPAKETAGTNGDTYH 180  
QY 52 -----NRAASVQDVNLNGWNIKGVKPGTTASDNV 80  
Db 181 LINGISTLTDTLNTGATVNTDNTYDDEKRRASVQDVNLNGWNIKGVKPGTTASDNV 240  
QY 81 DPAFTYDVEFLSADTKTTTVNVESKDNCKTEVIGAKTSVIERKDGKLVTKDGENG 140

Db 241 DPAFTYDVEFLSADTKTTTVNVESKDNCKTEVIGAKTSVIERKDGKLVTKDGENG 300  
QY 141 SSTDEGEGLVTAKEVIDAYNKAGWEMKTTTANGOTGQADKEFTYVSGTNVTFASG 200  
Db 301 SSTDEGEGLVTAKEVIDAYNKAGWEMKTTTANGOTGQADKEFTYVSGTNVTFASG 360  
QY 201 TVSKDDGDNITVMDVYNGDALNVNQLONSGWMLDSKAVAGSSGKVISGNVSPSK 260  
Db 361 TVSKDDGDNITVMDVYNGDALNVNQLONSGWMLDSKAVAGSSGKVISGNVSPSK 420  
QY 261 TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDNK 319  
Db 421 TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGKALNVGSKDNK 480  
QY 320 PVKITVAPKVEGVTVAQLKGVAQNLRNIDVNDGNARAGIAQAIATAGLVQ 379  
Db 481 PVKITVAPKVEGVTVAQLKGVAQNLRNIDVNDGNARAGIAQAIATAGLVQ 540  
QY 380 KSMMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433  
Db 541 KSMMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594

## RESULT 12

Q9JPH7 PRELIMINARY; PRT; 594 AA.  
AC Q9JPH7; 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992 (Nhla outer membrane protein).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BZ198, and 297-0;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tellelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.D., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -;  
DR EMBL: AF226369; AAF42518.1; -;  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 594 AA; 62361 MW; 436BDDDE68263C5C CRC64;

Query Match 92.2%; Score 2025.5; DB 2; Length 594;  
Best Local Similarity 70.9%; Pred. No. 3, 8e-86;  
Matches 421; Conservative 2; Mismatches 10; Indels 161; Gaps 2;

QY 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATLTLFAVYQASA----- 51  
Db 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATLTLFAVYQANATDDDLYLE 60

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QY 52 ----- 51
Db 61 PVQRTAVVLSFRSDKEGTEGETEDSDMWAVYFDEKRVLKAGATILKAGDNLKIKONTNE 120
QY 52 ----- 51
Db 121 NTNDSFTYSLKCDLTLDSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNDPTVH 180
QY 52 ----- 80
Db 181 INGISLTLDLTLNTGATTNTVNDVTDDEKKRAASVADVLNAGWNIKGVKPGTTASDNV 240
QY 81 DFNRYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVIREKDGKLVYTGKKG 140
Db 241 DFNRYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVIREKDGKLVYTGKKG 300
QY 141 SSTDGEGELVTAKEVIDAVNKGWMMKTTTANGOTGADKFEVTSCTNVTFAASKGTTA 200
Db 301 SSTDGEGELVTAKEVIDAVNKGWMMKTTTANGOTGADKFEVTSCTNVTFAASKGTTA 360
QY 201 TVSKDDGNTVTMDVNVGDLNVLNQLONGMNLDSKAVAGSSGKVISGNVSPSKGKDE 260
Db 361 TVSKDDGNTVTMDVNVGDLNVLNQLONGMNLDSKAVAGSSGKVISGNVSPSKGKDE 420
QY 261 TVNINAGNNIETIRNGKNIDATSMTPPOFSSVSLGAGADAPTLSDVDG-ALNVGSKDKND 319
Db 421 TVNINAGNNIETIRNGKNIDATSMTPPOFSSVSLGAGADAPTLSDVDGALNVGSKDKND 480
QY 320 PVRTINAVPGYKEDVTNVQOLKGYAQNLLNRINDVNDGNARIGIAQATATGLVQAYPG 379
Db 481 PVRTINAVPGYKEDVTNVQOLKGYAQNLLNRINDVNDGNARIGIAQATATGLVQAYPG 540
QY 380 KSMAAIGGTYRGAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
Db 541 KSMAAIGGTYRGAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 594
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## RESULT 13

```
QJUPR9 PRELIMINARY; PRT; 598 AA.
AC QJUPR9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Outer membrane protein GNA592.
GN GNA592.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226382; AAF42531.1; -.
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; YADA.1.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 92.1%; Score 2023.5; DB 2; Length 598;  
Best Local Similarity 70.4%; Pred. No. 4.8e-86;  
Matches 421; Conservative 2; Mismatches 10; Indels 165; Gaps 2;

```
QY 1 MNKTYRIIWSALNANVYVSELTNRNHTKRASATVTAVALTLFPATVQASA----- 51
Db 1 MNKTYRIIWSALNANVYVSELTNRNHTKRASATVTAVALTLFPATVQANATDDDDLYLE 60
QY 52 ----- 51
Db 61 PVQRTAVVLSFRSDKEGTEGETEDSDMWAVYFDEKRVLKAGATILKAGDNLKIKONTNE 120
QY 52 ----- 51
Db 121 NTNENTDSFTYSLKCDLTLDSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
QY 52 ----- 76
Db 181 PTVHLNGISLTLDLTLNTGATTNTVNDVTDDEKKRAASVADVLNAGWNIKGVKPGTTA 240
QY 77 SDNVDFVRYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVIREKDGKLVYTGKDK 136
Db 241 SDNVDFVRYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVIREKDGKLVYTGKDK 300
QY 137 GENGSSDDEGELVTAKEVIDAVNKGWMMKTTTANGOTGADKFEVTSCTNVTFAASKG 196
Db 301 DENGSSTDGEGELVTAKEVIDAVNKGWMMKTTTANGOTGADKFEVTSCTNVTFAASKG 360
QY 197 GTTATVSKDDGNTVTMDVNVGDLNVLNQLONGMNLDSKAVAGSSGKVISGNVSPSKG 256
Db 361 GTTATVSKDDGNTVTMDVNVGDLNVLNQLONGMNLDSKAVAGSSGKVISGNVSPSKG 420
QY 257 KMDEVTNINAGNNIETIRNGKNIDATSMTPPOFSSVSLGAGADAPTLSDVDG-ALNVGSK 315
Db 421 KMDEVTNINAGNNIETIRNGKNIDATSMTPPOFSSVSLGAGADAPTLSDVDGALNVGSK 480
QY 316 KDNKFEVRTINAVPGYKEDVTNVQOLKGYAQNLLNRINDVNDGNARIGIAQATATGLVQYA 375
Db 481 DFNKFEVRTINAVPGYKEDVTNVQOLKGYAQNLLNRINDVNDGNALAGIAQATATGLVQYA 540
QY 376 YLPKKSMAAIGGTYRGAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
Db 541 YLPKKSMAAIGGTYRGAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 598
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## RESULT 14

```
Q930Y2 PRELIMINARY; PRT; 592 AA.
AC Q930Y2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Outer membrane protein.
DE Mha outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H41;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF157609; AAK68870.1; -.
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; YADA.1.
SQ SEQUENCE 592 AA; 61869 MW; F9403A0BA18BEA7 CRC64;
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Query Match 91.7%; Score 2015.5; DB 2; Length 592;  
Best Local Similarity 70.8%; Pred. No. 1.1e-85;  
Matches 419; Conservative 3; Mismatches 11; Indels 159; Gaps 2;  
1 MNKTYRIIWSALNANVYVSELTNRNHTKRASATVTAVALTLFPATVQASA----- 51  
1 MNKTYRIIWSALNANVYVSELTNRNHTKRASATVTAVALTLFPATVQANATDEDEDEBEL 60

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QY 52 ----- 51
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QY 52 ----- 82
DB 181 GIGSTLTMLNTGATTNTNDVYDDEKRAASVKDVLNAGNNIGVPGTTASDNVDF 240
QY 83 VRTYDVEELSDFTKTTTVNVEESKDNCKTEVKIGAKTSYIKEDKILYTGKDKGENSS 142
DB 241 VRTYDVEELSDFTKTTTVNVEESKDNCKTEVKIGAKTSYIKEDKILYTGKDKGENSS 300
QY 143 TDEBGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGKTATV 202
DB 301 TDEBGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGKTATV 360
QY 203 SKDDGNITVMDVNVGDLNVNQLNSGNNLDSKAVAGSSGKVISGNSPSKGMDEYV 262
DB 361 SKDDGNITVMDVNVGDLNVNQLNSGNNLDSKAVAGSSGKVISGNSPSKGMDEYV 420
QY 263 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSKKDNKPY 321
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDGALNVGSKKDNKPY 480
QY 322 RTTNVAPVKEGDVTVNAOLKGVANLNRRIDNVNAGNAGIAOAIATAGLVQAYLPKGS 381
DB 481 RTTNVAPVKEGDVTVNAOLKGVANLNRRIDNVNAGNAGIAOAIATAGLVQAYLPKGS 540
QY 382 MMAIGGTYRGEAGYVAGYSISDGMWIIKGTASGNSRHFASASVGYQW 433
DB 541 MMAIGGTYRGEAGYVAGYSISDGMWIIKGTASGNSRHFASASVGYQW 592

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AC Q9JPS0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HI5;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226381; AAF42530.1; -

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DR EMBL: AF157607; AAK68868.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;

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Query Match 91.5%; Score 2010.5; DB 2; Length 598;
Best Local Similarity 69.9%; Pred. No. 1,9e-85;
Matches 418; Conservative 3; Mismatches 12; Indels 165; Gaps 2;

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QY 52 ----- 51
DB 61 PVQRTAVVLSFRSDKDEGTGEKTEEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
QY 52 ----- 51
DB 121 NTNENTNDSFTYSLKKDLTLDTLSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
QY 52 ----- 76
DB 181 PTVHLNGIGSTLTDLTLNTGATTNTNDVYDDEKRAASVKDVLNAGNNIGKVKPGTTA 240
QY 77 SDNVDFVRYDYVEFLSADTKTTTVNVEESKDNCKTEVKIGAKTSYIKEDKILYTGKDK 136
DB 241 SDNVDFVRYDYVEFLSADTKTTTVNVEESKDNCKTEVKIGAKTSYIKEDKILYTGKDK 300
QY 137 GENGSSSTDEBGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGK 196
DB 301 DENGSSSTDEBGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGN 360
QY 197 GTTATVSKDDGNITVMDVNVGDLNVNQLNSGNNLDSKAVAGSSGKVISGNSPSKGM 256
DB 361 GTTATVSKDDGNITVMDVNVGDLNVNQLNSGNNLDSKAVAGSSGKVISGNSPSKGM 420
QY 257 KMDFTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 315
DB 421 KMDFTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDGALNVGSK 480
QY 316 KDNKPVRTTNVAPVKEGDVTVNAOLKGVANLNRRIDNVNAGNAGIAOAIATAGLVQA 375
DB 481 DANKPVRTTNVAPVKEGDVTVNAOLKGVANLNRRIDNVNAGNAGIAOAIATAGLVQA 540
QY 376 YLPKGSMAIGGTYRGEAGYVAGYSISDGMWIIKGTASGNSRHFASASVGYQW 433
DB 541 YLPKGSMAIGGTYRGEAGYVAGYSISDGMWIIKGTASGNSRHFASASVGYQW 598

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Search completed: October 6, 2003, 09:30:42  
Job time : 34.8023 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 : Search time 43.1096 Seconds  
(without alignments)  
1848.329 Million cell updates/sec

Title: US-09-771-382-27  
Perfect score: 2544  
Sequence: 1 NKKYRIITMNSALNMMVYVS.....TASGNSRGHFGASASVGQW 502

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_19Jun03:\*

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24: /SIDSL/gcgdata/geneseq/genesqp-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2544	100.0	502	AAU06186	N. meningitidis PM
2	2459.5	96.7	591	AAV27202	Amino acid sequenc
3	2459.5	96.7	591	AAV23746	A surface protein
4	2459.5	96.7	591	AAU06171	N. meningitidis PM
5	2455	96.5	592	AAV23737	A surface protein
6	2452.5	96.4	591	AAV57045	BASB029 amino acid
7	2447.5	96.2	591	AAV23741	A surface protein
8	2447.5	96.2	591	AAU06175	N. meningitidis EG
9	2383	93.7	512	AAU06182	N. meningitidis PM

10	2371.5	93.2	599	20	AAV23743	A surface protein
11	2371.5	93.2	599	22	AAU06176	N. meningitidis H3
12	2366	93.0	594	22	AAV23740	A surface protein
13	2366	93.0	594	21	AAV57044	BASB029 amino acid
14	2366	93.0	594	22	AAU06174	N. meningitidis EG
15	2359	92.7	594	20	AAV23739	A surface protein
16	2359	92.7	594	22	AAU06179	N. meningitidis B2
17	2351	92.4	592	22	AAU06180	N. meningitidis Z2
18	2344	92.1	598	20	AAV23742	A surface protein
19	2344	92.1	598	22	AAU06177	N. meningitidis H1
20	2335	91.8	598	20	AAV23738	A surface protein
21	2335	91.8	598	22	AAU06178	N. meningitidis B2
22	2327	91.5	592	20	AAU23744	A surface protein
23	2327	91.5	592	22	AAU06172	N. meningitidis H4
24	2323	91.3	592	20	AAV27203	Amino acid sequenc
25	2317.5	91.1	589	20	AAV23745	A surface protein
26	2317.5	91.1	589	22	AAU06173	N. meningitidis P2
27	2255.5	88.7	513	22	AAU06183	N. meningitidis H4
28	2166	85.1	604	22	AAU06181	N. meningitidis su
29	2098.5	82.5	433	22	AAU06185	N. meningitidis PM
30	2005.5	78.8	407	22	AAU06184	N. meningitidis PM
31	1011.5	39.8	2411	21	AAV23860	Haemophilus influe
32	1009.5	39.7	2353	17	AAV9393	Haemophilus adhesi
33	974	38.3	1098	17	AAV9392	Haemophilus adhesi
34	906	35.6	1094	21	AAV23858	Haemophilus influe
35	847.5	33.3	679	17	AAV9394	Haemophilus adhesi
36	847.5	33.3	679	21	AAV23855	Haemophilus influe
37	690.5	27.1	245	20	AAV27201	Amino acid sequenc
38	682	26.8	1004	21	AAV23857	Haemophilus influe
39	661	26.0	1002	21	AAV23854	Haemophilus influe
40	600	23.6	116	21	AAV37832	Neisseria conserv
41	594	23.3	1104	21	AAV23856	Haemophilus influe
42	594	23.3	1104	21	AAV23859	Haemophilus influe
43	523.5	20.6	298	24	AAV30477	Haemophilus influe
44	374	14.7	2139	24	ABF71294	M. catarrhalis sur
45	372.5	14.6	2314	22	AAV69136	M. catarrhalis les

#### ALIGNMENTS

RESULT 1	
ID	AAU06186 standard; Protein; 502 AA.
AAU06186	
AC	AAU06186;
AC	
DT	24-OCT-2001 (first entry)
DT	
DE	N. meningitidis PMC21 Nhma deletion mutant #4.
DE	
KW	Surface antigen Nhma; meningococcal disease; meningitis vaccine;
KW	mutant; mutuin.
OS	Neisseria meningitidis strain PMC21.
OS	Synthetic.
PH	
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..49
FT	/label= Signal_peptide
FT	50..502
FT	/label= Mature_Nhma_deletion_mutant_#4
FT	/note= "Predicted mature protein, specifically
FT	claimed in claim 12"
PN	WO200155182-A1.
PN	
PD	02-AUG-2001.
PD	
PF	25-JAN-2001: 2001MO-AU00069.
PF	
PR	25-JAN-2000: 2000US-0177917.
PR	
XX	
XX	

PA (UYOU ) UNITV QUEENSLAND.  
XX  
XX PI Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
DR N-PSDB: AAS09176.  
XX  
XX New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 12; Fig 9; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhha deletion mutant #4.  
XX  
SQ Sequence 502 AA;  
  
Query Match 100.0%; Score 2544; DB 22; Length 502;  
Best Local Similarity 100.0%; Pred. No. 1.9e-152;  
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MNKIRIIMNSALNMAVYVSELTNRHNRASATVKTAVLTLFATVQASANTLKGDNL 60  
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DB 61 KIKQOTYSLKRDLDLTYSVGTCKLSFSANGKVNITSDTKGINFAKETAINGDTTVHLN 120  
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DB 121 GIGSLTPTDRAASVSKDVLANGMNKGKVNVDVFRITDYEFELSDADRTTTTVNESKDNCK 180  
OY 181 TEVKIGAKTSVKEKDKLVTKGDKGNGSSSTDEGEGLVTAKVIDAVNKAQMRKTTTA 240  
DB 181 TEVKIGAKTSVKEKDKLVTKGDKGNGSSSTDEGEGLVTAKVIDAVNKAQMRKTTTA 240  
OY 241 NGOTQADKFEFTVYSGTNTVTFASGKGTATVSKDOGNITVYDVNVDALNVLONSG 300  
DB 241 NGOTQADKFEFTVYSGTNTVTFASGKGTATVSKDOGNITVYDVNVDALNVLONSG 300  
OY 301 WNLDSKAVAGSSGKVIISGNVSPSKGMDVETVINAGNNIETIRNKNIDIASMTPOSS 360  
DB 301 WNLDSKAVAGSSGKVIISGNVSPSKGMDVETVINAGNNIETIRNKNIDIASMTPOSS 360  
OY 361 VSLGAGADAPTLISVDGDLNNGSKKDNKPVRTITNVAPEVKEGSDVTNVAQLKGAONLNR 420  
DB 361 VSLGAGADAPTLISVDGDLNNGSKKDNKPVRTITNVAPEVKEGSDVTNVAQLKGAONLNR 420  
OY 421 IDNVGNNRAGIAQAIATAGLVQATLPKGSMAAIGGTYRGEAGTAIGSSISDGNMTI 480  
DB 421 IDNVGNNRAGIAQAIATAGLVQATLPKGSMAAIGGTYRGEAGTAIGSSISDGNMTI 480  
OY 481 KGTASGNSRGHFGASASVGYOW 502  
DB 481 KGTASGNSRGHFGASASVGYOW 502  
  
RESULT 2  
AAY27202  
ID AAY27202 standard: Protein; 591 AA.  
XX

AC AAY27202;  
XX  
XX 24-SEP-1999 (first entry)  
XX  
XX Amino acid sequence of N. meningitidis protein ORF40-1.  
XX  
XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX  
XX Neisseria meningitidis.  
XX  
XX WO936544-A2.  
XX  
XX 22-JUL-1999.  
XX  
XX 14-JAN-1999; 99WO-IB00103.  
XX  
XX 09-OCT-1998; 98GB-0022143.  
XX  
XX 14-JAN-1998; 98GB-0000760.  
XX  
XX 01-SEP-1998; 98GB-0019015.  
XX  
XX (CHIR-) CHIRON SPA.  
XX  
XX Grandi G, Maignani V, Pizsa M, Rappuoli R, Scarlato V;  
PI WPI: 1999-444400/37.  
XX  
XX N-PSDB: AAX99124.  
XX  
XX New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX  
XX The invention provides proteins (AAY27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisseria  
CC bacteria, especially Neisseria meningitidis.  
XX  
SQ Sequence 591 AA;  
  
Query Match 96.7%; Score 2459.5; DB 20; Length 591;  
Best Local Similarity 84.9%; Pred. No. 5e-147;  
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;  
  
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DB 1 MNKIRIIMNSALNMAVYVSELTNRHNRASATVKTAVLTLFATVQASANNEOEEDL 60  
OY 53 -----TLAGDNLKIKQ 64  
DB 61 YLDPYQRTVAVLVNSDEGEGEKEKVEENSDMAVYFNEKGVLTARETTLAAGDNLKIKQ 120  
OY 65 ----FTYSIKKDLDTLSVGTCKLSFSANGKVNITSDTKGINFAKETAINGDTTVHLN 120  
DB 121 NGNTFTYSIKKDLDTLSVGTCKLSFSANGKVNITSDTKGINFAKETAINGDTTVHLN 180  
OY 121 GIGSLTPTD-----RAASVKDVLANGMNKGK-----ANDF 151  
DB 181 GIGSLTPTDLNTGATNTVNDNTVDDEKRAASVKDVLANGMNKGKPGTTASDNDV 240  
OY 152 VRTDYTFELSDADRTTTTVNESKDNCKTEVKIGAKTSVKEKDKLVTKGDKGNGSS 211  
DB 241 VRTDYTFELSDADRTTTTVNESKDNCKTEVKIGAKTSVKEKDKLVTKGDKGNGSS 300  
OY 212 TDEGEGLVTAKVIDAVNKAQMRKTTTANGOTGADKFEFTVSGTNTVTFASGKGTATV 271  
DB 301 TDEGEGLVTAKVIDAVNKAQMRKTTTANGOTGADKFEFTVSGTNTVTFASGKGTATV 360  
OY 272 SKDOGNITVYDVNVDALNVLONSGMNLDSKAVAGSSGKVIISGNVSPSKGMDVETV 331



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Qy      332 NINAGNNIETRRGNKNDIATSMTPQFSSVSLGAGADAPTLVDGALNVGSKKDKNRPVR 391
Db      421 NINAGNNIETRRGNKNDIATSMTPQFSSVSLGAGADAPTLVDGALNVGSKKDKNRPVR 480
Qy      392 ITNVAPGKRGDVTNVAQLKGVANLNNRIDNVGNNARAGIAQAIATAGLVQAYLPKSKM 451
Db      481 ITNVAPGKRGDVTNVAQLKGVANLNNRIDNVGNNARAGIAQAIATAGLVQAYLPKSKM 540
Qy      452 MAIGGTYRGEAGYAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 502
Db      541 MAIGGTYRGEAGYAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 591

RESULT 3
AAU23746
ID      AAY23746 standard; Protein; 591 AA.
XX
AC      AAY23746;
XX
DT      08-SEP-1999 (first entry)
XX
DE      A surface protein of Neisseria meningitidis.
XX
KM      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX      Neisseria meningitidis.
XX      WC0931132-A1.
XX      24-JUN-1999.
XX
PF      14-DEC-1998; 98WO-AU01031.
XX
PR      12-DEC-1997; 97GB-0026398.
XX
PA      (ISIS-) ISIS INNOVATION LTD.
PA      (UYOU) UNIV QUEENSLAND.
XX
PI      Jennings MP, Moxon ER, Peak IRA;
XX      WPI; 1999-418754/35.
XX      N-PSDB; AAX85798.
XX
DR      N-PSDB; AAX85798.
XX
PT      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX
PS      Claim 1; Page 127-128; 132pp; English.
XX
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX
SQ      Sequence 591 AA:
XX
Query Match 96.7%; Score 2459.5; DB 20; Length 591;
Best Local Similarity 84.9%; Pred. No. 5e-147;
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;
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Db      1 MNKIYRIIMNSALNAMYVSELFRNHRKRSATYKTAVALTLFATYQASANNEDEEDL 60
Qy      53 -----TLKAGDNLIKIQ 64

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Db      121 NGTFNYSILKKDLTDLTSVTEKLSFSANKNKNIISDTGLMFAKETAGTNGDTYHLN 180
Qy      121 GIGSTLTLD-----RAASVCKDLVLAAGNNIKGVK-----NVDF 151
Db      181 GIGSTLTDLTLLNKGATTTNVTNDVTDDEKRRASVCKDLVLAAGNNIKGVKPGTTASDNVDF 240
Qy      152 VRTYDVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYIKERDKLVTKDKGENGSS 211
Db      241 VRTYDVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYIKERDKLVTKDKGENGSS 300
Qy      212 TDEGEGLVTAKEVIDAVNKKGMKKTITANGQTGQADKFEYTVSGTWTATASCKGTATV 271
Db      301 TDEGEGLVTAKEVIDAVNKKGMKKTITANGQTGQADKFEYTVSGTWTATASCKGTATV 360
Qy      272 SKDDGNIITVMYDVNVDALNVNQLQNSGWNLDLSKAAVSSGKVIISGNVSPSKGKMDETV 331
Db      361 SKDDGNIITVMYDVNVDALNVNQLQNSGWNLDLSKAAVSSGKVIISGNVSPSKGKMDETV 420
Qy      332 NINAGNNIETRRGNKNDIATSMTPQFSSVSLGAGADAPTLVDGALNVGSKKDKNRPVR 391
Db      421 NINAGNNIETRRGNKNDIATSMTPQFSSVSLGAGADAPTLVDGALNVGSKKDKNRPVR 480
Qy      392 ITNVAPGKRGDVTNVAQLKGVANLNNRIDNVGNNARAGIAQAIATAGLVQAYLPKSKM 451
Db      481 ITNVAPGKRGDVTNVAQLKGVANLNNRIDNVGNNARAGIAQAIATAGLVQAYLPKSKM 540
Qy      452 MAIGGTYRGEAGYAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 502
Db      541 MAIGGTYRGEAGYAIQYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 591

RESULT 4
AAU06171
ID      AAU06171 standard; Protein; 591 AA.
XX
AC      AAU06171;
XX
DT      24-OCT-2001 (first entry)
XX
DE      N. meningitidis PMC21 surface antigen Noha polypeptide sequence.
XX
KM      Surface antigen Noha; meningococcal disease; meningitis vaccine.
XX
OS      Neisseria meningitidis strain PMC21.
XX
FH      Key
FT      Peptide
FT      1..51 Location/Qualifiers
FT      /label= Signal_peptide
FT      /label= C1
FT      /note= "Conserved region 1"
FT      51..108
FT      /label= V1
FT      /note= "Variable region 1"
FT      52..591
FT      /label= Mature_Noha
FT      /note= "Predicted mature protein, specifically
FT      claimed in claim 12"
FT      109..120
FT      /label= C2
FT      /note= "Conserved region 2"
FT      121..124
FT      /label= V2
FT      /note= "Variable region 2"
FT      125..188
FT      /label= C3
FT      /note= "Conserved region 3"
FT      189..210
FT      Region

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FT      /label= V3
FT      /note= "Variable region 3"
FT      211...229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..591
FT      /label= C5
FT      /note= "Conserved region 5"
FT      W020015182-A1.
FT      02-AUG-2001.
FT      25-JAN-2001; 2001WO-AU00069.
FT      25-JAN-2000; 2000US-0177917.
FT      (UYOU ) UNIV QUEENSLAND.
FT      Peak IRA, Jennings MP;
FT      WPI, 2001-488774/53.
FT      DR N-PSDB; AAS09161.
FT      New Nhma surface antigen polypeptides and polynucleotides from
FT      preventing broad spectrum of Neisseria meningitidis -
FT      Claim 9, Fig 1; 91pp; English.
FT      PS
FT      XX The present invention relates to the isolation of novel Neisseria
FT      CC meningitidis mutant polypeptides of the surface antigen Nhma
FT      CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
FT      CC characterised by deletions of non-conserved amino acids, particularly
FT      CC the deletion of variable regions. The deletion mutants are useful in
FT      CC diagnostics, therapeutic and prophylactic vaccines against a broader
FT      CC spectrum of N. meningitidis, and in designing and/or screening of
FT      CC medicaments. The mutant proteins when used as a vaccine can effectively
FT      CC immunise against a broader spectrum of N. meningitidis strains than
FT      CC would be expected from a corresponding wild-type surface antigen.
FT      CC The present sequence representing the wild type surface antigen Nhma
FT      CC from N. meningitidis strain PMC21 is 1 of 10 Nhma polypeptide sequences
FT      CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
FT      CC the present invention.
FT      SQ Sequence 591 AA:
FT      Query Match 96.7%; Score 2459.5; DB 22; Length 591;
FT      Best Local Similarity 84.9%; Pred. No. 5e-147;
FT      Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;
FT      QY 1 MNKIRITWNSALNAAVYSELTRNHTKRASATVAVLATILTRFVQASAN----- 52
FT      DB 1 MNKIRITWNSALNAAVYSELTRNHTKRASATVAVLATILTRFVQASANNEOEEDL 60
FT      QY 53 -----TLAGNMLKTIKQ 64
FT      DB 61 YLDPQRTVAVLVNSDKEGTEGKEKVEENSDMAVYFNEKGYLARETLLRAGDMLKIQ 120
FT      QY 65 ----FTVSLKRDLDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVMHN 120
FT      DB 121 NGTNTYSLKKDLDTLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVMHN 180
FT      QY 121 GIGSLTMD-----RAASYKDYLANGNWIKGYK-----NWDF 151
FT      DB 181 GIGSLTMDLNTGATTNVTNDNVTYDDEKRAASVYKDVLANGNWIKGYKPGTTASDNVDF 240
FT      QY 152 VRTDYVLEFSLADRTTTVNESKDNCKTEVKGAKSVYKEDGKLVTKDGENSS 211
FT      DB 241 VRTDYVLEFSLADRTTTVNESKDNCKTEVKGAKSVYKEDGKLVTKDGENSS 300

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QY      212 TDEGCLVTAKAEVIDAVNKAQMRMKTGTANGQTQADKFEYVTSNTVTFASGKGTATV 271
DB      301 TDEGCLVTAKAEVIDAVNKAQMRMKTGTANGQTQADKFEYVTSNTVTFASGKGTATV 360
QY      272 SKDDOGNITVAVDVGALVNLQNSGWNLSKAVAGSSGKVTSGVSPSKGMDTV 331
DB      361 SKDDOGNITVAVDVGALVNLQNSGWNLSKAVAGSSGKVTSGVSPSKGMDTV 420
QY      332 NINAGNNEITRNGKNIDIASMPPOFSSVSLGACADAPTLISVDDALNVSSKKDKPVR 391
DB      421 NINAGNNEITRNGKNIDIASMTPOFSSVSLGACADAPTLISVDDALNVSSKKDKPVR 480
QY      392 ITNVAQVKEGSDVTNVAQLKQVQNLNRRIDNVDSNARAGIAQATATAGLVQAYLPKSKM 451
DB      481 ITNVAQVKEGSDVTNVAQLKQVQNLNRRIDNVDSNARAGIAQATATAGLVQAYLPKSKM 540
QY      452 MAIGGGYTRGEGVATIGYSSISDGSNWLKGTASNSGKHFGASASVGYQW 502
DB      541 MAIGGGYTRGEGVATIGYSSISDGSNWLKGTASNSGKHFGASASVGYQW 591

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## RESULT 5

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AAV23737
ID AAV23737 standard; Protein; 592 AA.
XX
AC AAV23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX (UYOU ) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA.
XX
DR WPI; 1999-418754/35.
XX
DR N-PSDB; AAX85788.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS
PS Claim 1; Page 86-87; 132pp; English.
XX
XX
XX The present sequence represents a surface protein of Neisseria
XX meningitidis which is approximately 62 kDa. The N. meningitidis
XX surface glycoproteins, nucleic acids, the primers and optionally
XX a thermostable polymerase, or antibodies are useful in a kit for
XX the detection or diagnosis of N. meningitidis infection in humans.
XX The N. meningitidis surface glycoproteins can also be used to
XX prevent or treat N. meningitidis infection in humans, especially
XX in the form of vaccines. The proteins and antibodies can also
XX be used to identify immunoreactive peptides.
XX
XX
XX Sequence 592 AA:

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Query Match 96.5%; Score 2455; DB 20; Length 592;
Best Local Similarity 84.6%; Pred. No. 9.7e-147;
Matches 501; Conservative 0; Mismatches 1; Indels 90; Gaps 4;

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QY 1 MNKIYRIIWSALNAAWVVSLELFRNHTKRASATYKAVLATLLEFATYQASAN----- 52
DQ 1 MNKIYRIIWSALNAAWVVSLELFRNHTKRASATYKAVLATLLEFATYQASANNRPKKD 60
QY 53 -----TLKADNLKIK 63
DQ 61 LYLDPVORTVAVLIVNSDKEGTGEKEKEVEENSDMAVYFNEKGVLTAREITLAKADNLKIK 120
QY 64 Q----FTYSLKKDLTDLTSVTEKLSFSAANGKVNITSDPKGLNFAKETGNDPTVHL 119
DQ 121 QNGTNEFTYSLKKDLTDLTSVTEKLSFSAANGKVNITSDPKGLNFAKETGNDPTVHL 180
QY 120 NGIGSTLTD-----RAASVKDVLNAGWNIGVK-----NVD 150
DQ 181 NGIGSTLTDLTLNLTGATTTNTNDVNTDEKKRAASVADVLNAGWNIGVKRGTASDNVD 240
QY 151 FVRTDYVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYKEKDKLVTKDKGENGS 210
DQ 241 FVRTDYVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYKEKDKLVTKDKGENGS 300
QY 211 STDEGELVTAKEDIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKTAT 270
DQ 301 STDEGELVTAKEDIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKTAT 360
QY 271 VSKDQGNITVMYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSKGMDT 330
DQ 361 VSKDQGNITVMYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSKGMDT 420
QY 331 VNINAGNNIETTRNGKNIDATSMTPQSSVSIGAGADAPTLVSDGALNVGSKDKPKV 390
DQ 421 VNINAGNNIETTRNGKNIDATSMTPQSSVSIGAGADAPTLVSDGALNVGSKDKPKV 480
QY 391 RITNVAAGVEGDVTNVAOLKGVAQNINRINDVDNAGNIAQAIATAGIYQAYLPGKS 450
DQ 481 RITNVAAGVEGDVTNVAOLKGVAQNINRINDVDNAGNIAQAIATAGIYQAYLPGKS 540
QY 451 MMAIGGCTYGEAGAYGAGYSISDGNMIIKGTASGNSRGHFGASASGYQW 502
DQ 541 MMAIGGCTYGEAGAYGAGYSISDGNMIIKGTASGNSRGHFGASASGYQW 592

RESULT 6
AAV57045
ID AAV57045 standard; Protein: 591 AA.
XX
AC AAV57045:
XX
DQ 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by AAT"
FT Misc-difference 98 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AAC"
FT Misc-difference 123 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX

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PN W09558683-A2.
PD 18-NOV-1999.
XX
PE 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI; 2000-053103/04.
DR N-PSDB; AAZ39865.
XX
FT New polypeptide from neisseria meningitidis useful for diagnosis,
treatment or prevention of bacterial infections in mammal
Claim 4; Fig 2; 74pp; English.
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
serogroup B strain H44/76. The BASB029 protein is homologous to the
Haemophilus influenzae surface fibril (HSF) protein. The invention
relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
BASB029 polypeptides are useful in a method of diagnosing a Neisseria
meningitidis infection in a mammal. Compositions containing BASB029
polynucleotides and polypeptides are useful for generating an immune
response in an animal. A therapeutic composition comprising an antibody
directed against BASB029 is useful in treating humans with Neisseria
meningitidis disease. The polynucleotide is useful in the diagnosis of
the stage of infection, type of infection, susceptibility to an
infection which results from increased or decreased expression of the
polynucleotide, and for therapeutic or prophylactic purposes.
CC particularly genetic immunisation. Antibodies against BASB029
polynucleotides and polypeptides are also useful for treating infections
particularly bacterial infections. The protein is useful in the
screening and development of antibacterial drugs. Fused recombinant
protein is useful for the stimulation of the immune system of an organism
receiving the protein.
CC
XX
SQ Sequence 591 AA;
Query Match 96.4%; Score 2452.5; DB 21; Length 591;
Best Local Similarity 84.6%; Pred. No. 1.4e-146;
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;
QY 1 MNKIYRIIWSALNAAWVVSLELFRNHTKRASATYKAVLATLLEFATYQASAN----- 52
DQ 1 MNKIYRIIWSALNAAWVVSLELFRNHTKRASATYKAVLATLLEFATYQASANNRPKKD 60
QY 53 -----TLKADNLKIK 64
DQ 61 LYLDPVORTVAVLIVNSDKEGTGEKEKEVEENSDMAVYFNEKGVLTAREITLAKADNLKIK 120
QY 65 ----FTYSLKKDLTDLTSVTEKLSFSAANGKVNITSDPKGLNFAKETGNDPTVHL 120
DQ 121 NGSNFTYSLKKDLTDLTSVTEKLSFSAANGKVNITSDPKGLNFAKETGNDPTVHL 180
QY 121 GIGSTLTD-----RAASVKDVLNAGWNIGVK-----NVD 151
DQ 181 GIGSTLTDLTLNLTGATTTNTNDVNTDEKKRAASVADVLNAGWNIGVKRGTASDNVD 240
QY 152 VRTDYVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYKEKDKLVTKDKGENSS 211
DQ 241 VRTDYVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYKEKDKLVTKDKGENSS 300
QY 212 TDEGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKTATV 271
DQ 301 TDEGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKTATV 360
QY 272 SKDQGNITVMYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSKGMDT 331

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Db      361 SKDDGNTVMYDVNVGDLNVNQLONGSMNLSKRAVAGSSGKVISGNVSPSKGMDETIV 420
QY      332 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKKNKPYR 391
Db      421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKKNKPYR 480
QY      332 ITNVA PGVEGDVTNVAOLKGYAQNLLNNRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 451
Db      481 ITNVA PGVEGDVTNVAOLKGYAQNLLNNRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 540
QY      452 MAIGGCTYRGEAGYAI GYSSISDGNWIIKGTASGNSRHFASASVGYOW 502
Db      541 MAIGGCTYRGEAGYAI GYSSISDGNWIIKGTASGNSRHFASASVGYOW 591

RESULT 7
AAU23741
ID      AAU23741 standard; Protein; 591 AA.
XX
AC      AAU23741;
XX
DT      08-SEP-1999 (first entry)
XX
DE      A surface protein of Neisseria meningitidis.
XX
KM      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX
OS      Neisseria meningitidis.
XX
PN      W09931132-A1.
XX
PD      24-JUN-1999.
XX
PF      14-DEC-1998; 98MO-AU01031.
XX
PR      12-DEC-1997; 97GB-0026398.
XX
PA      (ISIS-) ISIS INNOVATION LTD.
XX      (UYGU ) UNIV QUEENSLAND.
XX
PI      Jennings MP, Moxon ER, Peak IRA;
XX
DR      WPI: 1999-418754/35.
XX      N-PSDB: AAX85793.
XX
PT      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX
PS      Claim 1; Page 104-106; 132pp; English.
XX
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX
SQ      Sequence 591 AA;

Query Match      96.2%; Score 2447.5; DB 20; Length 591;
Best Local Similarity 84.6%; Pred No. 2.9e-146;
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;
QY      1 MNKIYRIIWNLSALNMAVYSELTRNHTKRASATVTAVALTLFATVQASAN----- 52
Db      1 MNEIIRIIMNSALNMAVYSELTRNHTKRASATVTAVALTLFATVQASANNEQEDL 60
QY      53 -----TLKAGDNLIKIQ 64

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Db      61 YLDPVLRIVAVALLVNSDEKTEGKEKVEENSDMAVYFNEKGYLTAREITLKAGDNLIKIQ 120
QY      65 ----FTYSLKRDLTDLTSVGETEKLSEFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 120
Db      121 NGTNTFTSLKRLDLDLTSVGETEKLSEFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
QY      121 GIGSTLTLD-----RAASYKDLVLAGWNITKVK-----NDVF 151
Db      181 GIGSTLTDLTLNTGATTTVNTNDNVTTDDEKKRAASYKDVVLNAGWNITKVKPGTTASDNVDF 240
QY      152 VRTYPTVEFLSADTFTTVNVNVEKNGKTEVKGAKTSVIEKDKGLVTGDKENSS 211
Db      241 VRTYPTVEFLSADTFTTVNVNVEKNGKTEVKGAKTSVIEKDKGLVTGDKENSS 300
QY      212 TDEGGLVTAKEVIDAVNKAQWRMKTTHANGOTGADKFEVTSCTNTVFAAGKTATV 271
Db      301 TDEGGLVTAKEVIDAVNKAQWRMKTTHANGOTGADKFEVTSCTNTVFAAGKTATV 360
QY      272 SKDDGNTVMYDVNVGDLNVNQLONGSMNLSKRAVAGSSGKVISGNVSPSKGMDETIV 331
Db      361 SKDDGNTVMYDVNVGDLNVNQLONGSMNLSKRAVAGSSGKVISGNVSPSKGMDETIV 420
QY      332 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKKNKPYR 391
Db      421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKKNKPYR 480
QY      392 ITNVA PGVEGDVTNVAOLKGYAQNLLNNRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 451
Db      481 ITNVA PGVEGDVTNVAOLKGYAQNLLNNRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 540
QY      452 MAIGGCTYRGEAGYAI GYSSISDGNWIIKGTASGNSRHFASASVGYOW 502
Db      541 MAIGGCTYRGEAGYAI GYSSISDGNWIIKGTASGNSRHFASASVGYOW 591

RESULT 8
AAU06175
ID      AAU06175 standard; Protein; 591 AA.
XX
AC      AAU06175;
XX
DT      24-OCT-2001 (first entry)
XX
DE      N. meningitidis EG329 surface antigen Nhba polypeptide sequence.
XX
KM      Surface antigen Nhba; meningococcal disease; meningitis vaccine.
XX
OS      Neisseria meningitidis strain EG329.
XX
PS      Location/Qualifiers
XX      FH      1..50
XX      FT      Region
XX      FT      /label= C1
XX      FT      /note= "Conserved region 1"
XX      FT      /label= V1
XX      FT      /note= "Variable region 1"
XX      FT      /label= C2
XX      FT      /note= "Conserved region 2"
XX      FT      /label= V2
XX      FT      /note= "Variable region 2"
XX      FT      /label= C3
XX      FT      /note= "Conserved region 3"
XX      FT      /label= V3
XX      FT      /note= "Variable region 3"
XX      FT      /label= C4
XX      FT      /note= "Conserved region 4"
XX      FT      /label= V4

```

FT /note= "Variable region 4"  
 FT 237..591  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 XX  
 XX  
 PN WO200155182-A1.  
 XX  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 XX WPI; 2001-488774/53.  
 DR N-PSDB; AAS09165.  
 XX  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 PS Claim 9; Fig 1; 91pp; English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild-type surface antigen Nhha  
 CC from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 CC  
 XX  
 SQ Sequence 591 AA;  
 Query Match 96.2%; Score 2447.5; DB 22; Length 591;  
 Best Local Similarity 84.6%; Pred. No. 2.9e-146;  
 Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

DB 361 SKDDQGITVWYDVNVDALNVNOLONGWMLDRAVAGSSGKVISGNVSPSKGMDTV 420  
 QY 332 NINAGNNIETIRNKNIDIASMTPOSSVSLGAGAPPTLSVGDALNWGSKDKNPKVR 391  
 DB 421 NINAGNNIETIRNKNIDIASMTPOSSVSLGAGAPPTLSVGDALNWGSKDKNPKVR 480  
 QY 392 ITTVAPGVKESGDVTVNVAOLKVAQNLNRRIDNVGNARAGIAQAIATAGLVQAVLPCKSM 451  
 DB 481 ITTVAPGVKESGDVTVNVAOLKVAQNLNRRIDNVGNARAGIAQAIATAGLVQAVLPCKSM 540  
 QY 452 MAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 502  
 DB 541 MAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 591  
 RESULT 9  
 AAU06182  
 ID AAU06182 standard; Protein: 512 AA.  
 XX  
 AC AAU06182;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DE  
 XX N. meningitidis PMC21 Nhha deletion mutant #1.  
 DE  
 XX Surface antigen Nhha; meningococcal disease; meningitidis vaccine;  
 KW mutant; mutcin.  
 XX  
 OS Neisseria meningitidis strain PMC21.  
 OS Synthetic.  
 FH  
 FH Key Location/Qualifiers  
 FT Peptide 1..51  
 FT /label= Signal\_peptide  
 FT Protein 52..512  
 FT /label= Mature\_Nhha\_deletion\_mutant\_#1  
 FT /note= "Predicted mature protein, specifically  
 claimed in claim 12"  
 XX  
 FN WO200155182-A1.  
 XX  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 XX WPI; 2001-488774/53.  
 DR N-PSDB; AAS09172.  
 XX  
 XX  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 PS Claim 12; Fig 5; 91pp; English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence represents N. meningitidis strain PMC21 surface  
 CC antigen Nhha deletion mutant #1.  
 CC  
 XX

SO Sequence 512 AA:

Query Match 93.7%; Score 2383; DB 22; Length 512;  
 Best Local Similarity 90.6%; Pred. No. 2,8e-142;  
 Matches 481; Conservative 1; Mismatches 1; Indels 48; Gaps 3;

QY 1 MKKIRIITWNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOASANTLAKADNL 60  
 DB 1 MKKIRIITWNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52  
 QY 61 KIKOPTYSLKKDLMDLTSGTEKLSFSSANGNKVNTISPTKGINFAKFAKTAGTGTTHLN 120  
 DB 53 -----NEDLTSGTEKLSFSSANGNKVNTISPTKGINFAKFAKTAGTGTTHLN 101  
 QY 121 GIGSTLTLD-----RAASYKDVNLNMGWNLKGVK-----NVD 151  
 DB 102 GIGSTLTLDLTNTGATVNTDNTVTDDEKKRAASYKDVNLNMGWNLKGVKPGTTASDND 161  
 QY 152 VRTYTVTFELSDRTTTTVNVESSKNGKTEYKIGAKTSVYKEKDKGLVTGDKGENGSS 211  
 DB 162 VRTYTVTFELSDRTTTTVNVESSKNGKTEYKIGAKTSVYKEKDKGLVTGDKGENGSS 221  
 QY 212 TDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADKFEYVTSCTNTFFASGKGTATV 271  
 DB 222 TDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADKFEYVTSCTNTFFASGKGTATV 281  
 QY 272 SKDDOGNTVAVDVGDLNVLNOLONGMNLDSKAVAGSSGKVISGNVSPSKGMDET 331  
 DB 282 SKDDOGNTVAVDVGDLNVLNOLONGMNLDSKAVAGSSGKVISGNVSPSKGMDET 341  
 QY 332 NINAGNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGDLNMGSKKNKPYR 391  
 DB 342 NINAGNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGDLNMGSKKNKPYR 401  
 QY 392 ITTNAVPGKEGDTVVAOLKGYAONLNNRIDVNDGNARAGIAQAIAATAGLVQAYLPGRSM 451  
 DB 402 ITTNAVPGKEGDTVVAOLKGYAONLNNRIDVNDGNARAGIAQAIAATAGLVQAYLPGRSM 461  
 QY 452 MAIGGGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 502  
 DB 462 MAIGGGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 512

RESULT 10  
 AAY23743 standard; Protein; 599 AA.  
 AC AAY23743;  
 DT 08-SEP-1999 (first entry)  
 DE A surface protein of Neisseria meningitidis.  
 KW Surface protein: surface glycoprotein; infection; vaccine;  
 OS Neisseria meningitidis.  
 PN MO9931132-A1.  
 PD 24-JUN-1999.  
 PF 14-DEC-1998; 98WO-AU01031.  
 PR 12-DEC-1997; 97GB-0026398.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYOU) UNIV QUEENSLAND.  
 PI Jennings MP, Moxon ER, Peak IRA;  
 DR WPI: 1999-418754/35.  
 DR N-PSDB; AAX85795.

XX Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 PS Claim 1; Page 114-115; 132pp; English.

CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

SO Sequence 599 AA:

Query Match 93.2%; Score 2371.5; DB 20; Length 599;  
 Best Local Similarity 81.6%; Pred. No. 1.8e-141;  
 Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

QY 1 MKKIRIITWNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52  
 DB 1 MKKIRIITWNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOANADEDEEBEL 60  
 QY 53 -----TLKADNLIKIKO--- 64  
 DB 61 EPVVASALVLOFMIDKEGNGENESTGNIGWSIYDNNHMTLHGATVTLKAGDLKIKOMTN 120  
 QY 65 -----FTYSLAKDLDTLSVGTBKLSFSSANGNKVNTISPTKGINFAKFAKTAGT 113  
 DB 121 KNTNENTNDSSFTYSLAKDLDTLSVETBKLSFGANGKNKVNITSDTKGINFAKFAKTAGT 180  
 QY 114 DTTVHLNIGSTLTLD-----RAASYKDVNLNMGWNLKGVK----- 147  
 DB 161 DTTVHLNIGSTLTLDLTNTGATVNTDNTVTDDEKKRAASYKDVNLNMGWNLKGVKPGTT 240  
 QY 148 ---NVDFTYTVTFELSDRTTTTVNVESSKNGKTEYKIGAKTSVYKEKDKGLVTGKD 204  
 DB 241 ASDNDVFTYTVTFELSDRTTTTVNVESSKNGKTEYKIGAKTSVYKEKDKGLVTGKD 300  
 QY 205 KGENGSTDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADKFEYVTSCTNTFFASG 264  
 DB 301 KGENGSTDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADKFEYVTSCTNTFFASG 360  
 QY 265 KGTATVSKDDOGNTVAVDVGDLNVLNOLONGMNLDSKAVAGSSGKVISGNVSPSK 324  
 DB 361 KGTATVSKDDOGNTVAVDVGDLNVLNOLONGMNLDSKAVAGSSGKVISGNVSPSK 420  
 QY 325 GKMDETVINAGNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDG-DALNMG 383  
 DB 421 GKMDETVINAGNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGKALNMG 480  
 QY 384 KDKNKPVKITNAVPGYKGDVTVNAOLKGYAONLNNRIDVNDGNARAGIAQAIAATAGLVQ 443  
 DB 481 KDANKPVRITNAVPGYKGDVTVNAOLKGYAONLNNRIDVNDGNARAGIAQAIAATAGLVQ 540  
 QY 444 AYLPKSMATGCGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 502  
 DB 541 AYLPKSMATGCGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 599

RESULT 11  
 AAU06176 standard; Protein; 599 AA.  
 AC AAU06176;  
 DT 24-OCT-2001 (first entry)  
 DE N. meningitidis H38 surface antigen NhbA polypeptide sequence.  
 DR







```

Db      241 DFWRTYDTVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLTGTGDKEND
Qy      210 SSTDEGEGLYTAKEVIDAVNKAQMRKMTTANGOTGADKFEVYTSCTNTVTFASGKGTGTA
Db      301 SSTDKGEGLYTAKEVIDAVNKAQMRKMTTANGOTGADKFEVYTSCTNTVTFASGKGTGTA
Qy      270 TVSKDDOGNITVMTDVNVDGALNVNOLQNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD
Db      361 TVSKDDOGNITVMTDVNVDGALNVNOLQNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD
Qy      330 TVNINAGNNEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLTSDGD-ALNVGSKDKNK
Db      421 TVNINAGNNEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKDKANK
Qy      389 PVRTTNVAPGVKESGDVNTVAVOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLP
Db      481 PVRTTNVAPGVKESGDVNTVAVOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLP
Qy      449 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGSRGHRGASASVGYOW
Db      541 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGSRGHRGASASVGYOW

```

RESULT 14  
AAU06174  
ID AAU06174 standard; Protein: 594 AA.

XX AAU06174:

DT 24-OCT-2001 (first entry)

DE N. meningitidis EG327 surface antigen Nhma polypeptide sequence.

KM Surface antigen Nhma; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain EG327.

OS location/Qualifiers

FT 1.50 /label=C1 /note="Conserved region 1"

FT 51..104 /label=V1 /note="Variable region 1"

FT 105..116 /label=C2 /note="Conserved region 2"

FT 117..126 /label=V2 /note="Variable region 2"

FT 127..190 /label=C3 /note="Conserved region 3"

FT 191..212 /label=V3 /note="Conserved region 4"

FT 213..231 /label=C4 /note="Conserved region 5"

FT 232..238 /label=V4 /note="Variable region 3"

FT 239..594 /label=V5 /note="Variable region 4"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

FT /label=C5 /note="Conserved region 5"

```

PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYOU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP.
XX
DR WPI; 2001-488774/53.
XX
DR N-PSDB; AAS09164.
XX
PS
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain EG327 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 594 AA;

```

Query Match 93.0%; Score 2366; DB 22; Length 594;

Best Local Similarity 82.0%; Pred. No. 4e-141;

Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

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Qy      1 MNKIYRIIWNLSALNAAVVSSELTNRNHRASATVATVATLLEFATVQASAN-----52
Db      1 MNKIYRIIWNLSALNAAVVSSELTNRNHRASATVATVATLLEFATVQASATDDDDLYLE 60
Qy      53 -----TLKAGDNLIKQ-----64
Db      61 PVORTAVLSEFSDKEGTGEKEVTEEDSNMGVYFPDKKVLTAAGTTLTLAGDNLIKQNTNE 120
Qy      65 -----FTYSLKQDLTDLTSVGTSEKLSFSAANGKVNITSDPKGINFAKETAGTGDPTVH 118
Db      121 NTNASFTYSLKQDLTDLTSVGTSEKLSFSAANGKVNITSDPKGINFAKETAGTGDPTVH 180
Qy      119 LMGIGSTLTD-----RAASYKDYLNAGMNIKGVK-----NV 149
Db      181 LMGIGSTLTDLNTGATNTVNTNDVDEKKRAASVYKDYLNAGMNIKGVKPGTTASDNV 240
Qy      150 DFWRTYDTVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLTGTGDKENG 209
Db      241 DFWRTYDTVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLTGTGDKEND 300
Qy      210 SSTDEGEGLYTAKEVIDAVNKAQMRKMTTANGOTGADKFEVYTSCTNTVTFASGKGTGTA 269
Db      301 SSTDKGEGLYTAKEVIDAVNKAQMRKMTTANGOTGADKFEVYTSCTNTVTFASGKGTGTA 360
Qy      270 TVSKDDOGNITVMTDVNVDGALNVNOLQNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD 329
Db      361 TVSKDDOGNITVMTDVNVDGALNVNOLQNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD 420
Qy      330 TVNINAGNNEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLTSDGD-ALNVGSKDKNK 388
Db      421 TVNINAGNNEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKDKANK 480
Qy      389 PVRTTNVAPGVKESGDVNTVAVOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLP 448
Db      481 PVRTTNVAPGVKESGDVNTVAVOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLP 540
Qy      449 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGSRGHRGASASVGYOW 502

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```
DB 541 KSMMAIGGTYRGEAGYALGYSSISDGGNMIKGTASGNSRCHFGASASVGYOW 594
RESULT 15
AAV23739
ID AAV23739 standard; Protein; 594 AA.
XX
XX AAV23739;
AC
XX
XX 08-SEP-1999 (first entry)
DT
XX
XX A surface protein of Neisseria meningitidis.
DE
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
XX Neisseria meningitidis.
OS
XX
XX W09931132-A1.
XX
XX
XX 24-JUN-1999.
PD
XX
XX 14-DEC-1998; 98MO-AU01031.
PR
XX 12-DEC-1997; 97GB-0026398.
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85791.
XX
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX
XX Claim 1; Page 95-97; 132pp; English.
XX
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX
SQ Sequence 594 AA;
Query Match 92.7%; Score 2359; DB 20; Length 594;
Best Local Similarity 82.0%; Pred. No. 1,le-140;
Matches 487; Conservative 2; Mismatches 13; Indels 92; Gaps 5;
QY 1 MNKIRIIMNSALNMAVVVSELTNRNHTKRASATVKTAVLATLLEFATVOASAN-----52
DB 1 MNKIRIIMNSALNMAVVVSELTNRNHTKRASATVKTAVLATLLEFATVOANATDDDDLYLE 60
QY 53 -----TLKAGDNLIKIKO----64
DB 61 PVORTAVVLSFSPSDEKTEGTEGTEDSNMVAVFDEKRVLKAGAITLKLKAGDNLIKIKONTNE 120
QY 65 -----FTYSLKKDLTDLTSGVTEKLSFANGKNKVNITSDFKGLNPAKETAGTNGDPTVH 118
DB 121 NTNDSSTYSLKDLTDLTSGVTEKLSFANGKNKVNITSDFKGLNPAKETAGTNGDPTVH 180
QY 119 LNGIGSTLTD-----RAASVKKDVNLNAGNNIKGVK-----NV 149
DB 181 LNGIGSTLTDLTNLGATTTNTNNDVTDDEKKRAASVKKDVNLNAGNNIKGVKPGTASDNV 240
QY 150 DFVRTYDFVEFLSADTKTTTYNVVESKDKNGKTEVKIGAKTSYIKKDGKLVTKDKGENG 209
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DB 241 DFVRTYDFVEFLSADTKTTTYNVVESKDKNGKTEVKIGAKTSYIKKDGKLVTKDKGENG 300
QY 210 SSTDEGEGLVTAKEVIDAVNKRAGWNRKTTTANGOTGOADKFEFTVSGTNTVPASGKTTA 269
DB 301 SSTDEGEGLVTAKEVIDAVNKRAGWNRKTTTANGOTGOADKFEFTVSGTNTVPASGKTTA 360
QY 270 TVSKDDGNTIYMDVNVGDALNVNQLNSGNNLDSKAVAGSSGVISGVNPSRKGKMD 329
DB 361 TVSKDDGNTIYKVDVNVGDALNVNQLNSGNNLDSKAVAGSSGVISGVNPSRKGKMD 420
QY 330 TVNINAGNNIETTRNGKNIDITSMTPQFSSYSIGAGADAPTLSTVDGD-ALNVGSKKXNK 388
DB 421 TVNINAGNNIETTRNGKNIDITSMAPQFSSYSIGAGADAPTLSTVDGDALNVGSKKXNK 480
QY 389 PVRTINVAPGVKEGDTVNVNQLKGYAONLNRRIDNVNVDNARAGIAQAIATAGLVOAYLP 448
DB 481 PVRTINVAPGVKEGDTVNVNQLKGYAONLNRRIDNVNVDNARAGIAQAIATAGLVOAYLP 540
QY 449 KSMMAIGGTYRGEAGYALGYSSISDGGNMIKGTASGNSRCHFGASASVGYOW 502
DB 541 KSMMAIGGTYRGEAGYALGYSSISDGGNMIKGTASGNSRCHFGASASVGYOW 594
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Title: US-09-771-382-27  
Perfect score: 2544  
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2459.5	96.7	591	3	US-09-377-155-21 Sequence 21, Appl
2	2459.5	96.7	591	4	US-09-669-974-21 Sequence 21, Appl
3	2455	96.5	592	4	US-09-377-155-2 Sequence 2, Appl
4	2455	96.5	592	4	US-09-669-974-2 Sequence 2, Appl
5	2447.5	96.2	591	3	US-09-377-155-11 Sequence 11, Appl
6	2447.5	96.2	591	4	US-09-669-974-11 Sequence 11, Appl
7	2371.5	93.2	589	3	US-09-377-155-15 Sequence 15, Appl
8	2371.5	93.2	589	4	US-09-669-974-15 Sequence 15, Appl
9	2366	93.0	594	3	US-09-377-155-9 Sequence 9, Appl
10	2366	93.0	594	4	US-09-669-974-9 Sequence 9, Appl
11	2359	92.7	594	3	US-09-377-155-7 Sequence 7, Appl
12	2359	92.7	594	4	US-09-669-974-7 Sequence 7, Appl
13	2344	92.1	588	3	US-09-377-155-13 Sequence 13, Appl
14	2344	92.1	588	4	US-09-669-974-13 Sequence 13, Appl
15	2335	91.8	598	3	US-09-377-155-5 Sequence 5, Appl
16	2335	91.8	598	4	US-09-669-974-5 Sequence 5, Appl
17	2327	91.5	592	3	US-09-377-155-17 Sequence 17, Appl
18	2327	91.5	592	4	US-09-669-974-17 Sequence 17, Appl
19	2317.5	91.1	589	3	US-09-377-155-19 Sequence 19, Appl
20	2317.5	91.1	589	4	US-09-669-974-19 Sequence 19, Appl
21	1011.5	39.8	2411	4	US-09-268-347-36 Sequence 36, Appl
22	1009.5	39.7	2353	3	US-09-377-155-33 Sequence 33, Appl
23	1009.5	39.7	2353	4	US-08-913-942-4 Sequence 4, Appl
24	1009.5	39.7	2353	4	US-09-669-974-33 Sequence 33, Appl
25	1008.5	39.6	2354	4	US-09-268-347-47 Sequence 47, Appl
26	974	38.3	1098	3	US-08-409-995-2 Sequence 2, Appl
27	974	38.3	1098	4	US-08-685-467-2 Sequence 2, Appl

28	974	38.3	1098	3	US-09-377-155-32 Sequence 32, Appl
29	974	38.3	1098	4	US-08-913-942-2 Sequence 2, Appl
30	974	38.3	1098	4	US-09-669-974-32 Sequence 32, Appl
31	974	38.3	1098	4	US-09-268-347-44 Sequence 44, Appl
32	956	37.6	658	1	US-08-409-995-5 Sequence 5, Appl
33	956	37.6	658	1	US-08-685-467-5 Sequence 5, Appl
34	956	37.6	658	3	US-08-913-942-5 Sequence 5, Appl
35	947	37.2	607	1	US-08-409-995-6 Sequence 6, Appl
36	947	37.2	607	3	US-08-685-467-6 Sequence 6, Appl
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41	847.5	33.3	679	3	US-08-913-942-15 Sequence 15, Appl
42	847.5	33.3	679	4	US-09-268-347-26 Sequence 26, Appl
43	682	26.8	1004	4	US-09-268-347-30 Sequence 30, Appl
44	661	26.0	1002	4	US-09-268-347-24 Sequence 24, Appl
45	594	23.3	1104	4	US-09-268-347-28 Sequence 28, Appl

## ALIGNMENTS

RESULT 1									
US-09-377-155-21									
; Sequence 21, Application US/09377155									
; Patent No. 6197312									
; GENERAL INFORMATION:									
; APPLICANT: PEAK, Ian Richard Anselm									
; APPLICANT: JENNINGS, Michael Paul									
; APPLICANT: MOXON, E. Richard									
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN									
; FILE REFERENCE: 065064/0128									
; CURRENT APPLICATION NUMBER: US/09/377, 155									
; CURRENT FILING DATE: 1999-08-19									
; PRIOR APPLICATION NUMBER: PCT/AU98/01031									
; PRIOR FILING DATE: 1998-12-14									
; PRIOR APPLICATION NUMBER: GB 9726398.2									
; PRIOR FILING DATE: 1997-12-12									
; NUMBER OF SEQ ID NOS: 33									
; SOFTWARE: Patentin Ver. 2.0									
; SEQ ID NO 21									
; LENGTH: 591									
; TYPE: PRT									
; ORGANISM: Neisseria meningitidis									
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Query Match									
Best Local Similarity 96.7%; Score 2459.5; DB 3; Length 591;									
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;									
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DB	1	MNKIRIIMNSALNAMYVSELTRNTRKRASATVAVLATLLFATVQASANNEDEEDL	60						
QY	53	-----TKADNLIKIKQ 64							
DB	61	YIDPQRTAVAVLVNSDKTEGKEKEVEESMDAVFENEKGVLTARITLIKADNLIKIKQ	120						
QY	65	-----FTYSLKKLDLDLTSVTEKLSFESANGKNYVTSIDTKGLNPAKETAGTNGDTVHLN	120						
DB	121	NGTFYSLKKLDLDLTSVTEKLSFESANGKNYVTSIDTKGLNPAKETAGTNGDTVHLN	180						
QY	121	GIGSTLTLD-----RAASVKQVLAAGNNIGVK-----NVDF 151							
DB	181	GIGSTLTLDLTLTGATTTNTDNDVTDDEKRRASVKQVLAAGNNIGVKCTTASDVDF	240						
QY	152	VRTYDVEFLSADTKTTTVVESKDNKKTVEVIGAKTSYIKKDKGLVTKDKGENGSS	211						
DB	241	VRTYDVEFLSADTKTTTVVESKDNKKTVEVIGAKTSYIKKDKGLVTKDKGENGSS	300						
QY	212	TDEGEGLVTAKEYIDAVNKGGMKRTTANGGTGADKFTTVSGTNVTFASGKGTATV	271						

Db 301 TDEGGLVTAKEVIDAVNKAQWRMKTATTANGOTGADKFEYVTSCTNTVFASGKGTATV 360  
Qy 272 SKDDOGNITVMTDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVTISGNVSPSKGMDET 331  
Db 361 SKDDOGNITVMTDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVTISGNVSPSKGMDET 420  
Qy 332 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTLSVDDALNVGSKKKNKPV 391  
Db 421 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTLSVDDALNVGSKKKNKPV 480  
Qy 392 ITNVPAGYKEGDVTVVAOLKGVAVNOLNRRIDVNDGNARAGIAQAATATAGLVAYLPKSM 451  
Db 481 ITNVPAGYKEGDVTVVAOLKGVAVNOLNRRIDVNDGNARAGIAQAATATAGLVAYLPKSM 540  
Qy 452 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASNSRCHFGASASVGYW 502  
Db 541 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASNSRCHFGASASVGYW 591

RESULT 2  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 96.7%; Score 2459.5; DB 4; Length 591;  
Best Local Similarity 84.9%; Pred. No. 1.5e-187;  
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;

Qy 1 MKKIRIITNSALNMMVVVSELTNRHTRKASATVKTAVLATLLEFATVOASAN----- 52  
Db 1 MKKIRIITNSALNMMVVVSELTNRHTRKASATVKTAVLATLLEFATVOASANNEQEDL 60  
Qy 53 -----TLKAGDNLIKIK 64  
Db 61 IYLDVQRTVAVLIVNSDEKGEKKEVEBNSDMAVYFNEKGVLTAARETITLKAGDNLIKIK 120  
Qy 65 -----FTYSIKKDLTDLTSGTEKLSFSANGKNVITSDPTGKLNFAKETAGTNGDTTVHLN 120  
Db 121 NGTNTTYSIKKDLTDLTSGTEKLSFSANGKNVITSDPTGKLNFAKETAGTNGDTTVHLN 180  
Qy 121 GIGSTLTD-----RAASVQDVNLNAGNMIKGVK-----NVD 151  
Db 181 GIGSTLTDLTLNTGATVNTNDNTDDEKRAASVQDVNLNAGNMIKGVKPGTTASDNVD 240  
Qy 152 VRTVTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEREKGLVYTGKDKGENSS 211  
Db 241 VRTVTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEREKGLVYTGKDKGENSS 300  
Qy 212 TDEGGLVTAKEVIDAVNKAQWRMKTATTANGOTGADKFEYVTSCTNTVFASGKGTATV 271  
Db 301 TDEGGLVTAKEVIDAVNKAQWRMKTATTANGOTGADKFEYVTSCTNTVFASGKGTATV 360

Qy 272 SKDDOGNITVMTDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVTISGNVSPSKGMDET 331  
Db 361 SKDDOGNITVMTDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVTISGNVSPSKGMDET 420  
Qy 332 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTLSVDDALNVGSKKKNKPV 391  
Db 421 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTLSVDDALNVGSKKKNKPV 480  
Qy 392 ITNVPAGYKEGDVTVVAOLKGVAVNOLNRRIDVNDGNARAGIAQAATATAGLVAYLPKSM 451  
Db 481 ITNVPAGYKEGDVTVVAOLKGVAVNOLNRRIDVNDGNARAGIAQAATATAGLVAYLPKSM 540  
Qy 452 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASNSRCHFGASASVGYW 502  
Db 541 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASNSRCHFGASASVGYW 591

RESULT 3  
US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6197312

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 96.5%; Score 2455; DB 3; Length 592;  
Best Local Similarity 84.6%; Pred. No. 3.4e-187;  
Matches 501; Conservative 0; Mismatches 1; Indels 90; Gaps 4;

Qy 1 MKKIRIITNSALNMMVVVSELTNRHTRKASATVKTAVLATLLEFATVOASAN----- 52  
Db 1 MKKIRIITNSALNMMVVVSELTNRHTRKASATVKTAVLATLLEFATVOASANNEPRKKD 60  
Qy 53 -----TLKAGDNLIKIK 63  
Db 61 IYLDVQRTVAVLIVNSDEKGEKKEVEBNSDMAVYFNEKGVLTAARETITLKAGDNLIKIK 120  
Qy 64 Q-----FTYSIKKDLTDLTSGTEKLSFSANGKNVITSDPTGKLNFAKETAGTNGDTTVHL 119  
Db 121 QNGTNTTYSIKKDLTDLTSGTEKLSFSANGKNVITSDPTGKLNFAKETAGTNGDTTVHL 180  
Qy 120 NGIGSTLTD-----RAASVQDVNLNAGNMIKGVK-----NVD 150  
Db 181 NGIGSTLTDLTLNTGATVNTNDNTDDEKRAASVQDVNLNAGNMIKGVKPGTTASDNVD 240  
Qy 151 FVRTVTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEREKGLVYTGKDKGENSS 210  
Db 241 FVRTVTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVYKEREKGLVYTGKDKGENSS 300  
Qy 211 STDEGGLVTAKEVIDAVNKAQWRMKTATTANGOTGADKFEYVTSCTNTVFASGKGTAT 270  
Db 301 STDEGGLVTAKEVIDAVNKAQWRMKTATTANGOTGADKFEYVTSCTNTVFASGKGTAT 360  
Qy 271 VSKDDOGNITVMTDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVTISGNVSPSKGMDET 330  
Db 361 VSKDDOGNITVMTDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVTISGNVSPSKGMDET 420

Oy	331	NNNAGNNIETTRNCKNNDIATSMTPQPSVSSVLAGAGADAPTLVSOGDALNVGSKKONKPY	390
Db	421	VNINAGNNIETTRNCKNNDIATSMTPQPSVSSVLAGAGADAPTLVSOGDALNVGSKKONKPY	480
Oy	391	RITNAPPVCKEDVNVNVAOLKGVQNLNLRIDNVGNARAGIAQAIATATGIVQATYLPGRS	450
Db	481	RITNAPPVCKEDVNVNVAOLKGVQNLNLRIDNVGNARAGIAQAIATATGIVQATYLPGRS	540
Oy	451	MMAIIGGYRGDAGYAIGYSSISDGGNNMIRKGTASGNSRGHGASASVYQW	502
Db	541	MMAIIGGYRGDAGYAIGYSSISDGGNNMIRKGTASGNSRGHGASASVYQW	592

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RESULT 4
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/A098/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

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Query Match	96.5%	Score 2455:	DB 4:	Length 592:
Best Local Similarity	84.6%	Pred. No. 3.4e-187:		
Matches 501:	Conservative 0:	Mismatches 1:	Indels 90:	Gaps 4:
QY	1	MNKIYRIIMNSALNAMYVVSSELRNHTKRASATVKTAVLATLLEATVQASAN-----	52	
Db	1	MNKIYRIIMNSALNAMYVVSSELRNHTKRASATVKTAVLATLLEATVQASANERRPRKKD	60	
QY	53	-----TLKAGDNLIK 63		
Db	61	LYLDPVORTAVLYVNSDEKSTGEKEKVEENSDMAVYENEGVLTAREITTLKAGDNLIK	120	
QY	64	Q-----FTYSLKKDLDLDTSVGTEKLSFSANGKNVATSDTGLNFAKETAGNGDPTVHL	119	
Db	121	QNGRNFYTSLKKDLDLDTSVGTEKLSFSANGKNVATSDTGLNFAKETAGNGDPTVHL	180	
QY	120	NGISGTLD-----RAASVKVDLNAWNRKGVK-----NVD 150		
Db	181	NGISGTLDLTLNGCATTNVNTNDVTTDDEKKRAASVKVDLNAWNRKGVKPGTTASDNYD	240	
QY	151	FVRITDIYVEFLSADTKTTTVANVESDNGKRTIEVKIGACTSVYKEKDGKLYTGKDKGENGS	210	
Db	241	FVRITDIYVEFLSADTKTTTVANVESDNGKRTIEVKIGACTSVYKEKDGKLYTGKDKGENGS	300	
QY	211	STDECEGLVPTAKEVDAVNAKGMRRKTTTANGOTGOAKPELVNVSCTVNTFASGKGTAT	270	
Db	301	STDBEGGLVPTAKEVDAVNAKGMRRKTTTANGOTGOAKPELVNVSCTVNTFASGKGTAT	360	
QY	271	VSKDDQGNITWYDVNVGDALNVNQLQNSGWNLSKAAVSSGKVIISGNVSPSKKMDET	330	
Db	361	VSKDDQGNITWYDVNVGDALNVNQLQNSGWNLSKAAVSSGKVIISGNVSPSKKMDET	420	
QY	331	VWNAAGNIEITRNKNTDIATSMTPQFSSVSLGADAPTLSDGDALNVSCKDKNRPV	390	

Db 421 NINANGNMIETIRNCKNIDDIATSMPIQFSVSISLIGADAPLTLSVODDALNVSCKKONKPEY 480

Qy 391 RITNAPCPVKBEDYNNVAOLKGVANLNLRINDNVGNAAAGTAAOTATATGIVQVATYIPGGS 450

Db 481 RITNAPCPVKBEDYNNVAOLKGVANLNLRINDVDNANAGTAAOTATATGIVQVATYIPGGS 540

Qy 451 MAAIGGGYKRGAGYALIGSSISDGGNWTIKCTAGSNGSKHFGASASVGYQW 502

Db 541 MAAIGGGYKRGAGYALIGSSISDGGNWTIKCTAGSNGSKHFGASASVGYQW 592

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RESULT 5
US-09-377-155-11
: Sequence 11, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
:
: LENGTH: 591
:
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-11

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Query	Match	Similarity	Score	2447.5	DB	3	Length	591
Best Local	Similarity	84.6%	Pred. No.	1.3e-186				
Matches	500	Conservative	1	Mismatches	1	Indels	89	Gaps
Qy	1	MNKIYRIIWNLSALNAAVVVSELTNRNHRKASATYKTAVALATLLEFATVOASAN-----	52					
Db	1	MNEILRIIWNLSALNAAVVVSELTNRNHRKASATYKTAVALATLLEFATVOASANNEQEDL	60					
Qy	53	-----TLRAGDLNLIKIQ	64					
Db	61	YLDPLRTVAALLVNSDKEGTEKEKEVEENSDMAVYFNEKGVLAREITLNAAGDLNLIKIQ	120					
Qy	65	---FTYSLLKDLDELTIVSGTEKLSFSANGKNVITSPDKGLNFAKETAGTNGDTYHLN	120					
Db	121	NGTNFTYSLKKDLDTLIVSGTEKLSFSANGKNVITSPDKGLNFAKETAGTNGDTYHLN	180					
Qy	121	GIGSTLND-----RAASYKDVNLNAGNITKGYK-----NDF	151					
Db	181	GIGSTLNDTLNTGATNTVTDNVTYDDEKKRAASYKDVNLNAGNITKGYKPGTASTANDVF	240					
Qy	152	VRTDYVTEFLSADPTTIVNYESKONGKKTTEKICAKTSVYIKERKGLVYTGDKDENGSS	211					
Db	241	VRTDYVTEFLSADPTTIVNYESKONGKKTTEKICAKTSVYIKERKGLVYTGDKDENGSS	300					
Qy	212	TDEGEGLTAKEVIDAANKAGRMKRTTANGOTGADGFETVSGTNTVFASGKGTATV	271					
Db	301	TDEGEGLTAKEVIDAANKAGRMKRTTANGOTGADGFETVSGTNTVFASGKGTATV	360					
Qy	272	SKDOGNTITVAADVAVGALAVNQLQNSGWNLDKAAVAGSSSKVYISGVNVPBKGMDETV	331					
Db	361	SKDOGNTITVAADVAVGALAVNQLQNSGWNLDKAAVAGSSSKVYISGVNVPBKGMDETV	420					
Qy	332	NINAGNNIEIIRNCKNIDIAISMTPQFSSVSLGAGADAPTLSVDDALDNVSGKKKNKPYR	391					
Db	421	NINAGNNIEIIRNCKNIDIAISMTPQFSSVSLGAGADAPTLSVDDALDNVSGKKKNKPYR	480					
Qy	392	ITNAAPGVKEGDVTVAQLKQVAOHLNRRIDVNDGNARAGIAQAATATAGLVQAVYLPKGS	451					

Db 481 ITNAPGVKESDVTNVAQLKGVANLNNRIDNVGDNARAGIAQAATATAGLVQAYLPGRSM 540  
Qy 452 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 502  
Db 541 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 6  
US-09-669-974-11  
; Sequence 11, Application US/09669974  
; Patent No. 6333173

GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-11

Query Match 96.2%; Score 2447.5; DB 4; Length 591;  
Best Local Similarity 84.6%; Pred. No. 1.3e-186;  
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

Qy 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVAVLATLLFATVOASAN----- 52  
Db 1 MNELIRIIMNSALNMAVYVSELTRNHTKRASATVAVLATLLFATVOASANNEQEDEL 60  
Qy 53 -----TLKAGDNLKIKQ 64  
Db 61 YLDPLARTVAALVINSDEKTEKKEVENSMDWAYFENEKGLTAREITLKAGDNLKIKQ 120  
Qy 65 -----FTYSLKLDLDLTSVTEKLSFSANGKKNVITSPDKGLNFAKETAGTGTTHLN 120  
Db 121 NGTNFTYSLKLDLDLTSVTEKLSFSANGKKNVITSPDKGLNFAKETAGTGTTHLN 180  
Qy 121 GIGSTLND-----RAASVKDVLNAGWNKIGVK-----NYDF 151  
Db 181 GIGSTLPTLTLNTGATNTVNDNTYDDEKKRAASVKDVLNAGWNKIGVKPGTTASDNDF 240  
Qy 152 VRTYDVEFLSADTKTTTVNVEESKDNKKTEVKGAKTSVIERKDGKLVTKGKENGSS 211  
Db 241 VRTYDVEFLSADTKTTTVNVEESKDNKKTEVKGAKTSVIERKDGKLVTKGKENGSS 300  
Qy 212 TDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADFEFTVSTNTVTFASGKTTATV 271  
Db 301 TDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADFEFTVSTNTVTFASGKTTATV 360  
Qy 272 SKDDGNTITVAVNVGDALNVNOLONGSNWLDKRAVAGSSGKTVISGVNPSKGMDETV 331  
Db 361 SKDDGNTITVAVNVGDALNVNOLONGSNWLDKRAVAGSSGKTVISGVNPSKGMDETV 420  
Qy 332 NINAGNNIETIRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPEVR 391  
Db 421 NINAGNNIETIRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPEVR 480  
Qy 392 ITNAPGVKESDVTNVAQLKGVANLNNRIDNVGDNARAGIAQAATATAGLVQAYLPGRSM 451  
Db 481 ITNAPGVKESDVTNVAQLKGVANLNNRIDNVGDNARAGIAQAATATAGLVQAYLPGRSM 540

Qy 452 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 502  
Db 541 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 7  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312

GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 93.2%; Score 2371.5; DB 3; Length 599;  
Best Local Similarity 81.6%; Pred. No. 1.5e-180;  
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

Qy 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVAVLATLLFATVOASAN----- 52  
Db 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVAVLATLLFATVOANNTDEDEDEL 60  
Qy 53 -----TLKAGDNLKIKQ 64  
Db 61 EPYVSALVLPFMDKKEGNGENESTGNIGWSTIYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
Qy 65 -----FTYSLKLDLDLTSVTEKLSFSANGKKNVITSPDKGLNFAKETAGTNG 113  
Db 121 KNTNENTDSSFTYSLKLDLDLTSVTEKLSFGANGKKNVITSPDKGLNFAKETAGTNG 180  
Qy 114 DTVHALNGIGSTLND-----RAASVKDVLNAGWNKIGVK----- 147  
Db 181 DTVHALNGIGSTLND-----RAASVKDVLNAGWNKIGVK----- 240  
Qy 148 --NVDFFRTYDVEFLSADTKTTTVNVEESKDNKKTEVKGAKTSVIERKDGKLVTKGD 204  
Db 241 ASDNDFVHTYDVEFLSADTKTTTVNVEESKDNKKTEVKGAKTSVIERKDGKLVTKG 300  
Qy 205 KGENSSFTDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADFEFTVSTNTVTFASG 264  
Db 301 KGENSSFTDEGGLTAKEDVIDAVKAGRMKTTTANGOTGADFEFTVSTNTVTFASG 360  
Qy 265 KGTATVSKDDGNTITVAVNVGDALNVNOLONGSNWLDKRAVAGSSGKTVISGVNPSK 324  
Db 361 KGTATVSKDDGNTITVAVNVGDALNVNOLONGSNWLDKRAVAGSSGKTVISGVNPSK 420  
Qy 325 GKMDETVAINAGNNIETIRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVG 383  
Db 421 GKMDETVAINAGNNIETIRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGKALANGS 480  
Qy 384 KKNKPEVRITNAPGVKESDVTNVAQLKGVANLNNRIDNVGDNARAGIAQAATATAGLVQ 443  
Db 481 KKNKPEVRITNAPGVKESDVTNVAQLKGVANLNNRIDNVGDNARAGIAQAATATAGLVQ 540  
Qy 444 AYLPEKSMALIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 502  
Db 541 AYLPEKSMALIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599

RESULT 8  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 93.28; Score 2371.5; DB 4; Length 599;  
Best Local Similarity 81.68; Pred. No. 1.5e-180;  
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

QY 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVATLTLFATVQASAN----- 52  
DB 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVATLTLFATVQASANDEDEEEL 60  
QY 53 -----TLKAGNLKIKO--- 64  
DB 61 EPVRSALVLOFMIDKEGENESTGNIGSIYYDNHNTLHGATVTLKAGDNLIKQNTN 120  
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSANKNVNTSDTKGLNFAKETAGTNG 113  
DB 121 KNTNENTNDSSFYSLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
QY 114 DTTVHLNGISLTLD-----RAASVKDVLNAGNNIKGVK---- 147  
DB 181 DTTVHLNGISLTLDLNTGATNTVNDVTDKKRAASVADVLNAGNNIKGVKGT 240  
QY 148 ---NVDEFRTYDVEFLSADTKTTTVNVEESKDKNGKTEVKGAKTSYIKERDKLYTKGD 204  
DB 241 ASDNVDEFVHTYDVEFLSADTKTTTVNVEESKDKNGKTEVKGAKTSYIKERDKLYTKG 300  
QY 205 KGENGSTDEBGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEVTSNTVTFASG 264  
DB 301 KGENGSTDEBGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEVTSNTVTFASG 360  
QY 265 KGTATATSKDDGNTITFYVNVGDAALNVNOLONGSNNLDSKAVAGSSGVISGNVSPSK 324  
DB 361 KGTATATSKDDGNTITFYVNVGDAALNVNOLONGSNNLDSKAVAGSSGVISGNVSPSK 420  
QY 325 GKMDETVNIAGNNIEITRNGKNIDATSMTPOFSSVSLGADAPTLISVDG-DALNVGS 383  
DB 421 GKMDETVNIAGNNIEITRNGKNIDATSMTPOFSSVSLGADAPTLISVDKALNVGS 480  
QY 384 KKNKPPRTTNVAPVKEGVTNVAOLKGYAONLNHNDVNDGNAKGIQAATAGLVQ 443  
DB 481 KDNKPPRTTNVAPVKEGVTNVAOLKGYAONLNHNDVNDGNAKGIQAATAGLVQ 540  
QY 444 AYLPGKSMALIGGTYGEGAGYAGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 502  
DB 541 AYLPGKSMALIGGTYGEGAGYAGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 599

RESULT 9

US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 93.08; Score 2366; DB 3; Length 594;  
Best Local Similarity 82.08; Pred. No. 4.1e-180;  
Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

QY 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVATLTLFATVQASAN----- 52  
DB 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVATLTLFATVQASANDEDEEEL 60  
QY 53 -----TLKAGNLKIKO--- 64  
DB 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNMGVYFDPKKVYLAGTTLTLAGDNLIKQNTNE 120  
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSANKNVNTSDTKGLNFAKETAGTNGT 118  
DB 121 NTNASPTYSLSKKDLTDLTSVTEKLSFSANKNVNTSDTKGLNFAKETAGTNGT 180  
QY 119 LNGISLTLD-----RAASVKDVLNAGNNIKGVK---- 149  
DB 181 LNGISLTLDLNTGATNTVNDVTDKKRAASVADVLNAGNNIKGVKPGTTASDNV 240  
QY 150 DEVRTYDVEFLSADTKTTTVNVEESKDKNGKTEVKGAKTSYIKERDKLYTKGDENG 209  
DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKNGKTEVKGAKTSYIKERDKLYTKGDENG 300  
QY 210 SSTDEBGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEVTSNTVTFASGKTTA 269  
DB 301 SSTDEBGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEVTSNTVTFASGKTTA 360  
QY 270 TVSKDDGNTITVMDVNVGDAALNVNOLONGSNNLDSKAVAGSSGVISGNVSPSKGMD 329  
DB 361 TVSKDDGNTITVMDVNVGDAALNVNOLONGSNNLDSKAVAGSSGVISGNVSPSKGMD 420  
QY 330 TVNINAGNNIEITRNGKNIDATSMTPOFSSVSLGADAPTLISVDG-DALNVGS 388  
DB 421 TVNINAGNNIEITRNGKNIDATSMTPOFSSVSLGADAPTLISVDDEGALNVGS 480  
QY 389 PVRTTNVAPVKEGVTNVAOLKGYAONLNHNDVNDGNAKGIQAATAGLVQAVLP 448  
DB 481 PVRTTNVAPVKEGVTNVAOLKGYAONLNHNDVNDGNAKGIQAATAGLVQAVLP 540  
QY 449 KSMALIGGTYGEGAGYAGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 502  
DB 541 KSMALIGGTYGEGAGYAGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 10  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 594  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 93.0%; Score 2366; DB 4; Length 594;  
Best Local Similarity 82.0%; Pred. No. 4, 1e-180;  
Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

QY 1 NKKIIRIIMNSALNMAVVSSELTNRHTRKASATVATLTLFATVOASAN----- 52  
1 NKKIIRIIMNSALNMAVVSSELTNRHTRKASATVATLTLFATVOASATDDDDLYLE 60  
DB 1 NKKIIRIIMNSALNMAVVSSELTNRHTRKASATVATLTLFATVOASATDDDDLYLE 60  
QY 53 -----TLKAGDNLKIKO----- 64  
61 PVQRTAVVLSFRSDEKGEKEDSDMWVYFDEKRVLKAGATITLKAGDNLKIKONTNE 120  
DB 61 PVQRTAVVLSFRSDEKGEKEDSDMWVYFDEKRVLKAGATITLKAGDNLKIKONTNE 120  
QY 65 -----FTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNDPTVH 118  
121 NTNDSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNDPTVH 180  
DB 121 NTNDSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNDPTVH 180  
QY 119 LINGISSTLTLD-----RAASVQDVNAGNINIGV-----NV 149  
181 LINGISSTLTDLTNGATTNTNDVTDDEKRAASVQDVNAGNINIGVPGTTASDNV 240  
DB 181 LINGISSTLTDLTNGATTNTNDVTDDEKRAASVQDVNAGNINIGVPGTTASDNV 240  
QY 150 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLVTKDKGENG 209  
241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLVTKDKGENG 300  
DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLVTKDKGENG 300  
QY 210 SSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGQGTGADKFEPTVSGTNVTFASGKGT 269  
301 SSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGQGTGADKFEPTVSGTNVTFASGKGT 360  
DB 301 SSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGQGTGADKFEPTVSGTNVTFASGKGT 360  
QY 270 TVSKDQGNITVYVYVNGDALNVQNLQNSGWNLDSSKAVAGSSGKVIISGNVSPSKGK 329  
361 TVSKDQGNITVYVYVNGDALNVQNLQNSGWNLDSSKAVAGSSGKVIISGNVSPSKGK 420  
DB 361 TVSKDQGNITVYVYVNGDALNVQNLQNSGWNLDSSKAVAGSSGKVIISGNVSPSKGK 420  
QY 330 TVNINAGNIIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGD-ALNVGSKK 388  
421 TVNINAGNIIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKK 480  
DB 421 TVNINAGNIIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKK 480  
QY 389 PVRTINVAPVYEGGVTVNAQOLKGYAQNLLNNRIDVNDGNARAGIAQATATAGLVAYLP 448  
481 PVRTINVAPVYEGGVTVNAQOLKGYAQNLLNNRIDVNDGNARAGIAQATATAGLVAYLP 540  
DB 481 PVRTINVAPVYEGGVTVNAQOLKGYAQNLLNNRIDVNDGNARAGIAQATATAGLVAYLP 540  
QY 449 KSMAIIGGGTYRGEAGYALIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 502  
541 KSMAIIGGGTYRGEAGYALIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594  
DB 541 KSMAIIGGGTYRGEAGYALIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594

RESULT 11  
US-09-377-155-7  
Sequence 7, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 594  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 92.7%; Score 2359; DB 3; Length 594;  
Best Local Similarity 82.0%; Pred. No. 1, 5e-179;  
Matches 487; Conservative 2; Mismatches 13; Indels 92; Gaps 5;

QY 1 NKKIIRIIMNSALNMAVVSSELTNRHTRKASATVATLTLFATVOASAN----- 52  
1 NKKIIRIIMNSALNMAVVSSELTNRHTRKASATVATLTLFATVOASATDDDDLYLE 60  
DB 1 NKKIIRIIMNSALNMAVVSSELTNRHTRKASATVATLTLFATVOASATDDDDLYLE 60  
QY 53 -----TLKAGDNLKIKO----- 64  
61 PVQRTAVVLSFRSDEKGEKEDSDMWVYFDEKRVLKAGATITLKAGDNLKIKONTNE 120  
DB 61 PVQRTAVVLSFRSDEKGEKEDSDMWVYFDEKRVLKAGATITLKAGDNLKIKONTNE 120  
QY 65 -----FTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNDPTVH 118  
121 NTNDSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNDPTVH 180  
DB 121 NTNDSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNDPTVH 180  
QY 119 LINGISSTLTLD-----RAASVQDVNAGNINIGV-----NV 149  
181 LINGISSTLTDLTNGATTNTNDVTDDEKRAASVQDVNAGNINIGVPGTTASDNV 240  
DB 181 LINGISSTLTDLTNGATTNTNDVTDDEKRAASVQDVNAGNINIGVPGTTASDNV 240  
QY 150 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLVTKDKGENG 209  
241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLVTKDKGENG 300  
DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLVTKDKGENG 300  
QY 210 SSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGQGTGADKFEPTVSGTNVTFASGKGT 269  
301 SSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGQGTGADKFEPTVSGTNVTFASGKGT 360  
DB 301 SSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGQGTGADKFEPTVSGTNVTFASGKGT 360  
QY 270 TVSKDQGNITVYVYVNGDALNVQNLQNSGWNLDSSKAVAGSSGKVIISGNVSPSKGK 329  
361 TVSKDQGNITVYVYVNGDALNVQNLQNSGWNLDSSKAVAGSSGKVIISGNVSPSKGK 420  
DB 361 TVSKDQGNITVYVYVNGDALNVQNLQNSGWNLDSSKAVAGSSGKVIISGNVSPSKGK 420  
QY 330 TVNINAGNIIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGD-ALNVGSKK 388  
421 TVNINAGNIIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKK 480  
DB 421 TVNINAGNIIETTRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKK 480  
QY 389 PVRTINVAPVYEGGVTVNAQOLKGYAQNLLNNRIDVNDGNARAGIAQATATAGLVAYLP 448  
481 PVRTINVAPVYEGGVTVNAQOLKGYAQNLLNNRIDVNDGNARAGIAQATATAGLVAYLP 540  
DB 481 PVRTINVAPVYEGGVTVNAQOLKGYAQNLLNNRIDVNDGNARAGIAQATATAGLVAYLP 540  
QY 449 KSMAIIGGGTYRGEAGYALIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 502  
541 KSMAIIGGGTYRGEAGYALIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594  
DB 541 KSMAIIGGGTYRGEAGYALIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594

RESULT 12  
US-09-669-974-7  
Sequence 7, Application US/09669974  
Patent No. 6333173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974





;; PRIOR FILING DATE: 1997-12-12  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 13  
;; LENGTH: 598  
;; TYPE: PRF  
;; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 92.1%; Score 2344; DB 4; Length 598;  
Best Local Similarity 80.9%; Pred. No. 2.3e-178;  
Matches 484; Conservative 3; Mismatches 15; Indels 96; Gaps 5;

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DB 1 MNKIRIIMNSALNMVYVSELTRNHTKASATVATLTLFATVOANATDDDDLYLE 60
QY 53 -----TLKAGDNLIKQ----- 64
DB 61 PVQRTAVVLSFRSDEKGEKTEGSDSNMAYVFDEKRVLKAGATILKAGDNLIKQNTNE 120
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSGANGKNYITSDTKGLNFAKETAGTNGD 114
DB 121 NTNENTNDSSFYSLKKDLTDLTSVTEKLSFGANGKNYITSDTKGLNFAKETAGTNGD 180
QY 115 TTVHLNGIGSTLTD-----RAASVYKDVLAGNNIGVK----- 147
DB 181 PTVHLNGIGSTLTDLTLNTGATTNTNDVTDDEKRAASVYKDVLAGNNIGVKPGTTA 240
QY 148 --NVDVFRTYDVEFLSADTKTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGKDK 205
DB 241 SONVDFVRTYDVEFLSADTKTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGKDK 300
QY 206 GENGSSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEETVTSCTNVTFSAGK 265
DB 301 DENGSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEETVTSCTNVTFSAGN 360
QY 266 GTTATVSKDDQGNITVMDVNVGDLNVNQLONGSMNIDSKAVAGSSGKVISGNVSPSKG 325
DB 361 GTTATVSKDDQGNITVMDVNVGDLNVNQLONGSMNIDSKAVAGSSGKVISGNVSPSKG 420
QY 326 KMDETVNIAGNNIEITRGNKIDTATSMTPOFSSVSLGAGADAPTLISVDGD-ALNVGSK 384
DB 421 KMDETVNIAGNNIEITRGNKIDTATSMTPOFSSVSLGAGADAPTLISVDGDALNVGSK 480
QY 385 KDNKVRITTNVAPGYKEGDVTNVAOLKGYAQNLMNRIDVNDGNARAGIAQAATATAGLYOA 444
DB 481 DANKVRITTNVAPGYKEGDVTNVAOLKGYAQNLMNRIDVNDGNARAGIAQAATATAGLYOA 540
QY 445 YLPGRSMAIIGGTYRGEAGVAGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
DB 541 YLPGRSMAIIGGTYRGEAGVAGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
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RESULT 15  
US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5

;; LENGTH: 598  
;; TYPE: PRF  
;; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 91.8%; Score 2335; DB 3; Length 598;  
Best Local Similarity 80.6%; Pred. No. 1.2e-177;  
Matches 482; Conservative 4; Mismatches 16; Indels 96; Gaps 5;

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DB 1 MNKIRIIMNSALNMVYVSELTRNHTKASATVATLTLFATVOANATDDDDLYLE 60
QY 53 -----TLKAGDNLIKQ----- 64
DB 61 PVQRTAVVLSFRSDEKGEKTEGSDSNMAYVFDEKRVLKAGATILKAGDNLIKQNTNE 120
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSGANGKNYITSDTKGLNFAKETAGTNGD 114
DB 121 NTNENTNDSSFYSLKKDLTDLTSVTEKLSFGANGKNYITSDTKGLNFAKETAGTNGD 180
QY 115 TTVHLNGIGSTLTD-----RAASVYKDVLAGNNIGVK----- 147
DB 181 PTVHLNGIGSTLTDLTLNTGATTNTNDVTDDEKRAASVYKDVLAGNNIGVKPGTTA 240
QY 148 --NVDVFRTYDVEFLSADTKTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGKDK 205
DB 241 SONVDFVRTYDVEFLSADTKTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGKDK 300
QY 206 GENGSSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEETVTSCTNVTFSAGK 265
DB 301 DENGSTDEGEGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEETVTSCTNVTFSAGN 360
QY 266 GTTATVSKDDQGNITVMDVNVGDLNVNQLONGSMNIDSKAVAGSSGKVISGNVSPSKG 325
DB 361 GTTATVSKDDQGNITVMDVNVGDLNVNQLONGSMNIDSKAVAGSSGKVISGNVSPSKG 420
QY 326 KMDETVNIAGNNIEITRGNKIDTATSMTPOFSSVSLGAGADAPTLISVDGD-ALNVGSK 384
DB 421 KMDETVNIAGNNIEITRGNKIDTATSMTPOFSSVSLGAGADAPTLISVDGDALNVGSK 480
QY 385 KDNKVRITTNVAPGYKEGDVTNVAOLKGYAQNLMNRIDVNDGNARAGIAQAATATAGLYOA 444
DB 481 DANKVRITTNVAPGYKEGDVTNVAOLKGYAQNLMNRIDVNDGNARAGIAQAATATAGLYOA 540
QY 445 YLPGRSMAIIGGTYRGEAGVAGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
DB 541 YLPGRSMAIIGGTYRGEAGVAGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
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Search completed: October 6, 2003, 09:35:51  
Job time : 15.4245 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 14.3699 Seconds  
(without alignments)  
3359.577 Million cell updates/sec

Title: US-09-771-382-27  
Perfect score: 2544  
Sequence: 1 MNKIYRIIWSALNAMYVVS.....TASGNSRGHFASASVGYQW 502

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2459.5	96.7	591	2 G81133	adhesin NMB0992 [i
2	2351	92.4	592	2 A81888	adhesin surface f
3	523.5	20.6	298	2 I64138	adhesin homolog HI
4	380.5	15.0	1190	2 A82615	surface protein XF
5	360.5	14.2	1588	2 A86036	probable adhesin X
6	350.5	14.2	1588	2 H91188	probable adhesin E
7	358.5	14.1	2059	2 D82671	surface protein XF
8	351.5	13.8	1107	2 AC0976	probable autotrans
9	346.5	13.6	658	2 AH0130	probable surface p
10	226.5	8.9	1325	2 A64905	yadek protein - Esc
11	224.5	8.8	1004	2 C82672	surface-exposed h
12	210.5	8.3	1910	2 AF0394	probable adhesin h
13	210	8.3	1286	2 S28634	adhesin ALDA-I pre
14	208.5	8.2	1343	2 E90893	hypothetical prote
15	208	8.2	1091	2 G64964	hypothetical prote
16	203.5	8.0	1343	2 D85724	hypothetical prote
17	197	7.7	1018	2 H83135	probable adhesin p
18	194	7.6	936	2 I40711	sapB protein - Cam
19	192	7.5	1417	2 A83080	hypothetical prote
20	192	7.5	3705	2 AD0123	probable autotrans
21	192	7.5	4919	2 T31105	hypothetical prote
22	191	7.5	1536	2 A43855	high-molecular-we
23	190	7.5	949	2 D90803	ALDA-I adhesin-lik
24	188.5	7.4	1005	2 H85611	probable adhesin z
25	188.5	7.4	365	2 AB3486	cell surface prote
26	188.5	7.4	1477	2 BA3855	high-molecular-we
27	185.5	7.3	585	2 P90961	flagellin [Importe
28	185.5	7.3	585	2 H85809	hypothetical prote
29	185.5	7.3	5291	2 F90696	hypothetical prote

30	183.5	7.2	1335	2 T17508	glycoprotein Vp260
31	182.5	7.2	920	2 I40614	surface array prot
32	181	7.1	584	2 C48658	flagellin - Escher
33	181	7.1	3029	2 S76109	hypothetical prote
34	180.5	7.1	5188	2 B85347	probable RTX fam1
35	180	7.1	1109	2 A56143	surface-array prot
36	180	7.1	3013	2 AB0480	adhesin/invasin y
37	178.5	7.0	364	2 A81019	probable adhesin p
38	176.5	6.9	1341	2 H98323	hypothetical prote
39	176	6.9	1275	2 T33369	hypothetical prote
40	175.5	6.9	2020	2 C48399	ABC-type transport
41	174	6.8	1487	2 A62560	hypothetical prote
42	173	6.8	1608	2 A28182	hemolysin A - Ser
43	173	6.8	2249	2 A41477	190K surface anti
44	172.5	6.8	1366	2 S57664	IGA-specific metal
45	172	6.8	1369	2 T17504	hypothetical prote

ALIGNMENTS

RESULT 1					
G81133					
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)					
C:Species: Neisseria meningitidis					
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001					
C:Accession: G81133					
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000					
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307					
A:Accession: G81133					
A:Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-591 <TEF>					
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAI41395.1; PID:g722					
A:Experimental source: serogroup B, strain MC58					
C:Genetics: A:Gene: NMB0992					
Query Match	96.7%	Score 2459.5	DB 2	Length 591	
Best Local Similarity	84.9%	Pred. No. 5.8e-124			
Matches 502	Conservative 0	Mismatches 0	Indels 89	Gaps 4	
QY	1	MNKIYRIIWSALNAMYVVS	ELTRNHTRKASATVKTAVLATLRFATYQASAN	-----	52
DB	1	MNKIYRIIWSALNAMYVVS	ELTRNHTRKASATVKTAVLATLRFATYQASANNEQEEDL		60
QY	53	-----	-----	TLAGNKLAKIQ	64
DB	61	YLDEPQRTVAVLIVNSDKEGTGEKEKVEENSDMAVFNENKCVLTAREITLAKGNLKKIQ			120
QY	65	-----FTYSLKKDLFDLISVGTSEKLSFSANGKRVNITSPTKGLNPAKETAAGTNGDTYHLN			120
DB	121	NGTFTYSLKKDLFDLISVGTSEKLSFSANGKRVNITSPTKGLNPAKETAAGTNGDTYHLN			180
QY	121	GIGSTLTD	-----RAASVKDVLNAGNIIKGVK	-----NVDF	151
DB	181	GIGSTLTDLTLLNFGATTNVTNDVTTDDEKKRAASVKDVLNAGNIIKGVKPTTASDNVDF			240
QY	152	VRTDYVEFLSADTKTTTVNVESKDNKGKTEVKTGAKTSVTKEDKGKLYTKDKGENSS			211
DB	241	VRTDYVEFLSADTKTTTVNVESKDNKGKTEVKTGAKTSVTKEDKGKLYTKDKGENSS			300
QY	212	TDEGEGLTAKVEIVDAVNAKGRMKTTTANCOGADFEFTVTSCTNTVTFASGKTATV			271
DB	301	TDEGEGLTAKVEIVDAVNAKGRMKTTTANCOGADFEFTVTSCTNTVTFASGKTATV			360
QY	272	SKDDGQNTVYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIISGNVSPSKGMDET			331

Db 361 SKDDGNTIVMTDVNVDALNNQOLNSGMNLDKRAVASSGKVIISGNSPSKCKMDEV 420

Qy 332 NINAGNNIEITRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPYR 391

Db 421 NINAGNNIEITRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPYR 480

Qy 392 ITNVAGVKEGDTNVAOLKGAOONLNRIIDVNGARAGIAQATITAGLVQAVLPGKSM 451

Db 481 ITNVAGVKEGDTNVAOLKGAOONLNRIIDVNGARAGIAQATITAGLVQAVLPGKSM 540

Qy 452 MAIGGTYRGEAGYATIGYSSISDGNWIKGTASGSRGHPGASASVGYOM 502

Db 541 MAIGGTYRGEAGYATIGYSSISDGNWIKGTASGSRGHPGASASVGYOM 591

RESULT 2

A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)

C:Species: Neisseria meningitidis

C:date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001

C:Accession: A81888

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A:title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:reference number: A81775; M01D:2022356; PMID:10761919

A:Accession: A81888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-references: GB:A162755; GB:A157959; NID:g7379742; PIDN:CAM84461.1; PID:g737989

A:Experimental source: serogroup A, strain Z2491

A:Genetics:

A:Gene: NMA1200

Query Match 92.4%; Score 2351; DB 2; Length 592;

Best Local Similarity 81.6%; Pred. No. 3.6e-118;

Matches 463; Conservative 6; Mismatches 13; Indels 90; Gaps 5;

Qy 1 MNKRIINNSALNMAVVSSELTRNHTKRASATVKTAVATLTLFATVQASAN----- 52

Db 1 MNKRIINNSALNMAVVSSELTRNHTKRASATVKTAVATLTLFATVQANATDEDEEEL 60

Qy 53 -----TLKAGDNILKIQ----- 64

Db 61 ESVORSVSGSIQASMGSELETTISLMTNDSKEFDPYIVYTLKAGDNILKIQNTNENT 120

Qy 65 -----FTYSLKDDLTDLISVGTETKLSANGKNVNIISDPKGLNFAETAGTNGDTTVHLN 120

Db 121 MASSFTYSLKDDLTGLINETEKLSPGANGKRVNIISDPKGLNFAETAGTNGDTTVHLN 180

Qy 121 GIGSTLTLD-----RAASVDYLNAGWNKIGVK-----NVDF 151

Db 181 GIGSTLTLDLASSASHVADAGNOSTHYTRAASIKVDLNMGMNKGKTKGTSSTTGQSNVDF 240

Qy 152 VRTYDVEFLSADFTKTYVNVESKNGKTEVKGAKTSVIEKKDGLVTGDKGENGSS 211

Db 241 VRTYDVEFLSADFTKTYVNVESKNGKTEVKGAKTSVIEKKDGLVTGDKGENGSS 300

Qy 212 TPBEGELTAKEVYAVNKGARMKTTTANGOTGADKREYVTSCTNNVTFASGKTATV 271

Db 301 TPBEGELTAKEVYAVNKGARMKTTTANGOTGADKREYVTSCTNNVTFASGKTATV 360

Qy 272 SKDDGNTIVMTDVNVDALNNQOLNSGMNLDKRAVASSGKVIISGNSPSKCKMDEV 331

Db 361 SKDDGNTIVMTDVNVDALNNQOLNSGMNLDKRAVASSGKVIISGNSPSKCKMDEV 420

Qy 332 NINAGNNIEITRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPYR 390

Db 421 NINAGNNIEITRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPYR 480

Qy 391 RTNVAPGVKEGDTNVAOLKGAOONLNRIIDVNGARAGIAQATITAGLVQAVLPGKS 450

Db 481 RTNVAPGVKEGDTNVAOLKGAOONLNRIIDVNGARAGIAQATITAGLVQAVLPGKS 540

Qy 451 MAIGGTYRGEAGYATIGYSSISDGNWIKGTASGSRGHPGASASVGYOM 502

Db 541 MAIGGTYRGEAGYATIGYSSISDGNWIKGTASGSRGHPGASASVGYOM 592

RESULT 3

A64138

adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997

C:Accession: I64138

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; M01D:95350630; PMID:7542800

A:Accession: I64138

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <TIGR>

A:Cross-references: GB:U32846; GB:LA2023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.6%; Score 523.5; DB 2; Length 298;

Best Local Similarity 43.5%; Pred. No. 4.2e-21;

Matches 128; Conservative 25; Mismatches 60; Indels 81; Gaps 7;

Qy 1 MNKRIINNSALNMAVVSSELTRNHTKRASATVKTAVATLTLFATVQ----- 49

Db 1 MNKRIINNSALNMAVVSSELTRNHTKRASATVKTAVATLTLFATVQ----- 49

Qy 50 -----SANTLKAGDNILKIQ-----KOPTYSLKDDLTDLISV 79

Db 61 STEDDIEDSAAIKRDKNKNALAGDTLTITKAGKNLAKAKIDGCKSVTFPLAADLDVKTAK 120

Qy 80 GTEKLSFSAN-----GNKVNITSPTKGLNFAETAGTNGDTTVHLNIGSTLTD---- 128

Db 121 VSDTLTIGGNTPAAGATPKVTSITSPADGLKLAK--GNGDPAVHLNGLASTLDVPTN 177

Qy 129 -----RAASVDYLNAGWNKIGVK-----NVDFVRTYDVEFLSAD 164

Db 178 TGASTVTFPSDIDETKRAATITKVDLNMGMNKGKTKGTSSTTGQSNVDF 237

Qy 165 TKTTVTVNVSCKNGKTEVKGAKTSVIEKKDGLVTGDK-----KGENGSTDEGE 216

Db 238 KNTLDVLTAKENGKTEVKGAKTSVIEKKDGLVTGDK-----KGENGSTDEGE 291

RESULT 4

A82615

surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: A82615

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000

A:title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:reference number: A82515; M01D:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1190 <SIM>

A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAFP4783.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carriero, D.M.; Carrier as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.  
 A.; Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.,  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A.  
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savaas  
 A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
 M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: xfl981

Query Match 15.0%; Score 380.5; DB 2; Length 1190;  
 Best Local Similarity 26.2%; Pred. No. 9.9e-13;

Matches 148; Conservative 72; Mismatches 211; Indels 133; Gaps 22;

QY 17 VVSELRNHTTKASATVTAVALTLFATVQASANTLKAQNLKIKOFTYS--LKKDLT 74  
 DB 682 VTSGISAGNOKITVNAAGTADDAVAFSOLAQVSSATSKGWLASGANSNVAPGESV 741  
 QY 75 DLTSV--GTEKLSFANGNKV--NITSPTKGLNFAKEAG-----TNGDT--VHLNGIG 123  
 DB 742 DLKNTGDNIVISKESGNDVLENDLS--SLKLDKLTVDGTVMTTNGVTVSGVTLGSMG 798  
 QY 124 STLDRASVYKDYLNAG--WNI-----KGVKNVDEVRVDTV 158  
 DB 799 LVITDPSVTSSSGINSOKITVNAAGTADDAVNLSQLNTAMAGSAKVVHYSTYD-- 856  
 QY 159 EFLSADTKTTTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDKGENG--STDEGEG 217  
 DB 857 ---GGTGGGNYNGDGTGRTSIAVGVGLTASA---EGATAVGSGMAAGSGKSTALGRN 908  
 QY 218 LVTAKETIDAVNKAKMTTTFANGOTGADKFEVTVSGTNVTFASGKGTATVSKNDG 277  
 DB 909 AVASAGSVALGD-GAKDGKCAESTTGKISGLNNTVGVSGDASKGRTVVS----- 962  
 QY 278 NITVMTDVNVDALNNQI---QNSGMNLSKAVAGSSGKVISGNVSPSKGMDTVNI 333  
 DB 963 NVADAKEAT--DAVNLRQDLDRVAQDANRYVDNKIESLSEQTF-----YKV 1006  
 QY 334 NAGNNEITRNKGNIDTATSMTPQFSSVSLGAGADAPTLVS-----DGALNNGSK--- 384  
 DB 1007 NSLNN-----SATP-----IAAGVDATAIGVATASGADSIAMGNKASAS 1046  
 QY 385 KDKKPV-----RITTVAPGVKEDGVNVAQKGVANQNLNRID 422  
 DB 1047 ADNAVAALGNHSAVDRANTVSVSASGSEROYTVNAAGTADDAVNVSLNOGLITAKOYTD 1106  
 QY 423 NVDGNAR---AGIAQAIATAGLVQAYLPKSKMAIGGTYRGEAGYAIGYSSISDGMV 478  
 DB 1107 GAVGSLRBDTGDGVAAAIATANLPQAYIPGRGMTSVGSYSRQSAIATVGVSSVSEGRV 1166  
 QY 479 IITGTASGNSRGHFGASASVGYOW 502  
 DB 1167 VFKFGSANTRSQVIGAGVGYOW 1190

## RESULT 5

A86036  
 Probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: A86036  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoultis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: A86036  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1588 <STO>  
 A:Cross-references: GB:AE005174; NID:G13518349; PIDN:AA658749.1; GSPDB:GN00145; UWGP:Z50

A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z5029

## Query Match

14.2%; Score 360.5; DB 2; Length 1588;  
 Best Local Similarity 28.3%; Pred. No. 1.7e-11;

Matches 141; Conservative 55; Mismatches 181; Indels 121; Gaps 21;

QY 46 TVQASANTLKAQNLKIKOFTYSLKDLDTLTVSGTEKLSFSA-----NGKK-----VNIT 96  
 DB 1171 TVRQLNALGAIVATTPPKYFHANSTEE--DSLAVGTDLSLAMGAKTVNGDKGIGIGYAY 1228  
 QY 97 SDPTKGLNFAKETAGTNGDVTVHLNGI-----GSTLDRASVYKDYLN--AGMNTKG---VK 147  
 DB 1229 VDNALNLNGI--ALGSNAQ-VIHNSTALIGSGSTTRKACQNTYATNMDAQNVSGERSVG 1285  
 QY 148 NVDFVRTVTVVEFLSADTKTTTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDKG- 206  
 DB 1286 SADGQROITVNAAGSADTDVAVNG-----OLKVTDAQVSONTQSITNLDR--VTNLDSRV 1339  
 QY 207 ---ENG-----STDEGGLVTAKEVIDAVNKAQKRMKTTTANGOTGADKFEVTVSGTNV 259  
 DB 1340 TNIENGIGDIIVTGTSTKRYFTNTDGVDA--SAQKDSVALGSISIAAD--NSVALDTG- 1394  
 QY 260 TPAAGKGTATVSKDDGNT--VMYDVNVGDALNNVQLONS---GMNLSKAVAGSSGKV 315  
 DB 1395 SVATFEENTISVSGSTNRRTTNVAGKNATDAVNAQKSEAGVRYDTKA----- 1446  
 QY 316 ISGNVSPSKGMDTVNINAGNIEITRNKGNIDTATSMTPQFSSVSLGAGADAPTLVD 375  
 DB 1447 -----DGSID-----YSNITLGGNGGTT----- 1465  
 QY 376 GDALNNGSKDKNPRTTNVAPGVKEDGVNVAQKGVANQNLNRIDV 424  
 DB 1466 -----RISNVAGVNNNDVNVQALQSVQVETQOYTDQREVDNKLST 1510  
 QY 425 DGNARAGIAQAIATAGLVQAYLPKSKMAIGGTYRGEAGYAIGYSSISDGMNIIKGT 484  
 DB 1511 ESKLSSGSIASAMMTGLPQAYIPGRTGASMASIGGTYRGEAGYAIGYSSISDGMNIIKGT 1570  
 QY 485 SGNSRGHFGASASVGYOW 502  
 DB 1571 STNSQGEYSALAGIOW 1588

## RESULT 6

H91188  
 Probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain R  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
 C:Accession: H91188  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g  
 A:Reference number: A9629; MUID:21156231; PMID:11258796  
 A:Accession: H91188  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1588 <HAY>  
 A:Cross-references: GB:BA000007; PIDN:BA637903.1; PID:G13363955; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RMD 0509952  
 C:Genetics:  
 A:Gene: ECs4480

## Query Match

14.2%; Score 360.5; DB 2; Length 1588;  
 Best Local Similarity 28.3%; Pred. No. 1.7e-11;

Matches 141; Conservative 55; Mismatches 181; Indels 121; Gaps 21;

QY 46 TVQASANTLKAQNLKIKOFTYSLKDLDTLTVSGTEKLSFSA-----NGKK-----VNIT 96  
 DB 1171 TVRQLNALGAIVATTPPKYFHANSTEE--DSLAVGTDLSLAMGAKTVNGDKGIGIGYAY 1228



QY 126 LTRDAASVKKDLNAGMNIKGVK-----NVDFRYTDFEFLSADTKTTTVN-----VE 173  
 Db 530 STDA-----INSQLETFETMLLSQYNESISQLAGDISEYITFENGTVKIR 576  
 QY 174 SKDNGKTEVKIKAKTSVIEKDGKLVYTKDK-----GENGSSTDEG----- 215  
 Db 577 TNDNGLEGO-----DAYATNGATVAGYDAVASGAGCLAGCNSSSSIEGSLALSGS 629  
 QY 216 -----EGLY-----TAKEVIDAVNKA-----GWRMTTNTANGOTGQ--- 246  
 Db 630 TSNRAITTTGIRETSATSDGVYIGYNTDRELGLSLCTDGESEYRQITTNVADSEADAV 689  
 QY 247 -----ADKFETVTSGTNTVTFASGKGTAA-----TVSKDDOG-----NITVM 282  
 Db 690 TVRQLONAIGAVTTTPTKRYHANSTEDSLAVGTDSLAMGAKTIVNADAGIGLINTLNM 749  
 QY 283 YDVAVGALNN-----OLNSGNWLDSK-----AVAGSSGK 314  
 Db 750 ADAINGIAIGSNABANHANSIANGNSQTRGACQTDYATVNMPTPONSVEGEFVSGEDQ 809  
 QY 315 VISGNVSPSKGKMDETVNING-----NNIETRRGKN----- 348  
 Db 810 RQITNVNAGSADTDA---VNGQLKVTDAQVSRNTOSTITNLTQVSNLDTVTNIENGIG 866  
 QY 349 DIATSMTPPF-----SSVSLGAGADAP-----TLVYGDALNYS 383  
 Db 867 DIVTGTSTKRYKKTNDGADANAGADSVAIIGSSIAAENSVALGTNSVADENATVVSQS 926  
 QY 384 KKDKNPVRITNVAPGVKEGDTNVNQLK----- 411  
 Db 927 STQOR--RITNVAGVNNVTDAVNVAQLKSEAGSVREYNADGSVNSVLMIGDGSQGT 984  
 QY 412 -----GVAO-----NINNRIDVNDGARNAGIAQATATA 439  
 Db 985 RIGVNSAANDTDAVNVAQLKRSVEANTTYTDQKMEKNKSKIGIKENKSGGSIAMAMA 1044  
 QY 440 GLVQAYLPKSKMAIGGTYRGEAGYAIYSSISDGNMIIKGTASGNSRHFASASVGC 499  
 Db 1045 GLPQAYAPGAMNTSIAGTGFGEASAVAIQVMSVSESGWYKLGCTSNISQDYSALIGAG 1104  
 QY 500 YQW 502  
 Db 1105 FQW 1107

RESULT 9  
 AH0110  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
 C:Accession: AH0110  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,  
 Nature 413, 523-527, 2001.  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AH0110  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-658 <KUN>  
 A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: YP00902

Query Match 13.6%; Score 346.5; DB 2; Length 658;  
 Best Local Similarity 25.3%; Pred. No. 3.1e-11;  
 Matches 134; Conservative 76; Mismatches 198; Indels 121; Gaps 21;  
 QY 12 ALNMMVWVSELTNRHTRKASATVKT-----AVLATILPRTVQASANTLKAGCNLIKQPTTY 67  
 Db 213 ALGAGAVTSQ--ANSIALGAASIMTVGAQSSYSAYALTAPQASVGEIGIG----- 260

QY 68 SLKRDLDLTVSGTEKLSFSGANKNVNTSDTKLNFPAKETAGTNGD-----TVHLNGIG 123  
 Db 261 -----TALGRKRIKTVAGAG-----SASSDAVNVAQLTA--VGQVQONTANTISLG 304  
 QY 124 STLDRAASVKKDLNAGMNIKGVKNDVFTRTYDVEFLSADTKTTTVNESKDNKKT-- 181  
 Db 305 GRVTTIGSMAISANG-----GVRY--FHANSTOPDSVASTNSVAIGPASTLASGNALA 358  
 QY 182 -----EVKIGATSVIEKEDGKLVTKDKGKNGSSSTDEEGLVTKKEVIDAVNKAQWRKKT 237  
 Db 359 SGAGAVAIIG--DGAASADGSAIIGQSGDGKREVENTIG-----KYS 399  
 QY 238 TTANGQGOADKFEFTVTSGTNTVTFASGKGTATVSKDDQGNITVMYDVNVDALNVAQLQ 297  
 Db 400 NASNTSSG-----TVSGNAT-----GERTYSNVADG-----LQATDANVNLQDL 441  
 QY 298 NSGNWLDSKAVAGSSGKVIISGNVSPSKGKMDETVNINGNNI--BITRGNKIDI--ATSM 354  
 Db 442 G-----IAASIVVERNNVSGLQNGTGMFQVNNSSGLAKPSPATGANSATGAGSV 491  
 QY 355 TPQFSSVSLGAGADAP-----TLVYGDALNYSKKDKNPVRITNVAPGVKEGDV 404  
 Db 492 ASGNNSSTAFSGGARATANSALCANVANSVADRANSVSGVGNEN--DITNVAAPTQGTDA 549  
 QY 405 TNVAQLKGAQON-----LNMRIDVNDGNAR-----AGIAQIATAGIYQAYLPKSKMA 453  
 Db 550 VNFQOLKISQNTAATYNTQKSELKQDLKRNQSVLSACIASAMASLSITQYTGSSMTT 609  
 QY 454 IGGTYRGEAGYAIYSSISDGNMIIKGTASGNSRHFASASVQW 502  
 Db 610 IGAASVKGQASLSIGVSSISDSGRWVSKLQASMTQGFQIGVGVQW 658

RESULT 10  
 A64905  
 N:Alternate names: protein T  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: A64905; I52440; S34315  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: A64905  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1325 <BLAT>  
 A:Cross-references: GB:AE000248; GB:U00096; NID:g1787783; PIDN:ANC74583.1; PID:g17877  
 A:Experimental source: strain K-12, substrain MG1655  
 R:Cartwright, P.; Tims, M.; Litigow, T.; Hoj, P.; Hoogenraad, N.  
 Biochim. Biophys. Acta 1153, 345-347, 1993  
 A:Title: An Escherichia coli gene showing a potential ancestral relationship to the g  
 A:Reference number: I52440; MUID:94100243; PMID:8274505  
 A:Accession: I52440  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 <RES>  
 A:Cross-references: EMBL:X73295; NID:g312392; PIDN:CA651730.1; PID:g312393  
 A:Note: the difference in length is due to a frameshift error at pos 653  
 C:Genetics:  
 A:Gene: ydek  
 C:Function:  
 A:Description: probably involved in protein translocation apparatus  
 C:Keywords: nucleotide binding; P-loop  
 F:712-719/Region: nucleotide-binding motif A (P-loop)

Query Match 8.9%; Score 226.5; DB 2; Length 1325;  
 Best Local Similarity 24.8%; Pred. No. 0.00018;  
 Matches 146; Conservative 67; Mismatches 241; Indels 135; Gaps 27;  
 QY 1 MNKIYRIIMNSALNMMVWVSELTNR-----NHTKRASATVKT--VLATILPRTVQAS 50

```

Db      1 MRRITRVIMNCTLOVFOACSELTFRAGKTSVNLRRSSLLTFRSLTGLVLLALSAS 60
Qy      51 AATLAKAGDLAKIKOFTYSLKDKLDTLTSVTEKLSFASNGKNVNIISDPTKGNFAKETAG 110
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 GASLLEV-DMDQITNIDTVAAYDAYLVGWGTGVLNLAAGN-ASLFTITTSV-----IG 112
Qy      111 TNGDPTVHLNGIGST--LTDRASVYKVDLNA-----WNIKGVKNVD--FVRTYDVEF 160
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      113 AAEDESGTVNNVLGGTWRLTDSGNMNAAP-LNVGSGTGTILNIKQKHVDGGLR----- 164
Qy      161 LSADT- KTTTVVESDNKKTTEV-----KIGAKTS 190
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      165 LGSSTGCGVTVNVEGDSVLTLEFEIGSYGTGSLNTDKGYVTSIVAIIIGYQAGSNGQ 224
Qy      191 VKEKDKG-LTVNGDKG-----ENGSTDEGEGLVTAKEVIDAVNKAQRMKKTTPAN 241
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      225 VYVEKGEMLINKNDSISIEFOIGNOGTGEATIREGLVTAEMTIIIGNMTG-----IGTLN 280
Qy      242 GGTGQADKFEYTSSTNTVTFASGKGTATVASKDDGNTVMTDVNVDALN--VNOLONS 299
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      281 VO--DODSVYTVRRLYNGYFGNG--TVNISNNGLINNKESLVGVQDSHGCVNVTDKG 335
Qy      300 GNNL-----DSKAVAGSSGKVIISGNVSPSKGMDT-----V 331
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      336 HNNFLCTGEAFRYIYIGADGDELNVSSSEKVDSGITITG--MKETGTGNTTVKDKNSV 392
Qy      332 NINAGNNIEITRNKNIDTATSMTPQFSSVSLAGADAPTLTVDGDALNVGSKKD-NKPV 390
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      393 ITNLGTLNGIDHGEKNNISNOGLVYNSGGSSLGYG---ETGVGNVSIITGGMEWENKAV 448
Qy      391 RTTNVAPYKEDGYTNVAOLKGYAQNLRINVDGNARAGIAQAIATGLVQATLP--G 448
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      449 YTTIGVAGYGNLNIISDGG--KEVSQNIITPLGDKASIGTLNMDATSSSDTYGIVNGNG 506
Qy      449 KSMMAIGGCTYRGEAGYAT-----GYSSISDGSNMWIKKGASGNSR 489
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      507 SGIIVNSCATLNTSTGYGTGNGASGKGLVNISTDLSMLNK-TSSTNAQ 554

```

RESULT 11

C82672

surface-exposed outer membrane protein XF1516 [imported] - *Xylella fastidiosa* (strain 9e)

C:Species: *Xylella fastidiosa*

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: C82672

R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: C82672

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1004 <SIM>

A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001

R:Experimental source: strain 9a3c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Bilones, M.R.S.; Bueno, M.R.P.; Camargo, H.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H

as-Neto, E.; Docena, C.; El-Poriry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kiteajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiz

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

C:Genetics: annotation

A:Gene: XF1516

```

Query Match      8.8%; Score 224.5; DB 2; Length 1004;
Best Local Similarity 23.2%; Pred. No. 0.00017;
Matches 132; Conservative 74; Mismatches 207; Indels 157; Gaps 23;

Qy      2 NKIYRIINMSALNAVYVSELT-----RNHT-----K 28
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      4 NOIYRFFNLISGSSVASHMTNDGCSDDVLRHSGVRNRSVLVLAIGLTVSTHAQSVK 63
Qy      29 RASATVTPVATLTLFAVFOASANTLAKADNLKIKOFTYSLKDKLDTLTSVTEKLSFSA 88
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      64 SPAMTASGVMAVHAHVDQVNRTRADRIPIGDSEL-----MTHMALDKKFPF 110
Qy      89 NGKNVNTSDTKGLNFAKETAGTNGDTTVHLN--GISLTLDRAASVYKVDLNAQMNIKG 145
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      111 GNNISLIGYFSKAFAPNALALGYNSSVTQSANNGVALGSNST-----VSG 155
Qy      146 YKNVDFVRYDVEFLSADTKTITYNVESKDKGKTEYKIGAKTSVIKEKDKLYTGDK 205
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      156 VNSV-----ALGASMASELNVISVGSG--DGYTGPVRRIVNVGDG--IGNND 200
Qy      206 GENGSTDEGEGLVTAKEVIDAVNKAQRMKKTTPANGOTGQADKFEYTSSTNTVTFASGK 265
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      201 AYNKQLODS---VTA-----SYNDVAASVKTIALTNQ-----VTSSVASASGK 241
Qy      266 GTTATVVS-KDDGNTVMTDVNVDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSK 324
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      242 ESTALISGCAQAAVDWTVAF---GGRALINAVGASALGDFSHAKINSTVVGTSVSLQ 297
Qy      325 GKMDFTVNNAG-----NNIEITRNG--KNIDTATSMTPQFSSVSLAGADAPTLTV-- 374
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      298 GGVSLIGYNFVEGSEFNGALDSNLVLQGDV-----SVALGSGSMASEPNAV 347
Qy      375 --DGDALNVGSKDKNKPVRITVAPYKEDGYTNVAOLKGYAQNLRINVDN----- 424
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      348 VESGGLRQPAVR-----RIVAVGDGIGNNDVAVNKSQLDGYTASVNDVAVSKNIAAGAIQ 402
Qy      425 -DGNARAGIAQAIATAGLVQATLPCKSMATG-----GTTYGERAGYATGYSISDG 475
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      403 ITGSGVAVSYSGDSTPAGASAOAGDSSIALGARSRAVNISSALGVGDHAGANSTALG 462
Qy      476 GNMWIKGTA---SGNSRGH---FGASASVYG 499
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      463 G---QSTRISEGTSLGINSFVGQSATNG 488

```

RESULT 12

AF0394

probable adhesin hmwA [imported] - *Yersinia pestis* (strain C092)

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C:Accession: AF0394

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M

deno-Tarragat, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AF0394

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1910 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175

C:Genetics:

A:Gene: hmwA

Query Match 8.3%; Score 210.5; DB 2; Length 1910;

Best Local Similarity 22.6%; Pred. No. 0.0021;

Matches 133; Conservative 80; Mismatches 196; Indels 179; Gaps 26;

Qy 1 MNKIYRIINMSALNAVYVSE---LTRNHTKASATVTAVALT-----LLFATVQSA 51
 :
Db 734 LSKSGRVLPD--INGNIYKAVYGLRVNNSQLSARDKFAVAVNTGVDGFLRDSHYTATS 791





A:Gene: ECS2117

Query Match 8.2%; Score 208.5; DB 2; Length 1343;  
Best Local Similarity 23.6%; Pred. No. 0.0017;  
Matches 140; Conservative 72; Mismatches 239; Indels 141; Gaps 27;

QY 1 MKKIRIINSLAMVAVVSELT-----NHKRSATYKTA--VLATLLPFTQAS 50  
DB 1 MKKIRIINSLAMVAVVSELT-----NHKRSATYKTA--VLATLLPFTQAS 50  
QY 51 ANTLKAGDNLKIKQFTYSLKDKDLDLT-----SVTEKLSFSANGKNVNTSPDK 100  
DB 61 GASLEV-DNGQITNIDTVAIYAVGWTGVLNLAGSN-ASLITTTTSTV-----IG 112  
QY 111 TNGDPTVHLNGIGST--LTDRAASVYKVDVLAAGMNIKGVKNVDFRTYVEFLSADPKTT 168  
DB 113 GNEDESGTYVNLVGLTFWRLYDSCNNAP--LNVGSGGTGLINIKOKGHVDG-GYLRIGTQAA 170  
QY 169 ---TYNVEKDKGKTEV-KIG-----AKTSVKEKD 196  
DB 171 GVGTAVVEDESVLTLELFEISYGTSLNITDKGVTSIVAILGQYQANSKGVVVEKG 230  
QY 197 GK-LVTGKDKG-----ENGSTDEGEGLYTAKEVIDAVNKAAGRMKTTANGOTGA 247  
DB 231 GEMLIKNNDSSIEFOIGNOGTGBATIREGLITAEITIGGNATG---VGLTNDV--DQ 284  
QY 248 DKFEYVTSCTNVTFAAG-----KGTATVSKDDOGNITVAVDVN 286  
DB 285 DSVITVRLYNGYFGAVNISNGLINNKKEYSLVGVODGSHGVAVVTDKGMHNL---G 341  
QY 287 VDDALNVNOLNSGMNLDKAAVAGSSGKYISGNVSPSKKMDETVINANGN-----NIE 340  
DB 342 TEAFERYIYIGDAG--DDELNVSRGKVDSGIITAG--MKET--GTGNLTVDKDNV 392  
QY 341 ITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSK-----KDN 387  
DB 393 ITNLGNLGYDGHGEMINISNEGL-----VVSNGSSSLGGETGVGKYSITTGGEWEN 445  
QY 388 KPVRTITNAPGVKESDVTNVAOLKGYAQNLRIDNVGNARAGIAQATATAGLVQAYLP 447  
DB 446 KNYTTIGVAGVGNINISDGC--KFVSQNTFLGDKASIGITLNLMDATSSPDVGINVG 503  
QY 448 ---GKSMMAIGGTYRGEAGYAI-----GYSSISDGGNWIIGKASGNSR 489  
DB 504 NFGSGIVNNGATLNSTGYFTIGGNASGKGIIVNISTDSLMNKL-TSSSTNAQ 554

RESULT 15

G64964  
hypothetical protein b2000 - Escherichia coli (strain K-12)

C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: G64964

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
A:Rose, D.J.; Mau, B.; Shao, Y.

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G64964

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1091 <BLAT>

A:Cross-references: GB:AE000291; GB:U00096; NID:91788298; PIDN:MAC75061.1; PID:91788309;  
A:Experimental source: strain K-12, substrain MG1655

C:Keywords: nucleotide binding; P-loop  
F:683-690/Region: nucleotide-binding motif A (P-loop)

DB 57 LNTCYRLVNNHMTGAFVVAASELARRARKGVAVALSLAATVSLFVLAADIVYHGETVN 116  
QY 51 ANTLKAGDNLKIKQFTYSLKDKDLDLT-----SVTEKLSFSANGKNVNTSPDK 100  
DB 117 GGTLANHND---QIVFGTNGMTISTGLEYPDNEAMTGGQWODGGTANKTYYTSG-- 170  
QY 101 GINFAKETAGTNGDPTVHLNGIGSTLTLDRAASVYKVLNA-----GM 141  
DB 171 GIQ-RVNPBGSVSDPVISAGG-GOSLOGRA--VNTLLNGGEQOMHEGAIAATGTVINDGM 226  
QY 142 NI-----KGVKNVDFRTYVEFLSADPKTTTVNVEKDKGKTEVKIG-A 187  
DB 227 QYVKGCTVATDVTVAITGABGPDANGDTGQVRBDATKTTIN-----KNGRIYAAEGTA 282  
QY 188 KTSVIREKDKGLVTKDKGNGSSSTDE---GEGLV---TAKEVIDAVNKAAGM--- 235  
DB 283 NTTVV-----YAGDDQTVHGHALDPTLNGGYQYVHNGGFASDPV--VNSDGMQIVKNG 333  
QY 236 ---KTTTANGOTGQADKFEYVTSCTNVTFAAG-----KGTATVSKDDOG-NITVAVDVN 287  
DB 334 GVAGNTTVN-OKGRL-OVDAGGTATNVTLLKOGALVTSAAVTV-----GINRLGAFSVYE 387  
QY 288 GDALNVNOLNSGMNLDKAAVAGSSGKYISGNVSPSKKMDETVINANGNIEIRNGKN 347  
DB 388 GRADNV-VLENGG-RLD-----VLTGHTATN-----TRYDDGGTLDV-RNG-- 425  
QY 348 IDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSKKDKNKPVRTITNAPGVKESDVTNV 407  
DB 426 ---GTATL-----VSMGNG--VLLADSGAAVSGTRSDGK-----AFSIGGOADAL 467  
QY 408 AOLKGYAQNLRIDNVGNARAGIAQATATAGLVQAYLPKSKMAIGGTYRGEAGYAI 467  
DB 468 MLEKSSFTLN-----AGDTARDTT-----VNGGLETFARGTGLA 501  
QY 468 GYSSISDGGNWIIGKASGNSR 487  
DB 502 GTTTLNNGAIIILSGKTYVNN 521

Search completed: October 6, 2003, 09:33:25  
Job time : 17.3699 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.75217 Seconds  
(without alignments)  
3045.266 Million cell updates/sec

Title: US-09-771-382-27  
Perfect score: 2544  
Sequence: 1 MNKIYRIINWSALNANVVS.....TASGNSRGHFGASASVGYQM 502

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	226.5	8.9	1325	1 YDEK_ECOLI	P32051 escherichia
2	210	8.3	1286	1 AIDA_ECOLI	Q03155 escherichia
3	208	8.2	1039	1 AG43_ECOLI	P39180 escherichia
4	175.5	6.9	2003	1 YDBA_ECOLI	P33666 escherichia
5	173	6.8	1608	1 HLVA_SERMA	P15320 serratia ma
6	173	6.8	2249	1 OMPA_RICRI	P15921 rickettsia
7	172	6.8	1567	1 ICEN_XANCT	P18177 xanthomonas
8	169.5	6.7	1577	1 HLVA_PRCMT	P16466 proteus mir
9	169	6.6	1655	1 OMPB_RICCN	Q9K843 r outer mem
10	168.5	6.6	1654	1 OMPB_RICRI	Q53047 r outer mem
11	165	6.5	1645	1 OMPB_RICRY	P96989 r outer mem
12	165	6.5	2334	1 WAPA_BACSU	Q07883 bacillus su
13	164.5	6.5	1025	1 SLAP_CAOCR	P35828 caulobacter
14	164.5	6.5	1861	1 APU_THETU	P38536 t amylopull
15	164	6.4	1933	1 BIGA_SALTY	P25927 salmonella
16	163.5	6.4	9933	1 SLAP_CAMEF	P35827 campylobact
17	161.5	6.3	1148	1 ICER_PSEXS	Q30611 pseudomonas
18	161.5	6.3	2021	1 OMPA_RICCN	Q52657 rickettsia
19	160.5	6.3	1300	1 120K_RICRI	P14914 rickettsia
20	160.5	6.3	1643	1 OMPB_RICPR	Q53020 r outer mem
21	158.5	6.2	507	1 FLIC_SALON	Q06974 salmonella
22	158	6.2	1153	1 YPJA_ECOLI	P52143 escherichia
23	157	6.2	1153	1 PVDB_PLAKN	P50493 plasmodium
24	156.5	6.2	928	1 FLIC_SALBE	Q06968 salmonella
25	156.5	6.2	507	1 PM10_CHIRN	Q91B55 chlamydia p
26	156.5	6.2	1656	1 OMPB_RICJA	Q06653 r outer mem
27	155.5	6.1	350	1 FLIC_SALFL	Q08860 shigella fl
28	155.5	6.1	2358	1 YEED_ECOLI	P76347 escherichia
29	154	6.0	497	1 FLIC_SALRO	Q06982 salmonella
30	153.5	6.0	497	1 FLIC_ECOLI	P04949 escherichia
31	153	6.0	1200	1 ICEN_PSEXS	P06620 pseudomonas
32	152	6.0	504	1 FLIC_SALBU	Q06969 salmonella
33	152	6.0	504	1 FLIC_SALDU	Q06971 salmonella

34	151	5.9	1196	1 ICEN_PSEXS	Q33479 pseudomonas
35	151	5.9	1848	1 CBPA_CLOCL	P38058 clostridium
36	150.5	5.9	880	1 LYTD_BACSU	P39848 bacillus su
37	150.5	5.9	918	1 YMB_CAEEL	P34487 caenorhabdi
38	150	5.9	504	1 FLIC_SALMC	Q06981 salmonella
39	150	5.9	504	1 FLIC_SALSE	Q06983 salmonella
40	150	5.9	917	1 HXA3_HAEIN	P45355 haemophilus
41	149.5	5.9	1288	1 VACA_HELPJ	Q92KW5 helicobacte
42	149	5.9	504	1 FLIC_SALNA	O52959 salmonella
43	148.5	5.8	2660	1 YEED_ECO57	O8X8V7 escherichia
44	148	5.8	948	1 HPTI_DEIRA	P56867 deinococcus
45	147.5	5.8	1167	1 CAGA_HELPJ	Q9ZLE1 helicobacte

## ALIGNMENTS

RESULT 1  
YDEK\_ECOLI STANDARD: PRT; 1325 AA.  
AC P32051: P76140; P77168:  
DF 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical lipoprotein ydek precursor (ORF1).  
GN YDEK OR ORF1 OR B1510.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRATN-K12; MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 595-1325 FROM N.A.  
RX MEDLINE=94100243; PubMed=8274505;  
RA Cartwright P.J., Tjoms M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;  
RT "An Escherichia coli gene showing a potential ancestral relationship  
to the genes for the mitochondrial import site proteins ISP42 and  
KOW38.";  
RL Biochim. Biophys. Acta 1153:345-347(1993).  
CC - SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
(Potential).  
CC - SIMILARITY: TO E. COLI YFAL.  
CC - SIMILARITY: SOME TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  
ISP42 AND KOW38.  
CC - CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
FRAMESHIFT IN POSITION 653.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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CC EMBL; AF000248; AAC74583.1; -  
 CC EMBL; D90793; BAA15190.1; ALT\_INIT.  
 CC EMBL; D90794; BAA15197.1; ALT\_INIT.  
 CC EMBL; X73295; CAA51730.1; ALT\_FRAME.  
 CC PIR; A64905; A64905.  
 CC Ecocore; E611780; ydek.  
 CC PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 CC Hypothetical protein; Membrane; Lipoprotein; Signal;  
 CC Complete proteome.  
 CC SIGNAL 18  
 CC CHAIN 19 1325  
 CC LIPID 19 1325  
 CC CONFLICT 884 884  
 CC CONFLICT 1317 1317  
 CC SEQUENCE 1325 AA; 136514 MW; 26A3A06FA19AD7D CRC64;

Query Match 8.9%; Score 226.5; DB 1; Length 1325;  
 Best Local Similarity 24.8%; Pred. No. 0.0018;  
 Matches 146; Conservative 67; Mismatches 241; Indels 135; Gaps 27;

QY 1 MKKIRITWNSALNANWVSELT-----NHTKRASATYKTA--VIATLLEFATVOAS 50  
 DB 1 MKRIRIVNCTLOVFOACSELTFRAGKSTVNLKSSGLTFKRLTGLVLLALSGSAS 60  
 QY 51 ANTLKAGNLKIKOFTYSLKDLDTLTSVTEKLSFSANGKNVNTSDPKGILNFAKETAG 110  
 DB 61 GASLEV-DNDQITNIDTDAIDAYLVGWTGCVLITLILAGN-ASLTITITSV-----IG 112  
 QY 111 TNGDTVHLNGIGST-LTDRAASVKDVLNAG-----WIKGVNVD--FVRTYDVEF 160  
 DB 113 ANDESEGTVNVLGWTGRLYDSCNNARP-LNWQSGTGLTIKQKHVOGGLR-----164  
 QY 161 LSADP-KTTTVNVEKDKKTEV-----KIGAKTS 190  
 DB 165 LGSSTGVGVTVNVEGDSVLTLELFEIGSYGTSLINTDKGYVTSSIVAILGVOAGSNGQ 224  
 QY 191 VIKERDK-LVTGKRGK-----ENGSTDEGEGLVTAKEVIDAVNKAAGRMKTJAN 241  
 DB 225 VVEKGEEMLIKNNSSIEFOIGNOGTGEATIREGLVTAETITIGNATG-----IGILN 280  
 QY 242 GQFGADKFEVYVSTNVTFAVGKGTATVSKDDGNTVMYDVNVGDLN--VNQLONS 299  
 DB 281 VO--QDSVITVRLYNGYFGNG--TVNISNGLINKKEYSLVGVQDSHGCVNVTDKG 335  
 QY 300 GWNL-----DSKAVAGSSKVIYISGNVSPSKKMDT-----Y 331  
 DB 336 HNNFLGTGEAFRYIYIGADGDELNVSSSEKVDSSGIIITAG--MKETGTGNTVTKDNSV 392  
 QY 332 NINAGNINIEFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDDALNVGSKKD-NRPV 390  
 DB 393 ITNLGTNLGIDHGHGEMNINSGLVVSSNGSSSLGIG-ETGVGNVSTITGMEVKNV 448  
 QY 391 RTTNVAPVKEGDVTVAQLGVAQNLLNRIDNVGNARAGIAQAIATAGLVQAVLP--G 448  
 DB 449 YTTIGVAGVNLINISDGG--KFSQNTIFELGDKASGIGITLNLMDATSSPDVGIWVNGF 506  
 QY 449 KSMALIGGTYRGEAGYAI-----GYSSISDGGNNIILKTAGSNGSR 489  
 DB 507 SGIVNVSGATLNTSTGYGFIGGNASGKGIIVNISTDLSNLK-TSSTNAQ 554

## RESULT 2

AIDA-ECOLI STANDARD; PRT; 1286 AA.  
 AC Q03155;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adhesin aidA-1 precursor.

GN AIDA-1.  
 OS Escherichia coli.  
 OG Plasmid p186.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 CC NCBI\_taxid=562;  
 CC (1)  
 CC SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.  
 CC STRAIN=O126:H27 / 2787;  
 CC MEDLINE=92326638; PubMed=1625582;  
 CC RA Benz I, Schmidt M.A.;  
 CC RT "AIDA-1, the adhesin involved in diffuse adherence of the  
 CC diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is  
 CC synthesized via a precursor molecule."  
 CC Mol. Microbiol. 6:1539-1546(1992).  
 CC -1- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE  
 CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI  
 CC TO EPITHELIAL CELLS.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane.  
 CC  
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CC EMBL; X65022; CAA46156.1; -  
 CC PIR; S28634; S28634.  
 CC InterPro; IPR006315; Autotransport.  
 CC InterPro; IPR005546; Autotransporter.  
 CC InterPro; IPR004899; Pertactin.  
 CC Pfam; PF03797; Autotransporter; 1.  
 CC Pfam; PF03212; Pertactin; 1.  
 CC TIGRFAMS; TIGR01414; autotrans\_barl; 2.  
 CC Cell adhesion; Signal; Outer membrane; Plasmid.  
 CC SIGNAL 1 49  
 CC CHAIN 50 1286  
 CC PROPEP ? 1286  
 CC SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 8.3%; Score 210; DB 1; Length 1286;  
 Best Local Similarity 21.1%; Pred. No. 0.0012;  
 Matches 139; Conservative 83; Mismatches 226; Indels 210; Gaps 31;

QY 1 MKKIRITWNSALNANWVSELTNRH-----FKRASATYKTA--VIATLLEFATVOAS 51  
 DB 1 MKKAVSIITWNSRQMIYASSELARHGFLAKNTLLVLAVYSTIGNAFAVINSGLV-SSG 59  
 QY 52 NTLKAGDNLIKQFTYSLK-KDLDTLTSVTEKLSFSANGKNVNTSDPKGILNFAKETAG 110  
 DB 60 GYVSSGEL-----QIYVSGRGNMNAVNSGQIYV--NGKRTATVNSS--GSQVWG 109  
 QY 111 TNG---DTVHLNGIGSTLTDRAASVKDVLNAGNMIKGVNVDVRYTDYEFLSADPK- 166  
 DB 110 TSGATISTIVNSGQIQRVSSGVASATNLSCGAONIYMLGHAAS--NTVIFSGNQT 164  
 QY 167 -----TTTVNVEKDKKTEVIGKATSV-----IKERDKLVTKDNGEN--G 209  
 DB 165 FSGGTLTDSNTISSGGQOVYSSGVAISNTTINSSGACNLLSEGAISTHSSGNOYISAG 224  
 QY 210 SSTDEGEGLVTAKEVIDAVNKAAGRMKT-----TTANQOT-----GQADKFEVYVSG 256  
 DB 225 ANATP-----TIVNSGGFQRVNSGAVATGTVLSSGQONVSSGSAISVSVNSG 273  
 QY 257 TNVTFASGKGTATVYSKD-----DGNITVMYDVNV-----GDALNVN--QLOV 298  
 DB 274 VQVTFAGATVTDITVNSGONISSGGIVSETVAVSGTONIYSSGSAISANIKSQIYN 333  
 QY 299 S-GWMLDSKAVAG-----SSGKVI--SGNVSPSKKMDDEVNINAGNINIEITNG 345  
 DB 334 SEGTAINTLVSDGQYHIRNGIGASGTTVNSGIVNISSGGIYAESITINSGTILKVLSDG 393

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OY 346 -----KNID-----IATSMTPQPSVSLGAGAD 368
D 394 YARGTILNNSGRNENSGVSYNAMINTGNOXYIISDGEATAIVTSGQRIN--SGGT 451
OY 369 AP-----TLS-----VDGDLNNGSKK-----DNKPRVITNVPCKEGDVT 405
D 452 APQNSVWVYRTVSSAKPDAIEVSGKQTVYLMRGIMVSNFLTAVMSMFGTASGANY 511
OY 406 NVA-QIKVAVQNNNNKNDVNDGN-----ARACT 432
D 512 NLSGRNNAFNVGVTILNDEGRQYVSGATATSTVGNNGREYVLSGGITDGVLSNG 571
OY 433 AQAATATAGLQVAVL-----PGKSMAIG-----GGTYRGEAGYVAGYSISDGN 477
D 572 LQAVSSGGRASATVINEGGAQFYDGGQVYGTINKNGTIRVDSGASALNIALSSGN 629

RESULT 3
AG43_ECOLI STANDARD: PRT: 1039 AA.
ID AG43_ECOLI STANDARD: PRT: 1039 AA.
AC P39180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Flufling protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MCL655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G., Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horinouchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 mln region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
RT 43, a unique protein complex associated with the outer membrane of
RT Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;

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RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RP GENE NAME.
RX MEDLINE=97257509; PubMed=9103983;
RA Henderson I.R., Meehan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
RT determines colony morphology and autoaggregation in Escherichia coli
RT K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
CC FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
CC -1- SIMILARITY: TO ADHESIN AID-I AND TO BORDETTELLA PERTACTIN.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; AE000291; AAC75061.1; ALT_INIT.
DR EMBL; D90838; BAA15825.1; ALT_INIT.
DR EMBL; D90839; BAA15832.1; ALT_INIT.
DR EMBL; U24429; AAB47869.1; -.
DR HSSP; P07505; ISR.
DR Ecogene; EG12686; flu.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR004899; Pertactin.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03212; Pertactin; 1.
DR TIGRFAMs; TIGR01414; autotrans_barl; 1.
KW Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551
FT CHAIN 552 1039
FT VARIANT 2 2
FT VARIANT 41 42
FT VARIANT 46 46
FT VARIANT 157 157
FT VARIANT 188 188
FT VARIANT 303 305
FT VARIANT 320 320
FT VARIANT 372 372
FT VARIANT 493 493
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FT VARIANT 585 585
FT VARIANT 709 709
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FT VARIANT 829 835
FT VARIANT 845 847
FT VARIANT 855 855
FT VARIANT 888 888
FT VARIANT 1025 1025
FT CONFLICT 61 63
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBEO CRC64;
Query Match 8.28; Score 208; DB 1; Length 1039;
Best Local Similarity 23.28; Pred. No. 0.0012;
Matches 130; Conservative 65; Mismatches 197; Indels 168; Gaps 32;

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QY 1 MAKIIRITWNSALNMYVVSSELTNRNHTKASATVTAVALTLFATVQA-----S 50  
 DB 5 LNTCRLVNMHTGFAVSESLARARGRGVAVALSLAAVYSLPLVLAIVYHGETV 64  
 QY 51 ANTLKAGNLKIKOFTYSLKNDLTL-----SVGTCKLSFSGNKNVNTSDK 100  
 DB 65 GGTLANHNDL-----QIVFGTTNGMTISTIGLEVPDNEANGVODGGTANKTIVTSG-- 118  
 QY 101 GINFAKETAGTNGDTVHLNGISGTLTDRASVKKVLA-----GM 141  
 DB 119 GLQ-RVNPBGVSVDIVISAGG-QGSLQGRA--VNTTLNGEGQWMEGAATGTVINDKGM 174  
 QY 142 NI-----KQYKANDFVFTYVFEFLSADTKTTTVNVESSKNGKTEVYKIG-A 187  
 DB 175 QYVKKPGVATDVTVNTVGAEGGPDANCGDGFVRDPAVTTIN-----KNGROIYRAEGTA 230  
 QY 188 KTSVKEKDKGLVTKDKGNGSSTDE-----GEGLV-----TAKEYIDANVKAQWBM----- 235  
 DB 231 NTTV-----YAGDDQVYHGHADDTLNGSYQYVHNGTASDIY--VNSGMOIVKNG 281  
 QY 236 ---KTTTANGQTGAADKEFTVYSGTNYTFASG---KGTATVSKDDOG-NITVWYDVV 287  
 DB 282 GYAGNTTVN-QKGR-LQVAGGTATNTLKQGGALVTSTAATVT-----GINELGAFSYVE 335  
 QY 288 GDLVNVNLONGNMLDSKAVSSGKYISGNVSPSKKMDTVNINMGNIEITRNKGN 347  
 DB 336 GADNV-VLENG-RLD-----VLTGHTATN-----TRVDGGTLDV-RNG-- 373  
 QY 348 IDIATSMTPQFSSVSLAGADAPTLSDGDALNVGSKDKNKPVRATNVAPGVEGDVTV 407  
 DB 374 ---GTATL-----VSMGNG--VLLADSGAAVSGTTRSGK-----AFSIGGGQADAL 415  
 QY 408 AOLKVAONLNRIDNVGNARAGIAQAIATAGLVAVLPGKSMAGGGTYRGEAGYAI 467  
 DB 416 MLEKSSSEFLN-----AGDTATDT-----VNGLETFARGGTILA 449  
 QY 468 GYSSISDGNMIIKGTASGN 487  
 DB 450 GTTTLNNGAILTLTSGTYVN 469

RESULT 4  
 YDBA\_ECOLI  
 ID YDBA\_ECOLI STANDARD: PRT: 2003 AA.  
 AC P3366; P76087; P76088; P76856; P76857; P76859;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein ydba.  
 GN YDBA OR B1401/B1405.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97251357; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.,  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97251357; PubMed=9097039;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa K.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,

RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horichi T.;  
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 28.0-40.1 min region on the linkage map";  
 RL DNA Res. 3:363-377(1996).  
 RN [3]  
 RP SEQUENCE OF 464-2003 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=92190338; PubMed=1665988;  
 RA Moszer I., Glasner P., Danchin A.;  
 RT "Multiple I. insertion sequences near the replication terminus in  
 RT Escherichia coli K-12";  
 RL Biochimie 73:1361-1374(1991).  
 CC -I- SIMILARITY: TO S. TYPHIMORIUM ORF NEAR CYSG (AC P25928).  
 CC -I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR  
 CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
 CC BETWEEN AMINO ACIDS 839 AND 840.  
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Query Match 6.9%; Score 175.5; DB 1; Length 2003;  
 Best Local Similarity 22.8%; Pred. No. 0.12;  
 Matches 119; Conservative 69; Mismatches 184; Indels 151; Gaps 27;

QY 33 TYKTAVLATLLEFATVQAASANTLAKADNLKIKOFTYSLAK-----DLTDLTSVGTCKL 84  
 DB 151 TEKTLTIDSVFTYENADGTISLDS--NGRATINLMOIDEANNTVALEGSAGATRW 209  
 QY 85 SEFANGKNVNTSDTKGIN-----FAKETAGT-----NGDTVHLNGISGTL 126  
 DB 210 QYNHNGELY-ITGDAAVYNNNGKTYVDKSGTGINNGKVIQDGLDVSQGGHIGDI 268  
 QY 127 TDRAA-----SVKDVLMGWNITKQYKANDFVFTYVFEFLSADTKTTTVNVESSKNG 178  
 DB 269 TGDSATVNNKGTMTYTDSESMGQIDGDKAIYNNGEESTITNGGTGTQINGDPAVANNNG 328  
 QY 179 KTEVKIKAKTSV---IKEKDKGLVTKDKGNG-----SSTPEGGLVYAKE-- 223  
 DB 329 KTT---VQKDSGTGEINGNNGKVIQDGLDVSQGGHIGDITGDSATVNNKGTMTYDPE 385  
 QY 224 ---VID---AVNRAGMRKTTTANGQTGAADKEFTVYSGTNYTFASGKGTATVSKDD 275  
 DB 386 SIGIYDDGQAVVNNGG---ESALINGGT-----TQINGDPAV-ANNNGKTYVDKDS 435  
 QY 276 QCNITVMTDVNVGDLNVLNQLONGNMLDSKAVSSGKYI-SGNVSPSKKMDTVNIN 334  
 DB 436 TGT-----EIAGNNGKVIQDGLDVSQGG----- 458  
 QY 335 AGNNIEITRNKNIDTATSMT---PQFSSVSLAGADAPTLSDGDALNVGSKDKNKPVR 391  
 DB 459 -GHGIDITGDSATVNNKGTMTYDPE---SIG-----TQIDGQAVNNNGES---T 503  
 QY 392 ITNVAPGVEGDVTVNAOLKVAONLNR-IDNVGNARAGIAQAIATAGLVAVLPGKSMAG 450  
 DB 504 ITNGGTG-----TQINGDPAVANNNGKTYVDKSGTGTG-TKTAGNIGIYV--LDG-S 550

QY 451 MMAIGGTYRGEAGYAIYSSISDGGNMIKGTASGNSRCHFG 493  
Db 551 LFTVGG-----AHGVENIGDNGTVNNKGDIVYSDGSIG 584

RESULT 5  
HLA\_SERMA STANDARD: PRT; 1608 AA.  
ID HLA\_A\_SERMA  
AC P15320;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DE 01-NOV-1990 (Rel. 16, Last annotation update)  
DT Hemolysin precursor.  
GN SHLA.  
OS Serratia marcescens.  
OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
RX STRAIN-SNB;  
RX MEDLINE=88257037; Pubmed=3290200;  
RA Poole K., Schiebel E., Braun V.,  
RT "Molecular characterization of the hemolysin determinant of Serratia  
marcescens.";  
RL J. Bacteriol. 170:3177-3188(1988).  
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
DEFINED.  
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
REQUIRES SHLB FUNCTION.  
CC -1- SUBCELLULAR LOCATION: Outer membrane.  
CC -1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M22618; AAA50323.1; -  
DR PIR; A28182; A28182.  
KM Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL  
FT CHAIN 31 1608 HEMOLYSIN.  
SQ SEQUENCE 1608 AA; 165078 MW; D6698476FE7DAD51 CRC64;

Query Match 6.8%; Score 173; DB 1; Length 1608;  
Best Local Similarity 21.5%; Pred. No. 0.12; Indels 232; Gaps 30;  
Matches 141; Conservative 71; Mismatches 213;

QY 24 RNHTKR-----ASATVKTAVLATLFAVQASANTLAKGDNLIKQFTYSJKDL 73  
Db 460 RNTTSSLRTGRMSNDESESLKASLRS-----EGELTKKGRNVTGAGAVHQRL 512

QY 74 T-----DLTSVTEKLSFSANG--NKVNITSPTKLNFKEKTAGTNGDT 115  
Db 513 TIDADNOIOYOVKTANAKAVRDDKTSWGGIGGDNKN--SNRREISHASEL--TSGG- 567

QY 116 TVHLNG-IGSTLDRRAASVADVNLAMGNIKGVNVPFRV-----DVEPELSAD 164  
Db 568 TLRLNGOOGVTI-----GSKARGQGGVETATHGRLIDNALSTVDKIDAR 615

QY 165 TKTT---TVNESKDNKK-----TEVKGAKTSVIREKDEKLV-----TG 202  
Db 616 TGTAFNITSSSHKADNSYOSTASSELKSDTNLTLVSHKADVDIGSQVASGSELVSKEK 675

QY 203 K---DKGENSGSTDEBGLVT---AKEVIDAVNKAQWRM-----KTT----- 238  
Db 676 NINVKAEROQNIIDEKTAITLVNGYAKADKQYRAGLRIRIEHTRDSEKTYRTENSASLS 735

QY 239 -----TANGOTGQADKEFTYSGTNTVFAFGKGT----- 269  
Db 736 GGSVKLKAEDVTFSSGKLVADKGDASVSANKVSFLAADKTSNTEQRTIGGCFYTTGG 795

QY 270 -----TVSKDQGNITVMVDVNDALNVNQLONGSMND 304  
Db 796 IDKLSGVEAGEYENNNKTOAQSSKAITSGSDVKGNLT-----INRDKLTQOGAGHSVGAV 851

QY 305 SKVAGSSGKIVISGNVSPSKMDEYVNIAGNNIETTRGKNIDATSMTPPPSSVSLG 364  
Db 852 QENAGVDHLAADTASTTTTKTDVGNV-----GAVNDVSAVTRPVERAAGKA 900

QY 365 A-----GADPTLSVDGDLNVMSKK--DNKPYRITNVAPGV---KEGPV-- 404  
Db 901 AKLDATGVINDIGGICGAPNVGLDIGAGGSSSEKSSSAQVSSVQAQSIDINAKGEVRD 960

QY 405 -TNVAQLKGVAAONLN-----NRIDNVGNMRAGIQAIAVAGLVQAALPKSMM 452  
Db 961 QGTQYQASKG-AVNLTADSHRSEPAANRODEQSRDPR-----GSAG-VRYVTTGSDL 1011

QY 453 AIG-----GGTYREAGYAIYSSISDGGN-----IKGTASGNSRCHGASA 496  
Db 1012 TVDAKEGGTQQRNSNSASQAVTGSIDAANGINNVKKAIDYQGTALNGRGKTAVNA 1068

RESULT 6  
OMPA\_RICRI STANDARD: PRT; 2249 AA.  
ID OMPA\_RICRI  
AC P15921;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
antigen) (rOmpA) (rOmp A).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria: Proteobacteria: Alphaproteobacteria: Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-R;  
RX MEDLINE=90354033; Pubmed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.,  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990).  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PTM: GLYCOSYLATED (PROBABLE).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
CC  
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CC  
CC EMBL; M31227; AAA26380.1; -  
DR PIR; A41477; A41477.  
DR InterPro; IPR006315; Autotransport.  
DR InterPro; IPR005546; Autotransporter.  
DR Pfam; PF03797; Autotransporter; 1.  
DR TIGRFAMs; TIGR01414; autotransp; 3.  
KM Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28  
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.  
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 212 286 A (TYPE I).

FT REPEAT 287 358 B (TYPE II).  
FT REPEAT 359 430 C (TYPE II).  
FT REPEAT 431 505 D (TYPE I).  
FT REPEAT 506 577 E (TYPE II).  
FT REPEAT 578 652 F (TYPE II).  
FT REPEAT 653 724 G (TYPE II).  
FT REPEAT 725 799 H (TYPE I).  
FT REPEAT 800 874 I (TYPE I).  
FT REPEAT 875 949 J (TYPE I).  
FT REPEAT 950 1021 K (TYPE II).  
FT REPEAT 1022 1093 L (TYPE II).  
FT REPEAT 1094 1165 M (TYPE II).  
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).  
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.8%; Score 173; DB 1; Length 2249;  
Best Local Similarity 24.8%; Pred. No. 0.18; Mismatches 225; Indels 168; Gaps 31;

Matches 148; Conservative 56; Mismatches 225; Indels 168; Gaps 31;

QY 27 TKRASATVKTAVLATLLFATVOASANTLKAGDNLKIKOFTYSLK---DLTDLTSYGT 81  
DB 714 TFGTNSVTGTDIGNTNMLATVAVGATATLGAV-IRATFTKLNNASVLTLTNNANAVLT 772  
QY 82 EKLSFSANGKNVNTSDTKGNFA-KETAGTNGDT-----TVHLNG--IGSTLT 127  
DB 773 GADINTTGGDVGVLN---LNGALSOYTGDIGMTNSLATISVGAGTATLGAVIKATTT 828  
QY 128 --DRAASVKDLNAGMNIKGVKNDPFRITYDVEFLSADTKTTTVNESKNGKTEYKI 185  
DB 829 KLTNAASVLTLTNNANAVLTGA--VDNTTGGDNGVLNGLALSOYTGDIGMTNSLATISV 886  
QY 186 GAKT---SVYKEKDGKL-----V 200  
DB 887 GAGTATLGAVIKATTTKLNNASVLTLTNNANAVLTGADNTTGGDNGVLNGLALSOV 946  
QY 201 TGKXKNGSGST-DEGEGIVT---AKEVIDANNAKGMKRTTANGQGTGQAKFEVYT 254  
DB 947 TGDIGNTNSLATISVGAGTATLGAVIKATTTKLTDASAVKFTNPVYVGTALDNTGNAN 1006  
QY 255 SGTNVTFASGKGTATVASKDOGNITVYDVNVDALNVQNLQNSGMNLSKAVAGSSGK 314  
DB 1007 NGI-VTFGTNSTVGNV-----GNTNMLATVAVAGL--LQVGGVAVKANTINLTNDSA 1058  
QY 315 VISGNVSPSKGKMDIYNINAG-----NIEITRNGKNIDITATMTPOFSSVSLGAGADA 369  
DB 1059 VTFNPVYVGTALDNTGNANNGIYTFGTNSTVGNVGN-----TNALATVAVAG-- 1108  
QY 370 PTLSDVDGAL--NVGSKKDN-KPVRITNVAPGVKEGDTTNAQLKGVANQNLNRRIDNDG 426  
DB 1109 -LLQVGGVAVKANTINLTNDSAVTFTN--PVVVTGALDNTG-----NANNGIYFTTG 1158  
QY 427 NARA-----GIAQAIAT-----AGL-VOAYLPGKSMMA-----IGGTYRG 461  
DB 1159 NSTYTGDIGMTNMLATVAVAGITLQA---GGSLAANNIDFGASTLEFNPDLGG----- 1211  
QY 462 EAGTAIGT---SSISDGNWIK-----GTASGNSRGH---FGASASVG 499  
DB 1212 --GRAIPYFKGALANGNAILNNTKLTFTASHLTIETVAEINIGAGNLTFTDASVG 1266

RESULT 7

ID ICEN\_XANCT STANDARD; PRG; 1567 AA.

AC P18127;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ice nucleation protein.

GN INAX.

OS Xanthomonas campestris (pv. translucens).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI\_TaxID=343;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=X565;  
RX MEDLINE=91080859; PubMed=2259339;  
RA Zhao J., Orser C.S.;  
RT "Conserved repetition in the ice nucleation gene inax from  
RT Xanthomonas campestris pv. translucens.";  
RL Mol. Genet. 223:163-166(1990).  
CC -I- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE  
CC CRYSTALLIZATION IN SUPERCOOLED WATER.  
CC -I- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS  
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A  
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.  
CC -I- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE  
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.  
CC -I- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN  
CC FAMILY.

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CC EMBL; X52970; CAA37140.1; -.  
CC HSP; P06620; IINA.  
CC InterPro: IPR000258; Ice\_nucleatn.  
CC Pfam; PF00818; Ice\_nucleatn, 81.  
CC PRINTS; PR00327; ICENUCLEATN.  
CC PROSITE; PS00314; ICE\_NUCLEATION; 57.  
CC KW Ice nucleation; Repeat; Outer membrane.

SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;  
Query Match 6.8%; Score 172; DB 1; Length 1567;  
Best Local Similarity 20.9%; Pred. No. 0.13; Mismatches 237; Indels 94; Gaps 21;  
Matches 107; Conservative 74; Mismatches 237; Indels 94; Gaps 21;

QY 20 SELFRNHTKRASATVKTAVLATLLFATVOASANTLKAGDNLKIKOFTYSLKDLTDLT-- 77  
DB 808 SDITAGYSGTGTAAADSTLIAGYSGTGTSGDSSLTLAGY-----STQARSSDVTAG 861  
QY 78 -----SVTEKLSFANGKNVNTSDTKGNFAKETAGTNGDTTVHLNGJSTLTDRAS 132  
DB 862 YGSGTGAADSTLIAGY-----STQAGSDSLTA---GYGSGTARKGS 904  
QY 133 VKDVLNAGMNIKGVKND--FVRTYDVEFLSADTKTTTVNESKNGKTEYIKAKTS 190  
DB 905 --DV-TAGYSGTGAADSTLIAGYSGTGTSGDSSLTLAGYSGTGTARKGSDMTAGYGT 961  
QY 191 VIREKDKLVYKXKNGSGSTDEGELVAKVEIDVAVNKGAMKRTTANGQGTGQADKF 250  
DB 962 GTAGADSTLIAG-----YGTQTS-----DSSLTAGYSGTGTARSGSVTLAGY 1007  
QY 251 ETVTSGTNVTFASGKGTATVASKDOGNITVYDVNVDALNVQNLQNSGMNLSKAVAG 310  
DB 1008 STGTAGADSTLIAGYSGTGTAGSD--SSLTGY-----GSTGTARSGSDVTAGYSGT 1061  
QY 311 SSGKVISGNVSPSKGKMDIYNINAGNIEITRNGKNIDITATMTPOFSSVSLGAGADAP 370  
DB 1062 ADSTLIAGYSGTGTARSGSDSLTLAGYSGT--GTARSGSDI-----TAGYSGTGT-- 1113  
QY 371 TLSVDGALNVGSKKDKNPVITVAVGV-----KEGDTTNAQLKGVANQNLNRRIDN 423  
DB 1114 LIAGYSGTGTAGYD-----SULTAGYSGTGTARSGSDSLTLAGYSGTGTARSGHSLIAG 1165  
QY 424 VDGNAAGIAQAIATA--GLVQAYLPGKSMMAIGGTYRGAGY-----AIGYSSISDGG-- 476  
DB 1166 YGSGTGTAGYNSILTLTGYSGTGTAGESSLTLAGYSGT--STAGYDSTLTLAGYSGTGTAGYK 1223  
QY 477 NWITGTAGNSRGH-----FGASASVGYQ 501



Db 1224 STLTAGSGNSTAGHESSTLITAGSGSTQIACYE 1255

RESULT 8

HLVA\_PROMI STANDARD; PRT; 1577 AA.

AC P1646;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE Hemolysin precursor.

GN HPMa.

OS Proteus mirabilis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Proteus.

OC NCBI\_TaxID=584;

RN [1]

RP SEQUENCE FROM N.A.; AND SEQUENCE OF 30-43.

RC STRAIN-Isolate 477-12;

RX MEDLINE=90170827; PubMed=2407716;

RA Uphoff T.S., Welch R.A.;

RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serattia marcescens hemolysin genes (shlA and shlB).";

RL J. Bacteriol. 172:1206-1216(1990).

CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.

CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMa REQUIRES HPMB FUNCTION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMa MAY BE RESPONSIBLE FOR PORE FORMATION.

CC -1- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).

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CC EMBL: M30186; AAA25657.1; -

DR PTR; A35140; A35140.

KW Hemolysins; Toxin; Outer membrane; Signal.

FT SIGNAL

FT CHAIN 30 1577 HEMOLYSIN.

SO SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.78; Score 169.5; DB 1; Length 1577;

Best Local Similarity 21.7%; Pred. No. 0.18;

Matches 129; Conservative 72; Mismatches 196; Indels 197; Gaps 29;

QY 23 TRNHRKASATVAVLATLPAFYQASANTLK-----ADGNLKIKFYSIKKDLT 74

Db 710 TSTETEDANSTIGANVDLOANKDVTPFAGSDLTXTAGNASITGDNAFVSTENKKQDNT 769

QY 75 DLTSVGTETKLPFSANGKNVNTSD-----TKGLNFAKETAG----- 110

Db 770 DTTISG--GFSYGVADKVSADFOYDKQHTQTEVTKNNGSQTEVAGDLITRANLDLH 827

QY 111 -----TNGDTTVHLNGISLTLDRAASVKDVLNAGNINIKGVKAVDEPVRTYDTV 158

Db 828 EGASHVHEGRYQESGENIQHL-----AVNDETSKTDLSLWGVADV--GV-MLDYSGVTKPV 880

QY 159 EPLSADTKTTTVAVESDNGKK-----TEKKIAKTSVIRKED 196

Db 881 KKAIEDGVNTTKFGNNITDLTKKVTARDALNLANLSLETPNPGVEIGIGGSGSOSQTD 940

QY 197 GKLVY-----GK-----DKENGSTDEGEGLVTAKEVIDA--VNRAGRMKTTTA 240

Db 941 SQAVSTSIINACKIDIDSNNKLHDQTHYSTOEGISLTANTHTSEATLDRKQTFHETKG 1000

QY 241 NGQTGADKREFTYTSGNVTFE--SGKQTTA-----TVSKDDGQNTVMVDVYGDALNV 293

Db 1001 GGOIGVSTK-----TGSDDITVAIKREGQTTDMALMETKAGSFTSNGDISINVG---- 1051

QY 294 NOLNSGWNLSKRAVAGSSGKVISGNVSPSKMKDEFTVNINAGNNIEFTR----- 343

Db 1052 -NAHYEAOFPDAQ-----KGR---TV-INAGDGLTLAATDTHTSOS 1089

QY 344 -NGK-NIDATSWTPQSSVSLGADAPTL--SYDGDALNVSKRDNKPVRTINYPG 398

Db 1090 NVNGSANLKVGT--TPE--SKDYGGFNACTHTHSKQQTAKVGTITGSGIELNAGHL 1145

QY 399 VKEGDVTNVAOLKGVANLNLRID-----NVGNAKAGIAQ-----AATAG 440

Db 1146 TLQG--THLSSEDDIALNATNKVDLOSASSEHTKGNLISGVQVAGKRMPTDASSVNG 1203

QY 441 LVQAYLPKSGMMAIG-----GGTYGEGAYGAYGSSISDGMIIKGTG 484

Db 1204 L-----GSAQPAIKODEKSVSREGT-----INSGMLTINGS 1238

RESULT 9

OMPb\_RICCN STANDARD; PRT; 1655 AA.

AC Q9KKA3; Q9KX98; Q9XC45;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein) (surface protein antigen) (Cell surface antigen 5) (Scs5) (OMPb) (omp B) [contains: 120 kDa surface-exposed protein (surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].

DE OMPb OR RC1085.

GN Rickettsia conorii.

OS Rickettsia conorii.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OC NCBI\_TaxID=781;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Malish 7;

RX MEDLINE=21442074; PubMed=11557893;

RA Oyata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barde V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;

RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";

RL Science 293:2093-2098(2001).

RN [2]

RP SEQUENCE OF 33-1649 FROM N.A.

RC STRAIN=Indian tick typhus; and Malish 7;

RX MEDLINE=20393643; PubMed=10939649;

RA Roux V., Raoult D.;

RT "Phylogenetic analysis of members of the genus Rickettsia using the RT gene coding the outer-membrane protein ompB (ompB).";

RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).

RN [3]

RP SEQUENCE OF 353-1655 FROM N.A.

RC STRAIN=Malish 7;

RA Steenos J., Walker D.;

RT "The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group.";

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY SIMILARITY).

CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPb FAMILY.

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CC -----
DR EMBL; AE008659; AAL03623.1; -
DR EMBL; AF123721; AAF34124.1; -
DR EMBL; AF123726; AAF34129.1; -
DR EMBL; AF149110; AAD39533.1; -
DR PIR; E97835; E97835.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter. 1.
DR TIGRfams; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
FT VARIAT 1335 1655 32 kDa BETA PEPTIDE.
FT VARIAT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIAT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT CONFLICT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCB37 CRC64;

Query Match
Best Local Similarity 23.6%; Score 169; DB 1; Length 1655;
Matches 131; Conservative 67; Mismatches 235; Indels 114; Gaps 29;

10 NSALNAMYVSELTFRNHTKRASATV-----KTAVLATILFA--TVQASANTLKAGDMLK 61
314 NAGANAAYIG---TINNGAGRAAGFVSVYDNGNKVAITIDQYAKDAVIGSANA----- 362
62 IKQFTYSKKDITDITVSGETKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHNG 121
363 VGOVNF---RHIVDVGDTGT--TAKFTASAKVAITONS---NFGTDFGNLAQIL----- 410
122 IGSITLDRASAKVNLNAGMNIKGVKANDVFRTYTVFELSDTKTTTVN---VESKDN 177
411 VPNTMTLNGNFTGDSNPG--NTAGVTFD---ANGTTLASASADAVAVTNNITALESGA 466
178 G-----KTEVRIKARTSVIKEKDKGLVTKDKG-----ENGSTDEGEGLVTAK 222
467 GVOVLSGTHAEIRLIGMAGSVFKLADGVYINGKVOTALVGCALAGTITLIDGSAITTG- 525
223 EVIDAVNKRAGMRMKTITANGOTGAADKEFYV-----SGTWTFASGKTATATYSK 273
526 ---DIGNAGG---AAALGITLANDARKTLLIGGANITIGANGTINFGANGCTIKLS- 577
274 DDQGITITWYDV-----NWGDALNVQDLQNSGNLDSKAVAGSSGKVISGNSVPSK 326
578 -TÖNNIVVDFLATATDOTGVVDASSLTNAQTLTINGKIGTVGANGKNTLGGOFNISSKTV 636
327 M-DETVNIN---AGNN--IEITRNGKNIDIASTMPQ---FSSV-----SIGAGADAPT 371
637 LSDGVALINELVYINGNAVQFAHNTYLLTPTTNAAGQKIIFNPVYVNNNTTATCTNIGS 696
372 LSVGDALNVGSKDKNDKPVRTITNAPGVKEGDVTVNAQDKGAQNLNKRIDNVDS--NARA 430
697 ATNPLAEINFGSKGAANVDYLVNKGKYNL--YATNITTTDA---NVGSFTFAGSTNIVS 752
431 GIAQAIATAGLVQ-----ATLPGKSMALIGGGTVRGEAGYAIQYSSISDGNMIITGT 483
```

```
DB 753 G-----TVGQOQGNKFNVTALDNGTVKFLGNATFNNGNTTIAAN-STLQIGNTYADFV 805
QY 484 ASGNSRG 490
DB 806 ASADGTG 812

RESULT 10
OMP_RICRI
ID OMP_RICRI STANDARD; PRT; 1654 AA.
AC 053047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (OMPb)
DE (OMP B) (Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide).
GN OMPb.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (omp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMP/OMPb FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X16353; GAA34403.1; -
DR PIR; S18227; S18227.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter. 1.
DR TIGRfams; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 kDa BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 166184 MW; D7AB70FB7087F618 CRC64;

Query Match
Best Local Similarity 21.7%; Score 168.5; DB 1; Length 1654;
Matches 152; Conservative 79; Mismatches 233; Indels 239; Gaps 35;

7 IIMNSALNAMYVSE-----LTRNHTKRASATVKTAVLATILFAVQ 48
```

```

Db      92 LLNTANNLAVTSEDTTLGFTINNVNNAHSFNTLNAGKTLTTGQ-----GVTN 142
QY      49 ASANTLKAGDNLIKQFTYSLKKDLDLTSGV-----TEKL-----84
Db      143 AQAAPAKNAQNV-VQFENNGAALDNNDLKGVIRDEGAPASTVLENLAPTTQAPLLIG 201
QY      85 -SEFANG--NKVNT-----SDTKGLNFAKETAGTN-----GDT 115
Db      202 DNVIANGVNGTLNVTGFIQVSNKSFATYKAIINAGCGGIIFFITDANNANTLNLOAGT 261
QY      116 TVHLNGIGST-----LTDRAASYKVDL--NAGNINIKVKNVD-----VRYDYVELSLAD 164
Db      262 TINFETGDTGRLVLTSKHAATNFNTGSLGKLGV--IEFTVAVDQLTANAGAN 319
QY      165 TKTTTV-----VESKNGKTEV--KIGAKTSYIKERDKGLVYK-----KGE 207
Db      320 AVIGTNGAGRAAGFVSVNKGKATIDGOVYADWIOSAN--ATGOVNFRIHVDVGA 376
QY      208 NGS-----STDEGGLVTAKEVIDAV-----NKAGMR 234
Db      377 DGTAFKTAASKVTITQDSNFGNMDFG-NLAQIKVFNATLITGNFTGDASNPGNTAG-- 433
QY      235 MKTTTANG--QTQADKFEYVTSCTNTPASGKT-----TATVSKDDGNTVWYDV 285
Db      434 VTFPDANGTLESASADANVAVTNNITAEASGAGVOLSGTHAELRLGNAGSIFKLAD- 492
QY      286 NVGDALN--VNOLONSGWNLSKAVAGSSGKVISGKSPSKGM-----327
Db      493 -GTIVNGKYNQALVGAALAGTITLDGSAITITDIGNMGAALORITLANDAKTLT 550
QY      328 -----DEVNINA--GNNEITRNKNI-----DIATSMPEQFSVSLGAGADAPTL 372
Db      551 LGGANITGAGGFTIDLANGGTIKLTSTONNIIVDPDLALAI-TDQTEVAVASSLTNQT 609
QY      373 SVDC-----DALVGSK--DNKPVATVNAQVKEGV-----TNVA 408
Db      610 TINKICITIGANNKTLIGFNISSKTVLSNGNVAINELVIG-MDGAVOFAHDTYLITRT 668
QY      409 QLKGAONLNRIIDNVGNARAGIAQAIATAGLVOAVLPGK-----SMALIGGTYNGEA 463
Db      669 MAAGGKIIFNPVYNNCTTLAGTINLGSATNPILAETIFGSKGVAVDTLVNGESVNL--- 725
QY      464 GYA-----IGYSISDGGMWIIGTASGNSRGHFGASA 496
Db      726 -YATNITTTDANVGSFVFNAGGTIVSGTGGGQGNFNVYA 766

```

RESULT 11  
 OMPB\_RICTY STANDARD; PRT; 1645 AA.

AC P96989;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scat) (rOMP)  
 DE (Comp B) [Contams: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB OR SLP.  
 OS Rickettsia typhi.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_Taxid=785;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Williamston;  
 RX MEDLINE=94040787; PubMed=8224886;  
 RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;  
 RT Cloning and sequence analysis of the gene encoding the crystalline  
 RT surface layer protein of Rickettsia typhi.";  
 RL Gene 133:129-133(1993).  
 RN [2]

```

RP PARTIAL SEQUENCE.
RC STRAIN=Williamston;
RX MEDLINE=92114896; PubMed=1370573;
RA Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNR fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii."
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RX MEDLINE=92104668; PubMed=1729180;
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing."
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB-SIB.CH/ANNOUNCE/
CC OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).
CC -----
DR EMBL: L04661; JAB4987.1; -.
DR PIR: JN0896; JN0896.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRFAMs: TIGR01414; autotrans_bar1; 1.
KW Antigen; S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT TRANSEM 1354 1645 32 KDA BETA PEPTIDE.
FT CONFLICT 657 657 MEMBRANE ANCHOR (POTENTIAL).
FT CONFLICT 842 842 H -> N (IN REF. 2).
FT CONFLICT 1071 1071 V -> I (IN REF. 2).
FT CONFLICT 1306 1306 G -> A (IN REF. 2).
FT CONFLICT 1306 1306 G -> S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

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Query Match 6.5%; Score 165; DB 1; Length 1645;  
 Best local similarity 21.6%; Pred. No. 0.32;  
 Matches 117; Conservative 77; Mismatches 210; Indels 138; Gaps 25;

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QY      46 TVQASANTLKAAGDNLIKQFTYSLKKDLDLTSTGTEKLSFSANGKNVNTSDPKGLNFA 105
Db      141 TQAQAAAT-KSAQNVVSKVNGAALIND-NLDSGSGIDFPAAPVLEFENLNP-----T 193
QY      106 KETAGTNGDPTVHLNGIGSTL--TDRASVYKVDYLNAG--WNIGKVNVDVFRYDYVEF 160
Db      194 QEAPLTIGDNAKIYNGANGILINTNGFVYKSDKTFAGIKITINIDNGNGLMFNTPDANA 253
QY      161 LSAPTKTTTVNVESKD-----NGKTEVK--GAKTSYIKERD-----GKL- 199
Db      254 LNLGGGNTINFNGRDGTGLKLVLSKNGNATFENVGSLGNLKGVIETPTAAAGKILIA 313
QY      200 -----VTGKDKGENS-----STDG--EGLVTAKEVIDAVKAKGRMKTPTTANG 242
Db      314 NGGAANAIVGTDNAGRAAGFIYVDNGNNAATISGOVYADIV-----IQSANAGG 364
QY      243 QT-----GQADFEFTVSGTNTVFSAGKGTATVSKDDGNTVWYDV-----286
Db      365 QVTFEHLVDVGLGKTKTFKADSKVITTEANSEST-----DEGNLAVQIVPNNKILT 418
QY      287 ---VGDALNVNQLONSQWNLSKAVAGSSGKVISGKVNPS-----KGKDETVNI--- 333

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Db 419 GNFIDDA-----KNGG-NTAGVITFNANGTLVSGNTDPNIVTNIKAEVGGAGIYOLS 471
Oy 334 -----NAGNNIEITRNCKNIDITASMTPOSSVSLGADAPILSVGDL---N 380
Db 472 GHHGAEHLGNAGNSIFKLA-DGVINGPVNOMPLVNNNAAG-----STLDGSAITIGD 526
Oy 381 VGSKDKNPVTRITNVAPEVKEGDTNVAQLKGVAONLNNRIDVDGNARAGIAQAIAAG 440
Db 527 ICGAVNNAALDDITLA-----NDASKILTLSCA-----NIIGANAGAIHFQANCG 572
Oy 441 LVQALTPKSMMAIGCGTTRGAGAIYSSISDGNMIKT-----ASGSRHFQAS 495
Db 573 TQLTSTONNLLVDFDLDTDTQTSVAVSSLTNTQTLTNGSIGTIGANTKTIGRFNVG 632
Oy 496 AS 497
Db 633 SS 634

RESULT 12
WAPA_BACSU
ID WAPA_BACSU STANDARD: PRT: 2334 AA.
AC 007833:
DF 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Wall-associated protein precursor.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168:
RX MEDLINE=93302506; PubMed=8316082;
RA Foster S.D.;
RT "Molecular analysis of three major wall-associated proteins of
RT Bacillus subtilis 168: evidence for processing of the product of a
RT gene encoding a 258 kDa precursor two-domain ligand-binding
RT protein."
RL Mol. Microbiol. 8:299-310(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=95219088; PubMed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
RT genome containing the hut and wapa loci."
RL Microbiology 141:337-343(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=97124196; PubMed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RA Miwa Y., Fujita Y.;
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
RT containing the hic and cel loci, and creation of a 177 kb contig
RT covering the gut-sacxy region."
RL Microbiology 142:3113-3123(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boutsier L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Burschl C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerthon I.F., Cummings N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,

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RA Guisepi G., Guy B.J., Haga K., Hajeck J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parvo V., Pohl T.M., Portelle D., Porwollik S., Prescott A.M.,
RA Preece E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha F., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassaretti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zenchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -I- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION. MAY BE RELEASED
CC -I- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC INFO THE MEDIUM.
CC -I- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS: THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -I- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E.COLI RBS GROUP OF PROTEINS (RHSA-D).
CC -----
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CC -----
DR EMBL, L05634; AAA22883.1; -
DR EMBL, D31856; BAA06656.1; -
DR EMBL, D29985; BAA06260.1; -
DR EMBL, D83026; BAA11683.1; -
DR EMBL, Z99124; CAB15959.1; -
DR PIR, S32920; S32920.
DR Subtilist; BG10797; wapa.
DR InterPro; IPR003305; CBM_Cenc.
DR InterPro; IPR006530; YD.
DR Pfam; PF02018; CBM_4_9; 1.
DR TIGRFAMS; TIGR01643; YD_repeat_2x; 17.
KW Cell wall; Repeat; Signal; Complete proteome.
FT SIGNAL 1 28
FT CHAIN 29 2334
FT DOMAIN 504 869
FT REPEAT 504 605
FT REPEAT 636 736
FT REPEAT 769 869
FT DOMAIN 1021 2139
FT REPEAT 1021 1040
FT REPEAT 1042 1061
FT REPEAT 1063 1082
FT REPEAT 1083 1102
FT REPEAT 1109 1128
FT REPEAT 1129 1148
FT REPEAT 1150 1169
FT REPEAT 1174 1193
FT REPEAT 1199 1218
FT REPEAT 1219 1238
FT REPEAT 1646 1665
FT REPEAT 1667 1686
FT X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
FT 31 X 21 AA APPROXIMATE TANDEM REPEATS OF

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FT REPEAT 1690 1709 2-13.
FT REPEAT 1711 1730 2-14.
FT REPEAT 1732 1751 2-15.
FT REPEAT 1753 1772 2-16.
FT REPEAT 1795 1814 2-17.
FT REPEAT 1820 1839 2-18.
FT REPEAT 1840 1859 2-19.
FT REPEAT 1861 1880 2-20.
FT REPEAT 1887 1906 2-21.
FT REPEAT 1908 1927 2-22.
FT REPEAT 1929 1948 2-23.
FT REPEAT 1969 1982 2-24. (APPROXIMATE).
FT REPEAT 1983 2002 2-25.
FT REPEAT 2008 2027 2-26.
FT REPEAT 2028 2047 2-27.
FT REPEAT 2051 2070 2-28.
FT REPEAT 2071 2090 2-29.
FT REPEAT 2093 2112 2-30.
FT REPEAT 2120 2139 2-31.
SQ SEQUENCE 2334 AA; 258329 MW; B75138CD278BAA3 CRC64;

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Query Match 6.58; Score 165; DB 1; Length 2334;
Best Local Similarity 22.58; Pred. No. 0.49;
Matches 106; Conservative 64; Mismatches 181; Indels 120; Gaps 22;

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QY 23 TRNHTKRSATVK--TAVLATL-----LEATVQASAMTLKAGDNLK-----IKQ 64
DB 970 THRTTKRADGTGPTGVYLEFTTADOFLTKRQDQNAFENKKGKGLQVNDGHNNATV 1029
QY 65 FYTSLKADLTDLTSVTEKLSFS--ANGKNVNITS--DTKGLNFA-----KETAGTNGDT 115
DB 1030 YTYVNDKQNLTAITDASGRKLTFTYDENGHWTSITGPKNKVTVSYENDLLKVTDTGTV 1089
QY 116 TVH-----LNGISFLDRASAVDVLNAGNIN---GKRVNDEVRVRYDIYEFISAD 164
DB 1090 TSYDYDEGRILVQVYNSNSTEAKPFTETQYSGHLEKALNAKKEVTVSYD-----AD 1143
QY 165 TKTTTVAVESKDNKKTVEV--KIGAKTSVKEKDGKLVTV-----GKDKGENGSTDEG 215
DB 1144 KKITLTM---TQPNKRKQVQYVNEGNPIQVIYIDAEGLKITNTMYEGNNVVEDDPRDVG 1200
QY 216 EGLVTAKAVIDAVNKAQRMKTTTANGQGOADKFEVTVS-----GTVNTPFASGKTAT 270
DB 1201 TGRAT-----ESYQYDKQGNVTSVKDAYGTE--TTEYKKNNDVTV 1237
QY 271 VSKRDQGNIT--VMYDVAVGDLANVNOJLNSGMNLDKSAVAGSSGKTVSGANVSPKSG--KMD 328
DB 1238 KMKDTGEGNVTDIADV-----GLDAVSETDQSGKSSSAAYDKYGNQIQ 1280
QY 329 ETVINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLVGDALNVGSKKDNK 388
DB 1281 SSKRLSASTN--ILAKDG-----SFEAKSGMWLTSKDRKRKTSVADKSGVLSGSKAL 1331
QY 389 PVRITVNAVPGVKEG--DVTNVAQLKGVAQNLNINRDNVDGNARAGIAQATA 437
DB 1332 EVLSQSTASAGTDHGYSSATQTELE-----PNTTYLTSKIKTKDLAKSRA 1376

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RESULT 13
SLAP_CAUCR STANDARD; PRT; 1025 AA.
AC P35828; Q46015; Q9RF12;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (Paracrystalline surface layer protein).
GN RSPA OR CCI1007.
OS Caulobacter crescentus.
OC Bacteria: Proteobacteria: Alphaproteobacteria: Caulobacteriales:
CC Caulobacteriaceae: Caulobacter.
CX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.

```

```

RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=93007489; Pubmed-1393820;
RA Gilchrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RL crescentus paracrystalline surface layer protein."
RN Can. J. Microbiol. 38:193-202(1992).
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN-JS3001;
RA Bingle W.H., Awram P.A., Nornellini J.F., Smit J.K.;
RT "The secretion signal of C. crescentus S-layer protein is located in
RL the C-terminal 82 amino acids of the molecule."
RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RP [4]
RC SEQUENCE FROM N.A.
RP STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; Pubmed=11259647;
RA Niernann W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Onta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Debroy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RL "Complete genome sequence of Caulobacter crescentus."
RC Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN [5]
RC SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RP STRAIN-ATCC 19089 / CB15;
RX MEDLINE=8908089; Pubmed=3049545;
RA Fisher J.A., Smit J.K., Agabian N.;
RT "Transcriptional analysis of the major surface array gene of
RL Caulobacter crescentus."
RN J. Bacteriol. 170:4706-4713(1988).
RP [6]
RC CHARACTERIZATION.
RX STRAIN-ATCC 19089 / CB15;
RX MEDLINE=98292737; Pubmed=9620954;
RA Awram P., Smit J.K.;
RT "The Caulobacter crescentus paracrystalline S-layer protein is
RL secreted by an ABC transporter (type I) secretion apparatus."
RN J. Bacteriol. 180:3062-3069(1998).
RP [7]
RC FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
(TYPE I) SECRETION APPARATUS.
-1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
-----
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EMBL: AF062345; AAC38665.2; -
EMBL: AF193063; AA19365.1; -
EMBL: AE005779; AA82991.1; ALT_INIT.
PIR: A48995; A48995.
HSSP: P22629; 1SMC.
TIGR: CCI1007; -
InterPro: IPR001343; Hemlysn_Ca_bind.
Pfam: PF00353; hemolysincabind; 3.
PRINTS: PR00313; CAMDNGRPT.

```

KW Cell wall; S-layer; Calcium-binding; Complete proteome.  
 FT INIT\_MET 0  
 SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;  
 Query Match 6.5%; Score 164.5; DB 1; Length 1025;  
 Best Local Similarity 22.9%; Pred. No. 0.2; Mismatches 220; Indels 165; Gaps 28;  
 Matches 135; Conservative 66; Mismatches 220; Indels 165; Gaps 28;  
 QY 34 VKTAVIATLL-----FATVQAS-AMTLKAG---DNLK-IKOFYSLKDLTDLT 77  
 DB 191 VKAALIGITLINAATVSGIGVATATAAMINDSLDGLSDNAGVNLFAVSSGSGST 250  
 QY 78 ---SVTEKLSFSAN-----GKNVNTSDTKGLNFAKETAGTNGDTTV 117  
 DB 251 ISLTITGDTLITGTANDETFVAGEVAGAAATLVGDTLSGAGAGDVINWVQAAVATLPGIV 310  
 QY 118 HLNIGISLTLDRAASVKVDLNAAGNINIKGVK--NVDFVRITDVI-----EFLSADRTTV 170  
 DB 311 TISGLEIMNVISGAAL--TLNTSSGVTLTAINTISGAAGVTVAGAGONLTAATTAQAQA 368  
 QY 171 NVESKDNCKTEVKIGAKTSVIERKDKLVTKDKGENG-----SSTDEGEGLVTA 221  
 DB 369 NNVAVDGGAIVTV---ASTGV---TSQTIVGANSASGTSVSVAANSSTTTTGAIAVIG 422  
 QY 222 KEVIDAVNKAGRKAKTT-----TANG-----OTGADKEEYVTSCTN--VTF-- 261  
 DB 423 GTAVTVAQTAGNAVNTTLTADVTYVGNSSITAVTDTOTAAATAGATVAGRVGAVTTTD 482  
 QY 262 ---ASGKGTATVSKDOGNITV---MYDVNVD-----AL 291  
 DB 483 SAAASATTAGKAIATVTLTSGFCAATIDSSALITVNLISGIGTSIGIRGALTANPIANTLTL 542  
 QY 292 NVNOLONGSNLDSKAVAGS-----SGKVISGNVSPSKMKDETVINAGNIEITEN 344  
 DB 543 NVNGLTTGATIDSEAADDEFTTINAGSTASSTIASLVAAADATVNLISGARVTLTISH 602  
 QY 345 -----GKNI--DIATSMTPQFSSVSGAGADAPTLVSDDALNVGSKKDK 388  
 DB 603 TAAALTGITVNSVATIGALATGLV--FTG--GAGADSLILGATTAKIAYMGAGDDTV 657  
 QY 389 PVRTNNVAPG--VKEGDTVNNVQLKGVAONLNRRIDNV-----GNARAG--- 431  
 DB 658 TVSSATLGAAGSVNGDGDIV-----LVANVGSSFSADPARGGETTLRVAGAAAGSHN 712  
 QY 432 ----IAQAIATAGLVQ---AYLPKSKMAIGGCTYRGEAGYAIGYSSI 472  
 DB 713 ANGFTALDGAATGATFTTNVAVNVGLFLVLAFTGTTVTLTANAGTSDV 762  
 RESULT 14  
 APU\_THERU STANDARD; PRT; 1861 AA.  
 ID APU\_THERU  
 AC P38536;  
 DT 01-OCT-1994 (Rel. 30. Created)  
 DT 01-NOV-1995 (Rel. 32. Last sequence update)  
 DT 28-FEB-2003 (Rel. 41. Last annotation update)  
 DE Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].  
 GN AMYB.  
 OS Thermoaerobacter thermosulfurogenes (Clositridium  
 OS Thermosulfurogenes).  
 OC Bacteria; Firmicutes; Clostridia; Thermoaerobacteriales;  
 CC Thermoaerobacteriaceae; Thermoaerobacterium.  
 OX NCBI\_TaxID=33950;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 3896 / EML;  
 RX MEDLINE=9425298; PubMed=8195085;  
 RA Matuschek M., Burchardt G., Sahm K., Bahl H.;  
 RT "Pullulanase of Thermoaerobacterium thermosulfurogenes EML (Clositridium thermosulfurogenes): molecular analysis of the gene,

RT composite structure of the enzyme, and a common model for its attachment to the cell surface.";  
 RL J. Bacteriol. 176:3295-3302(1994).  
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.  
 CC -I- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic linkages in pullulan and in amylopectin and glycogen, and the alpha- and beta-limit dextrans of amylopectin and glycogen.  
 CC -I- SUBCELLULAR LOCATION: CELL-BOUND. IF C-TERMINUS MAY SERVE AS AN S-LAYER ANCHOR.  
 CC -I- PTM: GLYCOSYLATED.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -I- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -I- SIMILARITY: Contains 3 S-layer homology (SLH) domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/> or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC  
 DR EMBL: M57692; AAB00841.1; .  
 DR HSP: Q08751; IBV2.  
 DR Interpro: IPR006589; ALP\_amy1\_cat-sub.  
 DR Interpro: IPR006048; Alpha\_amy1\_C.  
 DR Interpro: IPR006047; Alpha\_amy1\_cat.  
 DR Interpro: IPR003961; FN\_III.  
 DR Interpro: IPR004185; Glyco\_hydro\_131g.  
 DR Interpro: IPR004193; Glyco\_hydro\_13N.  
 DR Interpro: IPR001119; SLH.  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR Pfam: PF02806; alpha-amylase; 1.  
 DR Pfam: PF02903; alpha-amylase; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF02922; Isoamylase; 1.  
 DR Pfam: PF02935; SLH; 3.  
 DR SMART: SM00642; Amy; 1.  
 DR SMART: SM00632; Amy; 1.  
 DR SMART: SM00600; FN3; 2.  
 DR PROSITE: PS01072; SLH\_DOMAIN; 3.  
 DR PROSITE: PS01072; SLH\_DOMAIN; 3.  
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;  
 KM Multifunctional enzyme; Glycoprotein.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1861  
 FT DOMAIN 928 1018  
 FT DOMAIN 1157 1248  
 FT ACT\_SITE 628 628  
 FT ACT\_SITE 657 657  
 FT ACT\_SITE 734 734  
 FT DOMAIN 1681 1739  
 FT DOMAIN 1740 1803  
 FT DOMAIN 1804 1861  
 FT CONFLICT 1734 1734  
 SQ SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;  
 Query Match 6.5%; Score 164.5; DB 1; Length 1861;  
 Best Local Similarity 20.8%; Pred. No. 0.4; Mismatches 229; Indels 155; Gaps 26;  
 Matches 122; Conservative 81; Mismatches 229; Indels 155; Gaps 26;  
 QY 2 NKIYRIWNSALNA-----WVVSSELTNRNHRKASATVKTAVL----- 39  
 DB 1208 NEVNYIDTVSYNGVYKVKVAVDLSNRTESNVVTKIPVYFNVTPDPTDA 1267  
 QY 40 ----ATLFAIVQASANTLKAGDNLIKQFIYSLKDLTDSVTEKLSANGNKNKI 95  
 DB 1268 VNLACTFPNATWDPQAQOM-----TKIDNNYTSITLTLDE---GTQLEYKVARCSMDKV 1318  
 QY 96 TSDTGLNFA---KTAGTNGDTVHLNGI-----GSTLT-DRAASVKDVL 137  
 DB 1319 EKDEYGNFASNRKATVYVNGNENKTIINDYIRKRDIFIFLYSPSSNMFTVDSNISTMEV- 1377



Mon Oct 6 12:38:31 2003

us-09-771-382-27.rsp

Page 14

Db 808 VANGSGLLIGDDSVVDVAVNSYIPTGYYTYNALLMADGECTSIENKGDITSHGVSYVRAD 867

Qy 468 GYSISIDGWNLIKCTASGNSRGHGASASVG 499

Db 868 NGSEVYNSGDIIVYATISSNSSEDRAITATASC 899

Search completed: October 6, 2003, 09:24:06  
Job time : 10.7522 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 36.8701 Seconds  
(without alignments)  
3513.485 Million cell updates/sec

Title: US-09-771-382-27  
Perfect score: 2544  
Sequence: 1 MKKIRIINNSALNMAWVVS.....TASGNSRGHFGASASVGYQM 502

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriopl:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2459.5	96.7	591	09JPR18	09JPR18 neisseria m
2	2455.5	96.5	591	09JPS7	09JPS7 neisseria m
3	2455	96.5	592	09AOF0	09AOF0 neisseria m
4	2447.5	96.2	591	09JQY3	09JQY3 neisseria m
5	2400	94.3	600	09JPS6	09JPS6 neisseria m
6	2388	93.9	590	09JPS3	09JPS3 neisseria m
7	2375.5	93.4	595	09JPH0	09JPH0 neisseria m
8	2371.5	93.2	599	09JPR8	09JPR8 neisseria m
9	2369	93.1	598	09JPR7	09JPR7 neisseria m
10	2367.5	93.1	599	09JPS2	09JPS2 neisseria m
11	2367	93.0	594	09JPS8	09JPS8 neisseria m
12	2365	92.9	594	09JQY4	09JQY4 neisseria m
13	2363	92.8	594	09JPR3	09JPR3 neisseria m
14	2361	92.7	592	09JPS9	09JPS9 neisseria m
15	2359	92.6	594	09JPH7	09JPH7 neisseria m
16	2357	92.6	598	09JPR9	09JPR9 neisseria m

17	2351	92.4	592	16	09JQW4	09JQW4 neisseria m
18	2344	92.1	598	2	09JPS0	09JPS0 neisseria m
19	2344	92.1	598	2	09JPR0	09JPR0 neisseria m
20	2335	91.8	598	2	09JQY5	09JQY5 neisseria m
21	2329.5	91.6	589	2	09JPR10	09JPR10 neisseria m
22	2327	91.5	592	2	09JQY1	09JQY1 neisseria m
23	2317.5	91.1	589	2	09JQY1	09JQY1 neisseria m
24	2317	91.1	600	2	09JPS5	09JPS5 neisseria m
25	2207.5	86.8	526	2	09JPS4	09JPS4 neisseria m
26	2205.5	86.7	530	2	09JPS1	09JPS1 neisseria m
27	1009.5	39.7	2353	2	P71401	P71401 haemophilus
28	974	38.3	1098	2	Q48152	Q48152 haemophilus
29	970	38.1	1096	2	Q8GM79	Q8GM79 haemophilus
30	901	35.4	1210	2	Q8GM74	Q8GM74 haemophilus
31	893	35.1	1210	2	Q8GM75	Q8GM75 haemophilus
32	888	33.7	1204	2	Q8GM76	Q8GM76 haemophilus
33	678	26.7	1004	2	Q8GM77	Q8GM77 haemophilus
34	663	26.1	1002	2	Q8GM78	Q8GM78 haemophilus
35	426.5	16.8	1299	16	Q9F3X6	Q9F3X6 pasteurella
36	380.5	15.0	1190	16	Q9PC04	Q9PC04 xylella fas
37	372.5	14.6	2314	2	Q8K0M8	Q8K0M8 moraxella c
38	370.5	14.6	1964	2	Q8K0M9	Q8K0M9 moraxella c
39	360.5	14.2	1588	16	Q8XDG4	Q8XDG4 escherichia
40	358.5	14.1	2059	16	Q9PD50	Q9PD50 xylella fas
41	352.5	13.9	1461	16	Q8ZL64	Q8ZL64 salmonella
42	351.5	13.8	1107	16	Q9F2D8	Q9F2D8 salmonella
43	351	13.8	1778	16	Q8FCB2	Q8FCB2 escherichia
44	346.5	13.6	641	16	Q8CKM1	Q8CKM1 yersinia pe
45	346.5	13.6	658	16	Q8ZHU0	Q8ZHU0 yersinia pe

## ALIGNMENTS

RESULT 1  
ID 09JPR18 PRELIMINARY: PRT: 591 AA.  
AC 09JPR18;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Outer membrane protein GNA992 (Adhesin) (Mha outer membrane protein).  
GN GNA992 OR NM009922 OR NMHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B, BZ169, BZ83, and H44/76;  
RX MEDLINE=20175756; Pubmed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Cepechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Brooker M., Hurd E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=20175755; Pubmed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B., Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,

RA Gill J., Scariato V., Masignani V., Pizza M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
RT MC58.";  
RL Science 287:1809-1815 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;  
RA Peak I.R., Strikhantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*.";  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.  
DR EMBL: AF226375; AAF42524.1; -  
DR EMBL: AE002450; AAF41395.1; -  
DR EMBL: AF226367; AAF42516.1; -  
DR EMBL: AF226370; AAF42519.1; -  
DR EMBL: AF226374; AAF42523.1; -  
DR EMBL: AF157611; AAK68872.1; -  
DR TIGR: NMB0992; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73BC6 CRC64;

Query Match 96.7%; Score 2459.5; DB 16; Length 591;  
Best Local Similarity 84.9%; Pred. No. 2.6e-100;  
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;

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DB 1 MNKIRIINNSALNMVYVSELTRNHTKRASATVTAVALTLFATVOASANNEQEDL 60  
OY 53 -----TLKAGDLKIKQ 64  
DB YLDPQRYAVAVLIVNSDEKGEKEKEVEENSDMAYVFNKEKGLTAREITLKKAGDLKIKQ 120  
OY 65 -----FTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTHLN 120  
DB 121 NGTNTFTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTHLN 180  
OY 121 GIGSTLTLD-----RAASYKDVLMAGMNKIGVK-----NYDF 151  
DB 181 GIGSTLTLDLNTGATNTVNDVTDDEKKRAASVKDVLMAGMNKIGVKPGTTASDNDF 240  
OY 152 VRTYDVEFLSADTKTTTVNVESSKDKGKTEVKGAKTSVIREKDGKLVTKGDKGENSS 211  
DB 241 VRTYDVEFLSADTKTTTVNVESSKDKGKTEVKGAKTSVIREKDGKLVTKGDKGENSS 300  
OY 212 TDEGGGLYAKAEVIDAVNKAAGWRMKTITANGOTGADKFEYVTSNTVTFASGKGTATV 271  
DB 301 TDEGGGLYAKAEVIDAVNKAAGWRMKTITANGOTGADKFEYVTSNTVTFASGKGTATV 360  
OY 272 SKDDGNTITVMDVNVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDET 331  
DB 361 SKDDGNTITVMDVNVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDET 420  
OY 332 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGACADAPTLSVDDALNVGSKKKNKPYR 391  
DB 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGACADAPTLSVDDALNVGSKKKNKPYR 480  
OY 392 ITNVAPEGVGVTVVAOLKGYAQNULNRRIDVNDGNARAGIAQAIAATAGLVQAYLPBGS 451  
DB 481 ITNVAPEGVGVTVVAOLKGYAQNULNRRIDVNDGNARAGIAQAIAATAGLVQAYLPBGS 540  
OY 452 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 502  
DB 541 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 591

RESULT 2  
ID 09JPS7  
AC 09JPS7;  
PRELIMINARY; PRT: 591 AA.

DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
ON NCBI\_TaxID=487;  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storti E., Zuo P.,  
RA Brocker M., Hündt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820 (2000).  
DR EMBL: AF226366; AAF42515.1; -  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 96.5%; Score 2455.5; DB 2; Length 591;  
Best Local Similarity 84.8%; Pred. No. 3.9e-100;  
Matches 501; Conservative 1; Mismatches 0; Indels 89; Gaps 4;

OY 1 MNKIRIINNSALNMVYVSELTRNHTKRASATVTAVALTLFATVOASAN----- 52  
DB 1 MNKIRIINNSALNMVYVSELTRNHTKRASATVTAVALTLFATVOASANNEQEDL 60  
OY 53 -----TLKAGDLKIKQ 64  
DB YLDPQRYAVAVLIVNSDEKGEKEKEVEENSDMAYVFNKEKGLTAREITLKKAGDLKIKQ 120  
OY 65 -----FTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTHLN 120  
DB 121 NGTNTFTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTTHLN 180  
OY 121 GIGSTLTLD-----RAASYKDVLMAGMNKIGVK-----NYDF 151  
DB 181 GIGSTLTLDLNTGATNTVNDVTDDEKKRAASVKDVLMAGMNKIGVKPGTTASDNDF 240  
OY 152 VRTYDVEFLSADTKTTTVNVESSKDKGKTEVKGAKTSVIREKDGKLVTKGDKGENSS 211  
DB 241 VRTYDVEFLSADTKTTTVNVESSKDKGKTEVKGAKTSVIREKDGKLVTKGDKGENSS 300  
OY 212 TDEGGGLYAKAEVIDAVNKAAGWRMKTITANGOTGADKFEYVTSNTVTFASGKGTATV 271  
DB 301 TDEGGGLYAKAEVIDAVNKAAGWRMKTITANGOTGADKFEYVTSNTVTFASGKGTATV 360  
OY 272 SKDDGNTITVMDVNVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDET 331  
DB 361 SKDDGNTITVMDVNVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDET 420  
OY 332 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGACADAPTLSVDDALNVGSKKKNKPYR 391  
DB 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGACADAPTLSVDDALNVGSKKKNKPYR 480  
OY 392 ITNVAPEGVGVTVVAOLKGYAQNULNRRIDVNDGNARAGIAQAIAATAGLVQAYLPBGS 451  
DB 481 ITNVAPEGVGVTVVAOLKGYAQNULNRRIDVNDGNARAGIAQAIAATAGLVQAYLPBGS 540  
OY 452 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 502  
DB 541 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 591

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RESULT 3
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AC Q9AOF0:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF125375; AAK09243.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
DR SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 96.5%; Score 2455; DB 2; Length 592;
Best Local Similarity 84.6%; Pred. No. 4;le-100;
Matches 501; Conservative 0; Mismatches 1; Indels 90; Gaps 4;

QY 1 MNKTYRIIWSALNAMYVSELTRNHTKRASATVKTAVLATLTFATVQASAN----- 52
DB 1 MNKTYRIIWSALNAMYVSELTRNHTKRASATVKTAVLATLTFATVQASANNEPCKD 60
QY 53 -----TLKAGDNLKIK 63
DB 61 LYLDPORTYAVLIIVNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIK 120
QY 64 Q-----FTYSLKKDLTDLTSVTEKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTYVHL 119
DB 121 QNGTFYSLKLDLTDLTSVTEKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTYVHL 180
QY 120 NGIGSTLTD-----RAASVKVLANAGNMIKGVK-----NVD 150
DB 181 NGIGSTLTDLTDLTNGATTNTNDVTDDEKKRAASVKVLANAGNMIKGVKPGTTASDNVD 240
QY 151 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEYKIGATSVYKEKDGKLVYTKDKGNGSS 210
DB 241 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEYKIGATSVYKEKDGKLVYTKDKGNGSS 300
QY 211 STDEGGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEFVTSCTNVTFAFGKGTAT 270
DB 301 STDEGGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEFVTSCTNVTFAFGKGTAT 360
QY 271 VSKDQGNITVWDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMDET 330
DB 361 VSKDQGNITVWDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMDET 420
QY 331 VNINAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLISVDGALNVGSKDKMPV 390
DB 421 VNINAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLISVDGALNVGSKDKMPV 480
QY 391 RITNAPGVKEGDVTNVNQAOLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 450
DB 481 RITNAPGVKEGDVTNVNQAOLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 540
QY 451 MAIIGGTYRGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 502
DB 541 MAIIGGTYRGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 592

RESULT 4
Q93QY3 PRELIMINARY; PRT; 591 AA.
ID Q93QY3
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AC Q93QY3:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157606; AAK68867.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
DR SEQUENCE 591 AA; 62048 MW; CDDC600798859C65 CRC64;

Query Match 96.2%; Score 2447.5; DB 2; Length 591;
Best Local Similarity 84.6%; Pred. No. 8;le-100;
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

QY 1 MNKTYRIIWSALNAMYVSELTRNHTKRASATVKTAVLATLTFATVQASAN----- 52
DB 1 MNKTYRIIWSALNAMYVSELTRNHTKRASATVKTAVLATLTFATVQASANNEQEDL 60
QY 53 -----TLKAGDNLKIK 64
DB 61 YLDPLVLTAVLIIVNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIK 120
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTYVHL 120
DB 121 NGTFYSLKLDLTDLTSVTEKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTYVHL 180
QY 121 GIGSTLTD-----RAASVKVLANAGNMIKGVK-----NVD 151
DB 181 GIGSTLTDLTDLTNGATTNTNDVTDDEKKRAASVKVLANAGNMIKGVKPGTTASDNVD 240
QY 152 VRTYDVEFLSADTKTTTVNVEKDKNGKTEYKIGATSVYKEKDGKLVYTKDKGNGSS 211
DB 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEYKIGATSVYKEKDGKLVYTKDKGNGSS 300
QY 212 TDEGGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEFVTSCTNVTFAFGKGTAT 271
DB 301 TDEGGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFEFVTSCTNVTFAFGKGTAT 360
QY 272 SKDQGNITVWDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMDET 331
DB 361 SKDQGNITVWDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMDET 420
QY 332 NINAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLISVDGALNVGSKDKMPV 391
DB 421 NINAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLISVDGALNVGSKDKMPV 480
QY 392 ITNAPGVKEGDVTNVNQAOLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 451
DB 481 ITNAPGVKEGDVTNVNQAOLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 540
QY 452 MAIIGGTYRGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 502
DB 541 MAIIGGTYRGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 5
Q9JPS6 PRELIMINARY; PRT; 600 AA.
ID Q9JPS6
AC Q9JPS6:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
```

DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria: Betaproteobacteria: Neisseriales;  
OC Neisseriaceae: Neisseria.  
NCBI\_TaxId=487;  
OK NCBI\_TaxId=487;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42520.1; -.  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0596CD1 CRC64;

Query Match 94.3%; Score 2400; DB 2; Length 600;  
Best Local Similarity 82.0%; Pred. No. 1.1e-97;  
Matches 492; Conservative 3; Mismatches 7; Indels 98; Gaps 4;

QY 1 MKKIRITNSALNMAVYSELTRNHTKRASATVATATLLFAVQASAN----- 52  
DB 1 MKKIRITNSALNMAVYSELTRNHTKRASATVATATLLFAVQASADN 60  
QY 53 -----TLKAGDNLK 61  
DB 61 EEEETLEPVVATAPLSPSAEDTGEKEVTEMTWGIYFDKNGYIKACTITLKAGDNLK 120  
QY 62 IKQ-----FTYSLKKDLTDLTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGT 111  
DB 121 IKQNTDENTNASSFTYSLKKELTDLTSVGTETKLSFGANGKNVITSDTKGLNFAKETAGT 180  
QY 112 NGDTTVHLNGTSTLT-----RAASVDVYLNAGNNIGVK-- 147  
DB 181 NGDTTVHLNGTSTLTDLTLLNGATTNTNDVTDDEKKRAASVDVYLNAGNNIGVKPG 240  
QY 148 -----NVDFVRYTVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLYTG 202  
DB 241 TTASNDVDFVRYTVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLYTG 300  
QY 203 KDKGENGSSTDEGEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVTSQTNVFA 262  
DB 301 KDKGENGSSTDEGEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVTSQTNVFA 360  
QY 263 SGKGTAAVSKDDQNTIVYMDVNVGDLNVLQNSGNLDSKAVAGSSGKVIYGNVSP 322  
DB 361 SGKGTAAVSKDDQNTIVYMDVNVGDLNVLQNSGNLDSKAVAGSSGKVIYGNVSP 420  
QY 323 SKGKDETVYNINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGALANG 382  
DB 421 SKGKDETVYNINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGALANG 480  
QY 383 SKKDKPVRITNVAPVEGDTNVAQLKGAQONLNRIIDNVGNARAGIAQAIATAGLV 442  
DB 481 SKDKAKPVRITNVAPVEGDTNVAQLKGAQONLNRIIDNVGNARAGIAQAIATAGLV 540  
QY 443 QAYLPGKSMMAIGGCTYRGEAGYATGYSSISDGGNMIITKGTASGNSRGHFGASASVGIOW 502  
DB 541 QAYLPGKSMMAIGGCTYRGEAGYATGYSSISDGGNMIITKGTASGNSRGHFGASASVGIOW 600

ID Q9JPS3 PRELIMINARY; PRT; 590 AA.  
AC Q9JPS3;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria: Betaproteobacteria: Neisseriales;  
OC Neisseriaceae: Neisseria.  
NCBI\_TaxId=487;  
OK NCBI\_TaxId=487;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -.  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 93.9%; Score 2388; DB 2; Length 590;  
Best Local Similarity 83.2%; Pred. No. 3.5e-97;  
Matches 491; Conservative 3; Mismatches 8; Indels 88; Gaps 5;

QY 1 MKKIRITNSALNMAVYSELTRNHTKRASATVATATLLFAVQASAN----- 52  
DB 1 MKKIRITNSALNMAVYSELTRNHTKRASATVATATLLFAVQASADN 60  
QY 53 -----TLKAGDNLK 64  
DB 61 DPVQRTAVAVLIYNSDKEGTGEKEVENSMAVYFNEKGVLTAGTTTLKAGDNLKIKQNG 120  
QY 65 --FTYSLKKDLTDLTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGTNGTTHLNGI 122  
DB 121 TNEFTYSLKKDLTDLTSVGTETKLSFSAANGKVNITSDTKGLNFAKETAGTNGTTHLNGI 180  
QY 123 GSTLND-----RAASVDVYLNAGNNIGVK-- 153  
DB 181 GSTLNDTLLNGATTNTNDVTDDEKKRAASVDVYLNAGNNIGVKPGTASDNVDYR 240  
QY 154 TYDVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLYTGKDKGENGSSTD 213  
DB 241 TYDVEEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKERDKLYTGKDKGENGSSTD 300  
QY 214 EEEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVTSQTNVFA 273  
DB 301 EEEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVTSQTNVFA 360  
QY 274 DDQGNITVYMDVNVGDLNVLQNSGNLDSKAVAGSSGKVIYGNVSPSKKMDETVNI 333  
DB 361 DDQGNITVYMDVNVGDLNVLQNSGNLDSKAVAGSSGKVIYGNVSPSKKMDETVNI 420  
QY 334 NAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDG-ALNVGSKDKKPVRI 392  
DB 421 NAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGALNVGSKDKKPVRI 480  
QY 393 TNVAPVEGDTNVAQLKGAQONLNRIIDNVGNARAGIAQAIATAGLVQAYLPGKSM 452  
DB 481 TNVAPVEGDTNVAQLKGAQONLNRIIDNVGNARAGIAQAIATAGLVQAYLPGKSM 540  
QY 453 AIGGCTYRGEAGYATGYSSISDGGNMIITKGTASGNSRGHFGASASVGIOW 502  
DB 541 AIGGCTYRGEAGYATGYSSISDGGNMIITKGTASGNSRGHFGASASVGIOW 590

RESULT 7  
ID Q9JPH0 PRELIMINARY; PRT: 595 AA.  
AC Q9JPH0;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=528, and 1000;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226360; AAF42509.1; -;  
DR EMBL: AF226356; AAF42505.1; -;  
DR InterPro: IPR005594; Yada.  
DR Pfam: PFO3895; Yada.  
SQ SEQUENCE 595 AA; 62120 MM; 8212C96380142BRC CRC64;

Query Match 93.4%; Score 2375.5; DB 2; Length 595;  
Best Local Similarity 81.6%; Pred. No. 1.2e-96;  
Matches 487; Conservative 7; Mismatches 8; Indels 93; Gaps 5;  
QY 1 MNKIRIIMNSALNANWVSELTRNHRKASATVKTAVLATLTFATVQASAN----- 52  
DB 1 MNKIRIIMNSALNANWVSELTRNHRKASATVKTAVLATLTFATVQASAN----- 52  
QY 53 -----TLKAGDNLKIKO--- 64  
DB 61 EPPVRSALVLOPMIDKNGENESTGDIQSIYYDHNTHLGAFTVTLKAGDNLKIKONTD 120  
QY 65 -----FTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDFKGLNFAKETAGTNGDTTV 117  
DB 121 ENTNASFTYSLKKDLTDLTSVGTETKLSFGANGKNVITSDFKGLNFAKETAGTNGDTTV 180  
QY 118 HLMGIGSTLTLD-----RAASYDVNLAGNNIKGV-----N 148  
DB 181 HLMGIGSTLTLDLAGSSAHVDAGNOSTHYTRRAASIKVDNLAGNNIKGVGTGTTGSGEN 240  
QY 149 VDFVRYTDVYEFISADTKTTTVNVEKDNCKTEVKIGAKTSYIKKEDGLVYKDGGEN 208  
DB 241 VDFVRYTDVYEFISADTKTTTVNVEKDNCKTEVKIGAKTSYIKKEDGLVYKDGGEN 300  
QY 209 GSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFETVTSGTNVTFAAGKGT 268  
DB 301 GSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFETVTSGTNVTFAAGKGT 360  
QY 269 ATYSKDDQGNITWYDVNVDALNVNOLONGNMLDSKAVAGSSGKATSGNVSFSKMD 328  
DB 361 ATYSKDDQGNITWYDVNVDALNVNOLONGNMLDSKAVAGSSGKATSGNVSFSKMD 420  
QY 329 ETVNINAGNNIETRNKNDIATSMTPQSSVSLGADAPLTSVGD-ALNVGSKDN 387  
DB 421 ETVNINAGNNIETRNKNDIATSMTPQSSVSLGADAPLTSVDEGALNVGSKDN 480  
QY 388 KPVRIITNAPGVKEGDTVNAQLKGAQNLNRIIDVGNARAGIAQAIATAGLVQAYLP 447

DB 481 KPVRIITNAPGVKEGDTVNAQLKGAQNLNRIIDVGNARAGIAQAIATAGLVQAYLP 540  
QY 448 GKSMMAIGCGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFASASVGYOM 502  
DB 541 GKSMMAIGCGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFASASVGYOM 595  
RESULT 8  
ID Q9JPR8 PRELIMINARY; PRT: 599 AA.  
AC Q9JPR8;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992 (Nhha outer membrane protein).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH38;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226383; AAF42532.1; -;  
DR EMBL: AF157608; AAF68869.1; -;  
DR InterPro: IPR005594; Yada.  
DR Pfam: PFO3895; Yada.  
SQ SEQUENCE 599 AA; 62844 MM; BBA16BBS3C1970C CRC64;  
Query Match 93.2%; Score 2371.5; DB 2; Length 599;  
Best Local Similarity 81.6%; Pred. No. 1.9e-96;  
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;  
QY 1 MNKIRIIMNSALNANWVSELTRNHRKASATVKTAVLATLTFATVQASAN----- 52  
DB 1 MNKIRIIMNSALNANWVSELTRNHRKASATVKTAVLATLTFATVQASAN----- 52  
QY 53 -----TLKAGDNLKIKO--- 64  
DB 61 EPPVRSALVLOPMIDKNGENESTGDIQSIYYDHNTHLGAFTVTLKAGDNLKIKONTN 120  
QY 65 -----FTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDFKGLNFAKETAGTNG 113  
DB 121 KTNENTNDSFYSLSKKDLTDLTSVGTETKLSFGANGKNVITSDFKGLNFAKETAGTNG 180  
QY 114 DTVYHLNGISTLTLD-----RAASYDVNLAGNNIKGV----- 147  
DB 181 DTVYHLNGISTLTLDLNTGAFTVNTDNDVTDKRRKASVKNVLAGNNIKGVKGT 240  
QY 148 ---NVDFVRYTDVYEFISADTKTTTVNVEKDNCKTEVKIGAKTSYIKKEDGLVYKGD 204  
DB 241 ASDNVDPVHRHYTDVYEFISADTKTTTVNVEKDNCKTEVKIGAKTSYIKKEDGLVYKGD 300  
QY 205 KGENGSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFETVTSGTNVTFAAG 264

Db 301 KGENGSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGADKFEVVTSGTNVTFASG 360  
Qy 265 KGTATVSKDDGNTITVMTDVNVGDALNVNQLONGSMWLDKAVAGSSGKVISGNVSPSK 324  
Db 361 KGTATVSKDDGNTITVMTDVNVGDALNVNQLONGSMWLDKAVAGSSGKVISGNVSPSK 420  
Qy 325 GKMDETIVNAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDG-DALNVSK 383  
Db 421 GKMDETIVNAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDGKDALNVSK 480  
Qy 384 KDNKPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGDNARAGIAQAIATAGLVQ 443  
Db 481 KDNKPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGDNARAGIAQAIATAGLVQ 540  
Qy 444 AYLPGKSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 502  
Db 541 AYLPGKSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 599

## RESULT 9

Q9JPR7 PRELIMINARY; PRT: 598 AA.  
ID Q9JPR7  
AC Q9JPR7;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SM2107;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.,  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226385; AAF42534.1; --  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 93.1%; Score 2369; DB 2; Length 598;  
Best Local Similarity 91.6%; Pred. No. 2.4e-96;  
Matches 488; Conservative 2; Mismatches 12; Indels 96; Gaps 5;

Qy 1 MNKIRIITNSALNMAVWVSELTRNHTKRASATVKTAVATLLFAFTVOASAN----- 52  
Db 1 MNKIRIITNSALNMAVWVSELTRNHTKRASATVKTAVATLLFAFTVOASAN----- 60  
Qy 53 -----TLKAGDNLKIKO----- 64  
Db 61 PVORTAVVLSFRAHSEGTGEKEVIGNTLGTYFEDEKRYLAKAGTTTLKAGDNLKIKQNDDE 120  
Qy 65 -----FTYSLKRDLDLTSVTEKLSFSGANGKVNITSPTKGLNFAKETAGTNGD 114  
Db 121 NTIDENTNASSFTYSLKRDLDLTSVTEKLSFSGANGKVNITSPTKGLNFAKETAGTNGD 180  
Qy 115 TTVHLNIGSTLTD-----RAASVDVNLNAGNINIGVK----- 147  
Db 181 TTVHLNIGSTLTDLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNINIKGVKTSSTGQ 240  
Qy 148 --NVDFTVTPVEFLSADTKTTTVNVSCKNGKTEVKIGAKTSVIEKDGKLTGTGDK 205  
|||||

Db 241 SENVDFTVTPVEFLSADTKTTTVNVSCKNGKTEVKIGAKTSVIEKDGKLTGTGCK 300  
Qy 206 GENGSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGADKFEVVTSGTNVTFASGK 265  
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGADKFEVVTSGTNVTFASGK 360  
Qy 266 GTTATVSKDDGNTITVMTDVNVGDALNVNQLONGSMWLDKAVAGSSGKVISGNVSPSK 325  
Db 361 GTTATVSKDDGNTITVMTDVNVGDALNVNQLONGSMWLDKAVAGSSGKVISGNVSPSK 420  
Qy 326 KMDDETIVNAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDG-DALNVSK 384  
Db 421 KMDDETIVNAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDGKDALNVSK 480  
Qy 385 KDNKPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGDNARAGIAQAIATAGLVQ 444  
Db 481 KDNKPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGDNARAGIAQAIATAGLVQ 540  
Qy 445 YLPGKSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 502  
Db 541 YLPGKSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 598

## RESULT 10

Q9JPS8 PRELIMINARY; PRT: 599 AA.  
ID Q9JPS8  
AC Q9JPS8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Outer membrane protein GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A22;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.,  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226385; AAF42513.1; --  
DR InterPro: IPR005594; Yada.  
DR Pfam: PF03895; Yada; 1.  
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 93.1%; Score 2367.5; DB 2; Length 599;  
Best Local Similarity 81.5%; Pred. No. 2.8e-96;  
Matches 488; Conservative 3; Mismatches 11; Indels 97; Gaps 5;

Qy 1 MNKIRIITNSALNMAVWVSELTRNHTKRASATVKTAVATLLFAFTVOASAN----- 52  
Db 1 MNKIRIITNSALNMAVWVSELTRNHTKRASATVKTAVATLLFAFTVOASAN----- 60  
Qy 53 -----TLKAGDNLKIKO----- 64  
Db 61 EPVKRTAVVLSFRSDKEGTGEKEVEDSHMGVYFPEKGVLAAGTTTLKAGDNLKIKQNTD 120  
Qy 65 -----FTYSLKRDLDLTSVTEKLSFSGANGKVNITSPTKGLNFAKETAGTNG 113  
Db 121 ENTIDENTNASSFTYSLKRDLDLTSVTEKLSFSGANGKVNITSPTKGLNFAKETAGTNG 180  
Qy 114 DTTVHLNIGSTLTD-----RAASVDVNLNAGNINIGVK----- 147  
|||||

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Db      181 DFTVHLNGIGSTLTDTLTLGSSASHVDAGNOSTHYTTPAASIKDVLNAGMNIKGVKSTTG 240
QY      148 ----NVDVFRTDVEFLSADTKTTTIVNVESSKDNKGKTEVKIGATSVIREKDKLTGKD 204
Db      241 QSENVDFTVTDVEFLSADTKTTTIVNVESSKDNKGKTEVKIGATSVIREKDKLTGKG 300
QY      205 KGENSSSTDEGEGLVTAKEVIDAVNKGMRMKTTPANGOTGQADKEFTVSGTNTVPASG 264
Db      301 KGENSSSTDEGEGLVTAKEVIDAVNKGMRMKTTPANGOTGQADKEFTVSGTNTVPASG 360
QY      265 KGTATFVSKDDGONTTVMYDVNVDALNNOLNONGMNLDSKAVAGSSGKVTISGNVSPSK 324
Db      361 KGTATFVSKDDGONTTVMYDVNVDALNNOLNONGMNLDSKAVAGSSGKVTISGNVSPSK 420
QY      325 GKMDEVNINAGNIEITRNKNIDTATSMTPOFSSVSLGAGADAPTLSDG- DALNVSS 383
Db      421 GKMDEVNINAGNIEITRNKNIDTATSMTPOFSSVSLGAGADAPTLSDG- DALNVSS 480
QY      384 KKDKNFVRTTNVAPGVKEGDTNVAQLKGVACNLNRIDNVDSNABAGIAQAATAGLVO 443
Db      481 KKANRKRVTITNVAPGVKEGDTNVAQLKGVACNLNRIDNVDSNABAGIAQAATAGLVO 540
QY      444 AYLPGKSMALIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
Db      541 AYLPGKSMALIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 11
Q9JPS2 PRELIMINARY; PRT; 594 AA.
ID 09JPS2 AC 09JPS2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Arico' B.,
RA Pizzo M., Scariato V., Maignani V., Giuliani M.M., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Rattl G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tetteijn H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada.1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 93.0%; Score 2367; DB 2; Length 594;
Best Local Similarity 82.2%; Pred. No. 2, 9e-96;
Matches 488; Conservative 1; Mismatches 13; Indels 92; Gaps 5;
QY 1 MNKIYIINNSALNANVAVVSELTRNHTKRASATVATLTLFATVOASAN----- 52
Db 1 MNKIYIINNSALNANVAVVSELTRNHTKRASATVATLTLFATVOASTDDDDLYLE 60
QY 53 -----TLKAGDNLKIKO----- 64
Db 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNMGVYFDKKGVLTAAGTITLKAGDNLKIKONTDE 120
QY 65 -----FTYSLKDLTDLTDSVGTETKLSFSANGKNKVNITSDPKLNAFAKETAGTNGDTT 118

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Db      121 MNASSFTYSLKDLTDLTDSVGTETKLSFGANGKRVNITSDPKLNAFAKETAGTNGDTT 180
QY      119 LNCIGSTLTD-----RAASVKDVLNAGMNIKGVK-----NY 149
Db      181 LNCIGSTLTDLTNLTGATTNVTNDVNTDDEKKAASVVKDVLNAGMNIKGVKPEPTTASDNV 240
QY      150 DFRVTDVTEFLSADTKTTTIVNVESSKDNKGKTEVKIGATSVIREKDKLTVGKDGENG 209
Db      241 DFRVTDVTEFLSADTKTTTIVNVESSKDNKGKTEVKIGATSVIREKDKLTVGKDGENG 300
QY      210 SSTDEGEGLVTAKEVIDAVNKGMRMKTTPANGOTGQADKEFTVSGTNTVPASGCTTA 269
Db      301 SSTDEGEGLVTAKEVIDAVNKGMRMKTTPANGOTGQADKEFTVSGTNTVPASGCTTA 360
QY      270 TVSKDDGONTTVMYDVNVDALNNOLNONGMNLDSKAVAGSSGKVTISGNVSPSKRMD 329
Db      361 TVSKDDGONTTVMYDVNVDALNNOLNONGMNLDSKAVAGSSGKVTISGNVSPSKRMD 420
QY      330 TVNINAGNIEITRNKNIDTATSMTPOFSSVSLGAGADAPTLSDG- ALNVGSKDKM 388
Db      421 TVNINAGNIEITRNKNIDTATSMTPOFSSVSLGAGADAPTLSDG- ALNVGSKDKM 480
QY      389 PVRTNVAPGVKEGDTNVAQLKGVACNLNRIDNVDSNABAGIAQAATAGLVOAYLP 448
Db      481 PVRTNVAPGVKEGDTNVAQLKGVACNLNRIDNVDSNABAGIAQAATAGLVOAYLP 540
QY      449 KSMMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
Db      541 KSMMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 12
Q930Y4 PRELIMINARY; PRT; 594 AA.
ID 0930Y4 AC 0930Y4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Nha outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E6327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada.1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD448B04B3A8BA2 CRC64;

Query Match 93.0%; Score 2366; DB 2; Length 594;
Best Local Similarity 82.0%; Pred. No. 3, 2e-96;
Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;
QY 1 MNKIYIINNSALNANVAVVSELTRNHTKRASATVATLTLFATVOASAN----- 52
Db 1 MNKIYIINNSALNANVAVVSELTRNHTKRASATVATLTLFATVOASTDDDDLYLE 60
QY 53 -----TLKAGDNLKIKO----- 64
Db 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNMGVYFDKKGVLTAAGTITLKAGDNLKIKONTNE 120
QY 65 -----FTYSLKDLTDLTDSVGTETKLSFSANGKNKVNITSDPKLNAFAKETAGTNGDTT 118
Db 121 NTAASSFTYSLKDLTDLTDSVGTETKLSFSANGKNKVNITSDPKLNAFAKETAGTNGDTT 180
QY 119 LNCIGSTLTD-----RAASVKDVLNAGMNIKGVK-----NY 149

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|||||
Db 181 LINGSTLTDLTLTGATTNVTNDVTDDEKRAASVADVLNAGMNIKGKPGTTASDNV 240
Oy 150 DFTVYDTVEFLSADTKTTTNNVESKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGNG 209
Db 241 DFTVYDTVEFLSADTKTTTNNVESKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGNG 300
Oy 210 SSTDEGGLYTAKEVDIAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVFAAGKTTA 269
Db 301 SSTDKGGLYTAKEVDIAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVFAAGKTTA 360
Oy 270 TVSKDDGNTVMDVNVGDLNVLNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGMD 329
Db 361 TVSKDDGNTVMDVNVGDLNVLNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGMD 420
Oy 330 TVNINAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKDNK 388
Db 421 TVNINAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDNK 480
Oy 389 PVRTTNVAPGVKEGDVTVNAQLKGVAQLNLRIDNVGNARAGIAQAIAATAGLVQAVLP 448
Db 481 PVRTTNVAPGVKEGDVTVNAQLKGVAQLNLRIDNVGNARAGIAQAIAATAGLVQAVLP 540
Oy 449 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOM 502
Db 541 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOM 594
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## RESULT 13

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09JPI3 PRELIMINARY; PRT; 594 AA.
AC 09JPI3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and B2322;
RX PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -
DR EMBL; AF226369; AAF42518.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 92.9%; Score 2363; DB 2; Length 594;
Best Local Similarity 82.0%; Pred. No. 4.4e-96;
Matches 487; Conservative 1; Mismatches 14; Indels 92; Gaps 5;
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Oy 1 MNKYIRIIMNSALNAAVVSSELTNRNHRKRASATVKTAVLATLFAVQASAN----- 52
Db 1 MNKYIRIIMNSALNAAVVSSELTNRNHRKRASATVKTAVLATLFAVQASATTTDDDLYLE 60
Oy 53 -----TLKGDMLKTKO----- 64
Db 61 PVORTAPVLPFHADESGEKEVTEEDSNMVGYPDKKGVLTAGTITLAKGDNLIKONTDE 120
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Oy 65 -----FTYSKDKDLDTLSVTEKLSFSAANGKRVNTTSOTKGNFAKETAAGTNGDTTV 118
Db 121 NTNASSFTYSKDKDLDTLSVTEKLSFSAANGKRVNTTSOTKGNFAKETAAGTNGDTTV 180
Oy 119 LINGSTLTD-----RAASVADVLNAGMNIKGKPGTTASDNV 149
Db 181 LINGSTLTDLTLTGATTNVTNDVTDDEKRAASVADVLNAGMNIKGKPGTTASDNV 240
Oy 150 DFTVYDTVEFLSADTKTTTNNVESKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGNG 209
Db 241 DFTVYDTVEFLSADTKTTTNNVESKDNKGKTEYKIGAKTSVIEKDKGLVTGDKGNG 300
Oy 210 SSTDEGGLYTAKEVDIAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVFAAGKTTA 269
Db 301 SSTDEGGLYTAKEVDIAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVFAAGKTTA 360
Oy 270 TVSKDDGNTVMDVNVGDLNVLNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGMD 329
Db 361 TVSKDDGNTVMDVNVGDLNVLNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGMD 420
Oy 330 TVNINAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKDNK 388
Db 421 TVNINAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDNK 480
Oy 389 PVRTTNVAPGVKEGDVTVNAQLKGVAQLNLRIDNVGNARAGIAQAIAATAGLVQAVLP 448
Db 481 PVRTTNVAPGVKEGDVTVNAQLKGVAQLNLRIDNVGNARAGIAQAIAATAGLVQAVLP 540
Oy 449 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOM 502
Db 541 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOM 594
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## RESULT 14

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09JPS9 PRELIMINARY; PRT; 592 AA.
AC 09JPS9;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;
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```
Query Match 92.8%; Score 2361; DB 2; Length 592;
Best Local Similarity 82.3%; Pred. No. 5.3e-96;
Matches 487; Conservative 2; Mismatches 13; Indels 90; Gaps 5;

Oy 1 MNKYIRIIMNSALNAAVVSSELTNRNHRKRASATVKTAVLATLFAVQASAN----- 52
Db 1 MNKYIRIIMNSALNAAVVSSELTNRNHRKRASATVKTAVLATLFAVQANATDDEDEEL 60
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QY 53 -----TLKAGDNLKIKQ----- 64  
 Db 61 ESWQSVVSGIQASMEGSELETISLMTNDSKEFVDPYIVTLAKADGNLKIKQNTMENT 120  
 QY 65 -----FTYSLKDKLDLTSVTEKLSFSANGKRVNITSOTKLNPAKETAGTNGTPTVHLN 120  
 Db 121 NASSFTYSLKDKLDLTSVTEKLSFGANGKRVNITSOTKLNPAKETAGTNGTPTVHLN 180  
 QY 121 GIGSTLTD-----RAASKVDVLANAGNIRKGV-----NVDF 151  
 Db 181 GIGSTLTDMLNTGATTNNTNDNTDDEKRRASAVKDVLANAGNIRKGVKPETTASDNVDF 240  
 QY 152 VRTYDVEFLSADTKTTTVNVEKSKDKTEVIGAKTSVTEKEDKLVTEKDKGENSS 211  
 Db 241 VRTYDVEFLSADTKTTTVNVEKSKDKTEVIGAKTSVTEKEDKLVTEKDKGENSS 300  
 QY 212 TDBEGGLVTAKEVIDAVNKAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 271  
 Db 301 TDBEGGLVTAKEVIDAVNKAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 360  
 QY 272 SKDDGNTVWYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIISGVNPSKGMDETV 331  
 Db 361 SKDDGNTVWYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIISGVNPSKGMDETV 420  
 QY 332 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 390  
 Db 421 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 480  
 QY 391 RITNVAQVKEGDDVTNVAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 450  
 Db 481 RITNVAQVKEGDDVTNVAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 540  
 QY 451 MMAIGGTYRGEAGTAIGYSSISDGNWIIKGTASGNSRGEFASASVGYOW 502  
 Db 541 MMAIGGTYRGEAGTAIGYSSISDGNWIIKGTASGNSRGEFASASVGYOW 592

RESULT 15

Q9JPH7 PRELIMINARY; PRT; 594 AA.  
 AC Q9JPH7;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
 DE Outer membrane protein GNA992 (Nha outer membrane protein).  
 GN GNA992 OR NHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_Taxid:487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B2198; and 297-0;  
 RC MEDLINE-20175756; PubMed-10710308;  
 RA Piza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B2198;  
 RA Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of Neisseria meningitidis.";  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF226358; AAF42507.1; -;  
 DR EMBL; AF226358; AAF42507.1; -;

DR EMBL; AF157604; AAK6865.1; -;  
 DR InterPro; IPR005594; Yada.  
 DR Pfam; PF03895; Yada; 1.  
 SO SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;  
 Query Match 92.7%; Score 2359; DB 2; Length 594;  
 Best Local Similarity 82.0%; Pred. No. 6,5e-96;  
 Matches 487; Conservative 2; Mismatches 13; Indels 92; Gaps 5;

QY 1 MNKIRIINNALNAAVYSELTRNRHTRKASATYKTAVALTLLEFATYQASNN----- 52  
 Db 1 MNKIRIINNALNAAVYSELTRNRHTRKASATYKTAVALTLLEFATYQASNN----- 60  
 QY 53 -----TLKAGDNLKIKQ----- 64  
 Db 61 PVORTAVVLSFRSDEKTEGEGEDSWMNAVYFDEKRVLRKAGATTLKAGDNLKIKQNTNE 120  
 QY 65 -----FTYSLKDKLDLTSVTEKLSFSANGKRVNITSOTKLNPAKETAGTNGTPTVH 118  
 Db 121 NTNDSFTYSLKDKLDLTSVTEKLSFGANGKRVNITSOTKLNPAKETAGTNGDPTVH 180  
 QY 119 LNGIGSTLTD-----RAASKVDVLANAGNIRKGV-----NV 149  
 Db 181 LNGIGSTLTDLTLTGATTNNTNDNTDDEKRRASAVKDVLANAGNIRKGVKPETTASDNV 240  
 QY 150 DVEFTYDVEFLSADTKTTTVNVEKSKDKTEVIGAKTSVTEKEDKLVTEKDKGENG 209  
 Db 241 DVEFTYDVEFLSADTKTTTVNVEKSKDKTEVIGAKTSVTEKEDKLVTEKDKGENG 300  
 QY 210 SSTDGEGLVTAKEVIDAVNKAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 269  
 Db 301 SSTDGEGLVTAKEVIDAVNKAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 360  
 QY 270 TVSKDDGNTVWYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIISGVNPSKGMDETV 329  
 Db 361 TVSKDDGNTVWYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIISGVNPSKGMDETV 420  
 QY 330 TVNINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 388  
 Db 421 TVNINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 480  
 QY 389 PVRTNVAQVKEGDDVTNVAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 448  
 Db 481 PVRTNVAQVKEGDDVTNVAQKRVNITANGOTGADKFEYVTSCTNVTFASSGKTATV 540  
 QY 449 KSMMAIGGTYRGEAGTAIGYSSISDGNWIIKGTASGNSRGEFASASVGYOW 502  
 Db 541 KSMMAIGGTYRGEAGTAIGYSSISDGNWIIKGTASGNSRGEFASASVGYOW 594

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 Job time : 39.8701 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 : Search time 46.3729 Seconds  
(without alignments)  
1848.329 Million cell updates/sec

Title: US-09-771-382-33  
Perfect score: 2757  
Sequence: 1 NNEEOEELYLHPVORTVAV.....TASGNSRGHGASASVGYQM 540

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
A.Geneseq\_19Jun03:\*  
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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2727	98.9	591	AA27202	Amino acid sequenc
2	2727	98.9	591	AA27376	A surface protein
3	2727	98.9	591	AA006171	N. meningitidis PM
4	2720	98.7	591	AA23741	A surface protein
5	2720	98.7	591	AA006175	N. meningitidis Eg
6	2705	98.1	591	AA57045	BA58029 amino acid
7	2695.5	97.8	592	AA23737	A surface protein
8	2512	91.1	594	AA23740	A surface protein
9	2512	91.1	594	AA57044	BA58029 amino acid

10	2512	91.1	594	AA006174	N. meningitidis Eg
11	2493	90.4	594	AA23739	A surface protein
12	2493	90.4	594	AA006179	N. meningitidis B2
13	2478	89.9	598	AA23738	A surface protein
14	2478	89.9	598	AA23742	A surface protein
15	2478	89.9	598	AA006177	N. meningitidis H1
16	2478	89.9	598	AA006178	N. meningitidis B2
17	2430.5	88.2	599	AA23743	A surface protein
18	2430.5	88.2	599	AA006176	N. meningitidis H3
19	2328	84.4	592	AA006182	N. meningitidis PM
20	2321	84.2	592	AA23744	A surface protein
21	2321	84.2	592	AA006172	N. meningitidis H4
22	2241.5	81.3	589	AA23745	A surface protein
23	2241.5	81.3	589	AA006173	N. meningitidis P2
24	2236.5	81.1	502	AA006186	N. meningitidis PM
25	2212	80.2	592	AA006180	N. meningitidis H4
26	2206	80.0	513	AA006183	N. meningitidis H4
27	2196	79.7	592	AA27203	Amino acid sequenc
28	2025.5	73.5	604	AA006181	N. meningitidis su
29	1941	70.4	433	AA006185	N. meningitidis PM
30	1822	66.1	407	AA006184	N. meningitidis PM
31	1153	41.8	245	AA27201	Amino acid sequenc
32	1033.5	37.5	241	AA23860	Haemophilus influe
33	1031.5	37.4	2353	AA23857	Haemophilus influe
34	927	33.6	1094	AA23858	Haemophilus influe
35	908	32.9	1098	AA23859	Haemophilus influe
36	809.5	29.4	679	AA23859	Haemophilus influe
37	809.5	29.4	679	AA23855	Haemophilus influe
38	600	21.8	116	AA23852	Haemophilus influe
39	598.5	21.7	1004	AA23857	Haemophilus influe
40	593.5	21.5	1104	AA23856	Haemophilus influe
41	593.5	21.5	1104	AA23859	Haemophilus influe
42	588	21.3	1002	AA23854	Haemophilus influe
43	451	16.4	298	AA23847	Haemophilus influe
44	383.5	13.9	2139	AA271294	M. catarrhalis sur
45	383	13.9	2314	AA269136	M. catarrhalis les

## ALIGNMENTS

RESULT 1	AA27202	standard; Protein: 591 AA.
ID	AA27202	
XX	AA27202:	
AC	24-SEP-1999	(first entry)
XX		
DT		
XX		
DE		Amino acid sequence of N. meningitidis protein ORF40-1.
XX		
KW		Neisseria meningitidis protein; pharmaceutical: vaccine; diagnosis;
KW		bacterial infection; treatment.
XX		
OS		Neisseria meningitidis.
PN	W09936544-A2.	
PD	22-JUL-1999.	
XX		
XX	14-JAN-1999;	99WO-IB00103.
PF		
XX		
PR	09-OCT-1998;	98GB-00022143.
PR	14-JAN-1998;	98GB-00000760.
PR	01-SEP-1998;	98GB-0019015.
XX		
PI	(CHIR-) CHIRON SPA.	
XX		
DR	Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;	
DR	WPI, 1999-444400/37.	
XX	N-PSDB; AA299124.	

PF New protein and its nucleotide sequence, useful in vaccines or  
PF diagnostic compositions for treating and/or preventing *Neisseria*  
PF meningitidis infections  
PS  
XX Claim 1; Page 62; 123pp; English.

XX The invention provides proteins (AAV27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AAV99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
CC  
XX

Sequence 591 AA:

Query Match 98.9%; Score 2727; DB 20; Length 591;  
Best Local Similarity 99.3%; Pred. No. 1.6e-157;  
Matches 536; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNEOEELYLHPVORTVAVLVNSDKGAGKEKEVEENSDMAVFNKGVLTAREITLK 60  
DB 52 NNEOEELYLDPVORTVAVLVNSDKGAGKEKEVEENSDMAVFNKGVLTAREITLK 111  
QY 61 AGDNKIKONGNFTYSLKKDLTDLTSVTEKLSFSAHGNKNYITSDPKGLNFAKETAGT 120  
DB 112 AGDNKIKONGNFTYSLKKDLTDLTSVTEKLSFSAHGNKNYITSDPKGLNFAKETAGT 171  
QY 121 NGDTTVHLNGIGSTLTDLTLNLTGATTNTNDVTDDEKKRAASVADVNLNAGNINIKVPRG 180  
DB 172 NGDTTVHLNGIGSTLTDLTLNLTGATTNTNDVTDDEKKRAASVADVNLNAGNINIKVPRG 231  
QY 181 TTASDNVDFVRTYDVEFLSADFTKTTVNVEESKDNKGKTEVIGAKTSVIREKDKLVTG 240  
DB 232 TTASDNVDFVRTYDVEFLSADFTKTTVNVEESKDNKGKTEVIGAKTSVIREKDKLVTG 291  
QY 241 KDKGENGSTDBEGELVTAKEVIDAVNKAQMKKTITANGOTGQADKRETVSGTNVFA 300  
DB 292 KDKGENSGSTDBEGELVTAKEVIDAVNKAQMKKTITANGOTGQADKRETVSGTNVFA 351  
QY 301 SGKGTATVSKDDQGNITVMYDVNGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSP 360  
DB 352 SGKGTATVSKDDQGNITVMYDVNGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSP 411  
QY 361 SKGKDETVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVG 420  
DB 412 SKGKDETVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVG 471  
QY 421 SKKDKKPVRTITNVAAGVEEGDVTNVAOLKGVANLNRRIDNDVGNARAGIAQAITAGLV 480  
DB 472 SKKDKKPVRTITNVAAGVEEGDVTNVAOLKGVANLNRRIDNDVGNARAGIAQAITAGLV 531  
QY 481 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGWMIITKGTASGNSRGHFGASASVGYOW 540  
DB 532 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGWMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 2  
AAV23746  
ID AAV23746 standard; Protein; 591 AA.

AC AAV23746;

DT 08-SEP-1999 (first entry)

DE A surface protein of *Neisseria meningitidis*.

KM Surface protein; surface glycoprotein; infection; vaccine;  
KM immunoreactive peptide.

OS *Neisseria meningitidis*.

PN W09931132-A1.

XX 24-JUN-1999.  
PD  
XX 14-DEC-1998; 98WO-AU01031.  
PF

XX 12-DEC-1997; 97GB-0026398.  
PR

XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX

PI Jennings MP, Moxon ER, Peak IRA;  
XX WPI: 1999-418754/35.  
DR

DR N-PSDB; AAV85798.  
DR

PT *Neisseria meningitidis* surface proteins useful for treating *N.*  
PT meningitidis infections  
PS Claim 1; Page 127-128; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX

Sequence 591 AA:

Query Match 98.9%; Score 2727; DB 20; Length 591;  
Best Local Similarity 99.3%; Pred. No. 1.6e-157;  
Matches 536; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNEOEELYLHPVORTVAVLVNSDKGAGKEKEVEENSDMAVFNKGVLTAREITLK 60  
DB 52 NNEOEELYLDPVORTVAVLVNSDKGAGKEKEVEENSDMAVFNKGVLTAREITLK 111  
QY 61 AGDNKIKONGNFTYSLKKDLTDLTSVTEKLSFSAHGNKNYITSDPKGLNFAKETAGT 120  
DB 112 AGDNKIKONGNFTYSLKKDLTDLTSVTEKLSFSAHGNKNYITSDPKGLNFAKETAGT 171  
QY 121 NGDTTVHLNGIGSTLTDLTLNLTGATTNTNDVTDDEKKRAASVADVNLNAGNINIKVPRG 180  
DB 172 NGDTTVHLNGIGSTLTDLTLNLTGATTNTNDVTDDEKKRAASVADVNLNAGNINIKVPRG 231  
QY 181 TTASDNVDFVRTYDVEFLSADFTKTTVNVEESKDNKGKTEVIGAKTSVIREKDKLVTG 240  
DB 232 TTASDNVDFVRTYDVEFLSADFTKTTVNVEESKDNKGKTEVIGAKTSVIREKDKLVTG 291  
QY 241 KDKGENGSTDBEGELVTAKEVIDAVNKAQMKKTITANGOTGQADKRETVSGTNVFA 300  
DB 292 KDKGENSGSTDBEGELVTAKEVIDAVNKAQMKKTITANGOTGQADKRETVSGTNVFA 351  
QY 301 SGKGTATVSKDDQGNITVMYDVNGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSP 360  
DB 352 SGKGTATVSKDDQGNITVMYDVNGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSP 411  
QY 361 SKGKDETVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVG 420  
DB 412 SKGKDETVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVG 471  
QY 421 SKKDKKPVRTITNVAAGVEEGDVTNVAOLKGVANLNRRIDNDVGNARAGIAQAITAGLV 480  
DB 472 SKKDKKPVRTITNVAAGVEEGDVTNVAOLKGVANLNRRIDNDVGNARAGIAQAITAGLV 531  
QY 481 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGWMIITKGTASGNSRGHFGASASVGYOW 540  
DB 532 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGWMIITKGTASGNSRGHFGASASVGYOW 591

	RESULT 3
ID	AA006171
XX	AA006171 standard; Protein: 591 AA.
XX	
AC	AA006171;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX	
OS	Neisseria meningitidis strain PMC21.
XX	
FH	Location/Qualifiers
FT	1..51
FT	/label= Signal_peptide
FT	1..50
FT	/label= C1
FT	/note= "Conserved region 1"
FT	51..108
FT	/label= V1
FT	/note= "Variable region 1"
FT	52..591
FT	/label= Mature_Nhha
FT	/note= "predicted mature protein, specifically claimed in claim 12"
FT	109..120
FT	/label= C2
FT	/note= "Conserved region 2"
FT	121..124
FT	/label= V2
FT	/note= "Variable region 2"
FT	125..188
FT	/label= C3
FT	/note= "Conserved region 3"
FT	189..210
FT	/label= V3
FT	/note= "Variable region 3"
FT	211..229
FT	/label= C4
FT	/note= "Conserved region 4"
FT	230..236
FT	/label= V4
FT	/note= "Variable region 4"
FT	237..591
FT	/label= C5
FT	/note= "Conserved region 5"
XX	
PN	WO20015182-A1.
XX	
PD	02-AUG-2001.
XX	
PE	25-JAN-2001; 2001WO-AU000069.
XX	
PR	25-JAN-2000; 2000US-0177917.
XX	
PA	(UYQU ) UNIV QUEENSLAND.
XX	
PI	Peak IRA, Jennings MP;
XX	
DR	WPI; 2001-488774/53.
XX	
DR	N-PSDB; AAS09161.
XX	
PT	New Nhha surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis .
XX	
PS	Claim 9; Fig 1; 91pp: English.
CC	The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AA006182-AA006186). The modified or mutant Nhha polypeptides are

Query Match	Best Local Similarity	98.9%;	Score 2727;	DB 22;	Length 591;				
Matches	536;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1	NNEDEEYLYLHPVORTVAVLIVNSDKGAGEKEVEENSDMAVYFNEKGYLTAREITLK	60						
Db	52	NNEDEEDLYLDPOQRTVAVLIVNSDKGEGTEKEVEENSDMAVYFNEKGYLTAREITLK	111						
QY	61	AGDNKIKIONGTNPFYSLSKKDLTDLTSTGTEKLSASGKNVNIISDPRKGLFAKETAGT	120						
Db	112	AGDNKIKIONGTNPFYSLSKKDLTDLTSTGTEKLSASGKNVNIISDPRKGLFAKETAGT	171						
QY	121	NGDPTVHLNGIGSTLTDTLTLMTGATTNTNDNVTDDEKRRASVAKDVLNAGNNIGVAPG	180						
Db	172	NGDPTVHLNGIGSTLTDTLTLMTGATTNTNDNVTDDEKRRASVAKDVLNAGNNIGVAPG	231						
QY	181	TTASDNDVFPRTYDTVERFLSADFTKTTVNVESKDKGKTEYKIGAKTSVIEKDKGLVTG	240						
Db	232	TTASDNDVFPRTYDTVERFLSADFTKTTVNVESKDKGKTEYKIGAKTSVIEKDKGLVTG	291						
QY	241	KDKGNGSSSTGEGEGLTAKEYLDAVKNAGAMKTTTANGCGQADKEETVSGTNVFA	300						
Db	292	KDKGNGSSSTGEGEGLTAKEYLDAVKNAGAMKTTTANGCGQADKEETVSGTNVFA	351						
QY	301	SGKGTATVSKDDQGNITVMYDVANVGDALNVNQLONGMNLDSKAVAGSSGKIVISGNVSP	360						
Db	352	SGKGTATVSKDDQGNITVMYDVANVGDALNVNQLONGMNLDSKAVAGSSGKIVISGNVSP	411						
QY	361	SKGKDETVININAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGALNVG	420						
Db	412	SKGKDETVININAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGALNVG	471						
QY	421	SKKDKKPVRTINVAVGVEKEDVTNAOIKGVANQNLNNPILDNVDGARRAGIAQAITAGLV	480						
Db	472	SKKDKKPVRTINVAVGVEKEDVTNAOIKGVANQNLNNPILDNVDGARRAGIAQAITAGLV	531						
QY	481	QAYLPGKSMMAIGGTYRGEAGYAIGYSSISDGCNMIIKGTASGNSRGHFGASASVGQW	540						
Db	532	QAYLPGKSMMAIGGTYRGEAGYAIGYSSISDGCNMIIKGTASGNSRGHFGASASVGQW	591						
RESULT 4									
AA23741									
ID AA23741 standard; Protein: 591 AA.									
XX AA23741;									
AC									
XX									
DT 08-SEP-1999 (first entry)									
XX									
DE A surface protein of Neisseria meningitidis.									
XX									
KM Surface protein; surface glycoprotein; infection; vaccine;									
XX									
OS Immunoreactive peptide.									
XX									
OS Neisseria meningitidis.									
XX									
PN WO9931132-A1.									
XX									
PD 24-JUN-1999.									

XX 14-DEC-1998; 98WO-AU01031.  
 PF  
 XX 12-DEC-1997; 97GB-0026398.  
 PR  
 XX (ISIS-) ISIS INNOVATION LTD.  
 PA (UYOU ) UNIV QUEENSLAND.  
 RA  
 XX Jennings MP, Moxon ER, Peak IRA;  
 PI  
 XX MPI: 1999-418754/35.  
 DR  
 DR N-PSDB: AAX85793.  
 FT  
 FT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 PS  
 PS Claim 1, Page 104-106; 132pp; English.  
 CC  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 XX  
 XX Sequence 591 AA;

Query Match 98.7%; Score 2720; DB 20; Length 591;  
 Best Local Similarity 99.1%; Pred. No. 4.3e-157;  
 Matches 535; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 NNEOEELLYHPORFVAVLVINSDEKAGEKEKEVENSOMAYVENEKGLTAREITLK 60  
 DB 52 NNEOEELLYDPLKRYAVLVINSDEKGEKEKEVENSOMAYVENEKGLTAREITLK 111  
 QY 61 AGDLKIKQNGTNTFTYSLKLDLTLTSVTEKLSFAHKNVNTSPTKGLNFAKETAGT 120  
 DB 112 AGDLKIKQNGTNTFTYSLKLDLTLTSVTEKLSFAHKNVNTSPTKGLNFAKETAGT 171  
 QY 121 NGDTTTHLNGIGSTLTDTLMTGATNTNTNDVDEKRAAYKDYVLMAGNLIKGVKPG 180  
 DB 172 NGDTTTHLNGIGSTLTDTLMTGATNTNTNDVDEKRAAYKDYVLMAGNLIKGVKPG 231  
 QY 181 TTASDNVDFRTYDTEFLSADTKTFTYVNESKDKGKTEKIGAKTSVIREKDKLVTG 240  
 DB 232 TTASDNVDFRTYDTEFLSADTKTFTYVNESKDKGKTEKIGAKTSVIREKDKLVTG 291  
 QY 241 KDKGENGSTDEGEGGLVTAKEVIDAVNKAQRMTTTANGOTGADKEFTVTSCTNTPFA 300  
 DB 292 KDKGENGSTDEGEGGLVTAKEVIDAVNKAQRMTTTANGOTGADKEFTVTSCTNTPFA 351  
 QY 301 SKGTATATVSKDDGNTVTMDVNVGALNNOLNSGMNLDKRAVAGSSGKVISGNVSP 360  
 DB 352 SKGTATATVSKDDGNTVTMDVNVGALNNOLNSGMNLDKRAVAGSSGKVISGNVSP 411  
 QY 361 SKGMDEVTNINAGNIEITRNKNRIDATSMTPQFSSVSLGAGADATLTVSDGALNVG 420  
 DB 412 SKGMDEVTNINAGNIEITRNKNRIDATSMTPQFSSVSLGAGADATLTVSDGALNVG 471  
 QY 421 SKDNKPVRTINNVAPGVKEGDTNVVAOLKGYAONLNRRIDNVGNAARAGIAQALATATLV 480  
 DB 472 SKDNKPVRTINNVAPGVKEGDTNVVAOLKGYAONLNRRIDNVGNAARAGIAQALATATLV 531  
 QY 481 QAYLPGRSMAIIGGCTYRGEAGIAGYSSISDGNWIIKGTASGNSRGHFGASASVGIOW 540  
 DB 532 QAYLPGRSMAIIGGCTYRGEAGIAGYSSISDGNWIIKGTASGNSRGHFGASASVGIOW 591

RESULT 5  
 AAU06175

ID AU06175 standard; Protein; 591 AA.  
 AC AAU06175;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DE N. meningitidis EG329 surface antigen Nhha polypeptide sequence.  
 XX  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 KW  
 XX  
 OS Neisseria meningitidis strain EG329.  
 XX  
 XX Key  
 FH Location/Qualifiers  
 FT 1..50  
 FT /label= C1  
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 PN WO200155182-A1.  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 XX MPI: 2001-488774/53.  
 DR N-PSDB: AAS09165.  
 PT  
 PT New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 PS  
 PS Claim 9; Fig 1; 91pp; English.  
 XX  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha